Industria y Comercio

SUPERINTENDENCIA

Delegatura de Propiedad Industrial
División de Nuevas Creaciones

SOLICITUD

PATENTE DE INVENCIÓN

21. **EXPEDIENTE No.** 10-48790

54. **TÍTULO** PROTEINAS DE UNION A ANTIGENO DE FACTOR DE CRECIMIENTO TIPO FACTOR DE CRECIMIENTO EPIDERMICO DE UNION A HEPARINA

51. **CLASIFICACIÓN INTERNACIONAL**

71. **SOLICITANTE** U3 PHARMA GMBH AG Y AMGEN INC.

DOMICILIO MARTINSRIED, ALEMANIA Y THOUSAND OAKS, CALIFORNIA, U.S.A.

74. **APODERADO** LUZ CLEMENCIA DE PAEZ
C.C. 35.456.344 de Usaquén

22. **BOGOTÁ, D.C.,** 26-04-2010

(FORMA P-10)

Industria y Comercio
SUPERINTENDENCIA

PETITORIO

SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO
No. 10-048790- -00000-0000
Fecha: 2010-04-26 16:26:55 Dep: 2020 DIR.NUEVASCR
Tra. 11 PATENTEIYII Eve: 378 FASENACIONALI
Act. 411 PRESENTACION Folios: 2752

FORMULARIO UNICO DE SOLICITUD DE PATENTE PCT ENTRADA EN FASE NACIONAL

1 SOLICITUD DE:

☒ Patente de Invención. ☐ Patente de Modelo de Utilidad.
☒ Capítulo I. ☐ Capítulo II.

2 SOLICITANTE (71)

Nombre: **U3 PHARMA GMBH Y AMGEN INC.**
Sociedades constituidas y existentes bajo las leyes de Alemania y del Estado de Delaware, Estados Unidos de América.

Dirección: Fraunhoferstr. 22,
82152 Martinsried,
Alemania

y

One Amgen Center Drive,
Thousand Oaks,
California 91320-1799,
Estados Unidos de América

Respectivamente

Domicilio: Martinsried,
Alemania

y

Thousand Oaks,
California 91320-1799,
Estados Unidos de América

Respectivamente

IDENTIFICACIÓN
C.C. ☐ NIT ☐
C.E. ☐ Otro ☐
Cual ____
Número ____

3 REPRESENTANTE O APODERADO

Nombre: LUZ CLEMENCIA DE PAEZ
Dirección: Carrera 4ª. No. 72-35
Teléfono: 347 36 11
Fax: 211 86 50
E-mail: clientes@cavelier.com
Domicilio: Bogotá, Colombia.

IDENTIFICACIÓN
C.C. ☒ NIT ☐
C.E. ☐ Otro ☐
Cual ____
Número 35.456.344 T.P 23.555

4 INVENTOR (ES) (72)

1. **Mike ROTHE**
Elisenstrasse 4,
82152 Krailing,
Dinamarca

2. **Norbert PRENZEL**
Pentenriedderstr. 32,
82152 Krailing
Dinamarca

3. **Eric BORGES**
Roseggergasse 25,
A-2344 Maria Enzersdorf,
Austria

4. **Thore HETTMANN**
Am Stadtpark 38D,
81243 München,
Dinamarca

5. **Orit FOORD**
712 Cayman Lane,
Foster City,
California 94404,
Estados Unidos de América

(Folio 2757)

5 **PCT (86)**
Solicitud Internacional No. PCT/EP2008/008233 Fecha: 26 de septiembre de 2008
Publicación Internacional No. WO 2009/040134 A1 Fecha: 02 de abril de 2009

6 **Título (54)**
PROTEINAS DE UNION A ANTIGENO DE FACTOR DE CRECIMIENTO TIPO FACTOR DE CRECIMIENTO EPIDERMICO DE UNION A HEPARINA

7 **Clasificación Internacional (51)** C07K 016/022

8 **Prioridad** SI☒ NO☐

(33) País de Origen	(32) Fecha	(31) Número de Solicitud
EP	26 de septiembre de 2007	07018946.9
US	26 de septiembre de 2007	60/975,485

9
Comprobante de pago No.: 10-24,711 **Fecha:** 05 de abril de 2010
Comprobante de pago No.: 10-20,579 **Fecha:** 15 de marzo de 2010
Comprobante de pago No.: 10-20,607 **Fecha:** 15 de marzo de 2010
Comprobante de pago No.: 10-27,472 **Fecha:** 12 de abril de 2010

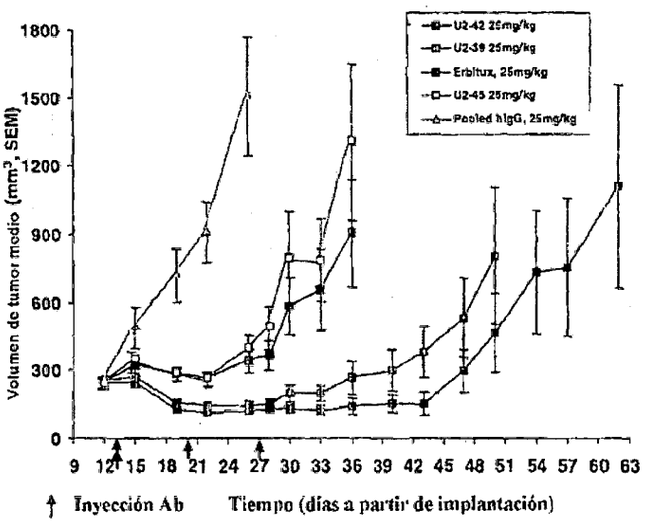
10 **Anexos:**

☒ Comprobante de pago de la tasa de presentación de la solicitud por $ 554.000.oo.
☒ Comprobante de pago por 64 reivindicaciones adicionales después de la décima reivindicación por $1.664.000.
☒ Documento que acredita la existencia y representación legal cuando el solicitante sea persona jurídica.
☒ Poderes de las sociedades **U3 PHARMA** y **AMGEN INC.**
☐ Documento de cesión del inventor al solicitante o a su causante.
☐ Declaraciones.
☒ Copia de la solicitud internacional. (Resumen, descripción, reivindicaciones, dibujos)
☒ Traducción de la solicitud internacional al castellano. (Resumen, descripción, reivindicaciones, dibujos)
☐ Copia del examen preliminar efectuado por la IPEA.
☐ Traducción del examen preliminar efectuado por la IPEA.
☐ De ser el caso, copia del contrato de acceso.
☐ De ser el caso, documento que acredite la licencia o autorización de uso de conocimientos tradicionales de las comunidades indígenas.
☐ De ser el caso, certificado de depósito del material biológico.
☒ Arte final 12x12
☐ De ser el caso, información sobre otras solicitudes de patente o títulos obtenidos en el extranjero por el mismo titular o su causante, relacionadas parcial o totalmente con la invención de esta solicitud.
☒ Otros: VER HOJA DE DOCUMENTOS ANEXOS

11

FIGURA CARACTERÍSTICA

FIGURA 38A



3x10⁶ sc, matrigel, ratones SCID, n=9; Inicio de tratamiento(d13) @ ~ 250 mm³
Dosis Inicial (ip): 50 mg/kg; Dosis semanal (ip): 25 mg/kg,
Combinación de αHBEGF con Erbitux se dio a 12.5 mg/kg cada uno
Cisplatino administrado una vez por semana a 5 mg/kg

12 Solicito la concesión de la patente,

NOMBRE: LUZ CLEMENCIA DE PAEZ

FIRMA : Luz Clemencia de Paez

C.C. 35.456.344 de Usaquén T.P. 23.555

SCT

DOCUMENTOS ANEXOS

1. ☒ Publicación Internacional WO 2009/040134 A1

   Descripción:

   Páginas 118 en el idioma original

   Páginas 246 en español

   Reivindicaciones: Número (s) 74

   Figuras: Número (s) 43

2. ☒ **Forma PCT/ISA/210.** Informe de Búsqueda Internacional.

3. ☒ Listado de secuencias.

4. ☒ **Forma PCT/IB/306.** Notificación de la inscripción del cambio de dirección del solicitante **U3 PHARMA GMBH.**

5. ☒ **Forma PCT/IB/306.** Notificación de la inscripción donde se adiciona el inventor **ORIT FOORD.**

6. ☒ Extracto de publicación.

NO SE REALIZARON MODIFICACIONES EN LA FASE INTERNACIONAL

5

Notaría Sexta (6) DEL CIRCULO DE BOGOTA, D.C.

COPIA NUMERO 3

DE LA ESCRITURA NUMERO: 1098
FECHA: 01/Marzo/2010

ACTO O CONTRATO:
PODER GENERAL
OTORGANTES:
CAVELIER ABOGADOS
NIDIA OSORIO LOPEZ

ICONTEC
CERTIFICADO
DE GESTION
DE LA CALIDAD
CERTIFICADO SC 3980-1
PRESTACION DEL SERVICIO PUBLICO NOTARIAL
ISO 9001:2000
NTC-ISO 9001:2000

CERTIFIED IQNet MANAGEMENT SYSTEM

AMPARO QUINTERO ARTURO

NOTARIA SEXTA

CARRERA 9 No. 69-31 - PBX: 317 01 00 - FAX: 314 56 41
Correo Electrónico: notaria6debgta@etb.net.co

6.

ESCRITURA PUBLICA NUMERO - - -1098 - - - - - -

- - - - - -MIL NOVENTA Y OCHO - - - - - - -

DE FECHA: MARZO PRIMERO (1) - - - - - - - - -

DEL AÑO DOS MIL DIEZ (2.010) - - - - - - - - -

OTORGADA EN LA NOTARIA SEXTA (6a) DEL CIRCULO DE BOGOTA D.C. ----------

CLASE DE ACTO O CONTRATO: **PODER ESPECIAL** ----------

DE: **CAVELIER ABOGADOS** ----------

A : **LUZ CLEMENCIA DE PÁEZ, NIDIA OSORIO LÓPEZ, OSCAR FERNANDO CORREA BARBOSA, EDNA DARMELY SARMIENTO CHARRY y JORGE CHAVARRO ARIZTIZABAL** ----------

En la ciudad de Bogotá D.C. República de Colombia, ante mí, AMPARO QUINTERO ARTURO ——— Notaria sexta (6a.) ——— de éste círculo notarial, se otorgó la presente escritura pública que se consigna en los siguientes términos: ----------

COMPARECENCIA: Con minuta escrita, compareció el señor **CARLOS ALBERTO GALLÓN GIRALDO**, mayor de edad, vecino de esta ciudad, casado, identificado con la cédula de ciudadanía No. 19.066.425 de Bogotá, y dijo:----------

ESTIPULACIONES: ----------

PRIMERA.- Que obra en su calidad de representante legal de la sociedad denominada **CAVELIER ABOGADOS** domiciliada en la **Carrera 4 No. 72-35, Bogotá, Colombia.** ----------

SEGUNDA: Que **U3 PHARMA GMBH** ——————— ., sociedad constituida y existente bajo las leyes de Alemania, domiciliada en Fraunhoferstr 22 82152 Martinsried, Alemania, designó a **CAVELIER ABOGADOS** como su representante para la Propiedad Industrial en Colombia con facultades de nombrar apoderados tal como consta en la copia auténtica del documento de representación que se protocoliza. ----------

TERCERA.- Que en su carácter de representante legal de **CAVELIER ABOGADOS**, y en desarrollo de la facultad otorgada por **U3 PHARMA GMBH** ——————— , confiere poder a los abogados **LUZ CLEMENCIA DE PAEZ**, T.P.A. No. 23.555, identificada con cédula de ciudadanía número 35.456.344 de Usaquen, **NIDIA OSORIO LOPEZ**, T.P.A. No.73.366, identificada con cédula de ciudadanía número 39.787.682 de Bogotá, **OSCAR FERNANDO CORREA**

NOTARIA SEXTA DE BOGOTÁ

PAPEL DE USO EXCLUSIVO DEL PROTOCOLO NOTARIAL . NO TIENE COSTO PARA EL USUARIO

IMPRESO EN DICIEMBRE 1° DE 2009 POR POLYPRINT EDITORIAL LTDA. - NIT 830.029.959-5

BARBOSA, T.P.A. No. 71.027 identificado con cédula de ciudadanía número 79.524.634 de Bogotá, **EDNA DARMELY SARMIENTO CHARRY**, T.P.A. 65.794 identificada con cédula de ciudadanía número 52.006.265 de Bogotá y **JORGE CHAVARRO ARIZTIZABAL**, T.P.A. No. 40.119, identificado con cédula de ciudadanía número 16.209.380 de Cartago (Valle), mayores de edad, vecinos de Bogotá, para que representen a la sociedad a cuyo nombre actúa, ante cualesquiera entidades o personas, ejerzan o no jurisdicción, incluyendo las del orden administrativo, contencioso administrativo y judicial, así como los tribunales de arbitramento, en todo lo concerniente a los siguientes asuntos: ----------

a) Obtención de patentes de invención, modelos de utilidad, diseños industriales, trazado de circuitos integrados, secretos industriales; el registro de marcas de fábrica, colectivas, defensivas, de servicio, lemas comerciales, nombres comerciales, enseñas, variedades vegetales, denominaciones de origen e indicaciones de procedencia, su renovación, traspaso, cambio de nombre o domicilio, cancelación voluntaria; y el registro de licencias de uso de esos derechos ----------

b) Las acciones de competencia desleal, protección del consumidor, oposiciones, cancelación administrativa o judicial, nulidad, medidas cautelares, concesión de licencias, la tutela, la protección de secretos industriales y de nombres de dominio junto con su administración y pago; y en general los procesos civiles, penales, administrativos o contencioso- administrativos, de conciliación, arbitramento, tutela relacionados con estos derechos; acciones y procesos que promovamos o se nos promuevan. ----------

CUARTO.- Que los apoderados designados están facultados en todos los asuntos arriba determinados para sustituir este mandato, transigir, conciliar, arbitrar, admitir los hechos del proceso, desistir, cancelar, recibir, renunciar y ratificar los actos de agentes oficiosos. ----------

QUINTO- Que protocoliza con la presente escritura, un certificado expedido por la Cámara de Comercio de Bogotá, que acredita la constitución y personería de la sociedad **CAVELIER ABOGADOS,** igualmente protocoliza copia autenticada del documento de representación otorgado el día 22 de Diciembre de 2009 - - - por **U3 PHARMA GMBH** , ———————— documento que está debidamente

7

62

S3546

CAVELIER
ABOGADOS
EDIFICIO SISKI
CARRERA 4a N° 72-35
BOGOTA, 8 – COLOMBIA

REPRESENTACION

REPRESENTATION

Yo (nosotros), abajo firmado (s)/I (we), the undersigned

U3 PHARMA GMBH

domiciliado (s) en/of FRAUNHOFERSTR. 22 82152 MARTINSRIED

GERMANY

Por el presente nombramos a CAVELIER ABOGADOS, sociedad colectiva constituida de conformidad con las leyes de la República de Colombia, mediante Escritura Pública No. 6233 del 10 de septiembre de 1974, otorgada en la Notaría Sexta del Círculo de Bogotá, domiciliada en Bogotá D.C., con matrícula mercantil No. 00820237 y NIT 860041367-3, domiciliada en la Carrera 4a N° 72-35, Bogotá, Colombia, como nuestra representante en todos los asuntos de Propiedad Industrial, con facultad para recibir notificaciones y nombrar apoderados judiciales o extrajudiciales.

CAVELIER ABOGADOS también podrá representarnos, con las mismas facultades arriba indicadas, ante cualesquiera entidades o personas, ejerzan o no jurisdicción, autoridades administrativas o jurisdiccionales, tribunales de arbitramento, en asuntos de naturaleza civil, comercial, penal, constitucional, competencia, competencia desleal, administrativa, contencioso administrativa, protección del consumidor, variedades vegetales, nombres de dominio, oposiciones u observaciones, cancelación administrativa y judicial, nulidad, medidas cautelares, concesión de licencias, acciones de tutela, la protección de secretos industriales, derecho regulatorio y en general para que nos represente en cualesquiera acciones y procesos que promovamos o se nos promuevan.

La representante podrá, en nuestro nombre, designar apoderados para actuar ante autoridades administrativas y judiciales, por vía extrajudicial y también procesalmente en nuestro nombre, como demandantes, como demandados, como litisconsortes, como agentes oficiosos, como terceros, por llamamiento en garantía o como intervinientes ad excludendum. Dentro de esta autorización, la representante podrá facultar a los apoderados que ella designe para transigir, conciliar,

Do hereby appoint CAVELIER ABOGADOS, a general partnership organized under the laws of the Republic of Colombia by means of Public Deed No. 6233 of September 10, 1974, granted at Notary Sixth of the Bogota Circuit, domiciled in Bogota D.C., with Mercantile Registration No. 00820237 and Taxpayer Identification Number 860041367-3, domiciled at Carrera 4a N° 72-35, Bogota, Colombia, as our representative for all Industrial Property matters with faculty to receive notifications and appoint attorneys in and out of Court.

CAVELIER ABOGADOS may also represent us, with the same faculties stated above, before any entities or persons, with or without jurisdiction, administrative or jurisdictional authorities, courts of arbitration, in civil, commercial, criminal, constitutional, competition, unfair competition, administrative, administrative contentious, consumer protection, plant varieties, domain names, opposition or observation matters, administrative and Court cancellation, nullity, precautionary measures, licensing, action for writ mandamus, protection of trade secrets, regulatory law and in general represent us in any actions and suits instituted by us or against us.

The representative may, in our name, designate attorneys to act before administrative and judicial authorities, through out-of-court channels, and also procedurally in our name as plaintiff, defendant, joint litigant, representative without power of attorney, third party, when summoned to appear in court or as intervener ad excludendum. Under this authorization, the representative may empower the attorneys appointed thereby to compromise, conciliate, admit the facts of the

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COMO NOTARIA SEXTA DEL CIRCULO DE BOGOTA D.C. HAGO CONSTAR QUE LA FOTOCOPIA COINCIDE CON EL ORIGINAL QUE HE TENIDO A LA VISTA BOGOTA D.C. REPUBLICA DE COLOMBIA

- 1 MAR. 2010

ARTURO QUINTERO ARTURO
NOTARIA

NOTARIA SEXTA DE BOGOTA

admitir los hechos del proceso, desistir, cancelar, recibir, renunciar y sustituir el poder que se le otorgue. Así mismo, la representante tendrá la facultad para revocar el poder así otorgado en el momento que considere pertinente. La representante en todo caso podrá ratificar los actos de agentes oficiosos.

case, desist, cancel, receive, resign and substitute the power of attorney granted thereto. Likewise, the representative shall have the faculty of revoking the power of attorney thus granted at any time it may deem convenient. The representative may in any case ratify the acts of representatives without a power of attorney.

Dado y firmado hoy/Given and signed this 22.12.2009

En/in _____

Por/by _____

Firma/Signature _____

Nota:

PARA SOCIEDADES

El documento de Representación deberá ser firmado por el representante legal de la compañía. Deberá ser presentado ante Notario Público para que certifique que la persona que firma es quien dice ser. La firma del señor Notario deberá ser legalizada*.

Adicionalmente deberá anexarse copia legalizada* del documento que pruebe la existencia y representación legal de la sociedad.

*La legalización podrá ser por Apostilla si el país del otorgante hace parte de la Convención de La Haya del 5 de octubre de 1961 o ante el Cónsul de Colombia en caso contrario. Una sola legalización que incluya ambos documentos sería suficiente.

PARA PERSONAS NATURALES

El documento de Representación deberá ser firmado por el otorgante: El Notario Público deberá certificar que la persona que firma es quien dice ser.

Posteriormente el documento de Representación deberá ser legalizado por Apostilla si el país del otorgante hace parte de la Convención de La Haya del 5 de octubre de 1961 o ante el Cónsul de Colombia en caso contrario.

Note:

FOR CORPORATIONS

The Representation document should be signed by the Legal Representative of the company. It should be produced before a Notary Public, who should certify that the person signing the same is in fact who he/she purports to be. The Notary's signature should then be legalized*.

In addition a legalized copy* of the document proving the existence and legal representation of the company should also be attached.

*Legalization may be made by Apostille if the issuing country is a member of the The Hague Convention of October 5, 1961, or before the Colombian Consulate if otherwise. A single legalization that would include both documents would be sufficient.

FOR INDIVIDUALS

The Representation should be signed by the grantor. The Notary Public should certify that the person signing is who he/she purports to be.

Subsequently, the Representation document should be legalized by Apostille if the issuing country is a member of the The Hague Convention of October 5, 1961 or before the Colombian Consulate if otherwise.

COMO NOTARIA SEXTA DEL CIRCULO DE BOGOTA D.C., HAGO CONSTAR QUE LA FOTOCOPIA COINCIDE CON EL ORIGINAL QUE HE TENIDO A LA VISTA
BOGOTA D.C., REPUBLICA DE COLOMBIA
- 1 MAR. 2010
ARTURO QUINTERO ARTURO
NOTARIA

© CAVELIER ABOGADOS

8.

URNr. S 3546 /2009

I hereby certify that the above are the true signatures, subscribed in my presence, of

1. Mr. Dr. Johannes Albrecht Bange, of Fraunhoferstr. 22, 82152 Planegg OT Martinsried,
   born at 06.02.1969,
   personally known,
2. Mr. Dr. Koichi Akahane, of Fraunhoferstr. 22, 82152 Planegg OT Martinsried,
   born at 12.05.1955,
   personally known,

acting on behalf of "U3 Pharma GmbH" a private limited company having its principal place of business in Planegg OT Martinsried/Munich, Germany.

From inspection of the Commercial Register of the District Court of Munich on the 22nd of November 2009, I hereby certify that the said firm "U3 Pharma GmbH ", having is principal place of business in Planegg OT Martinsried/Munich, is entered in Section B of the said Register under No 177122, and Mr. Dr. Johannes Albrecht Bange as managing director and Mr. Dr. Koichi Akahane as managing director are jointly authorized to represent it.

Munich, 22nd of Dezember 2009

Schmitt, Notary

COMO NOTARIA SEXTA DEL CIRCULO DE BOGOTA D.C., HAGO CONSTAR QUE LA FOTOCOPIA COINCIDE CON EL ORIGINAL QUE HE TENIDO A LA VISTA
BOGOTA D.C. REPUBLICA DE COLOMBIA
- 1 MAR. 2010
AMPARO QUINTERO ARTURO
NOTARIA

NOTARIA SEXTA DE BOGOTA

APOSTILLE

(Convention de La Haye du 5 octobre 1961)

1. Land: Bundesrepublik Deutschland

   Diese öffentliche Urkunde

2. ist unterschrieben von Notar **Bernd Schmitt**

3. in seiner Eigenschaft als **Notar**

4. Sie ist versehen mit dem Siegel des **Notars Bernd Schmitt in München**

Bestätigt

5. in München
6. am 21. Januar 2010
7. durch den Präsidenten des Landgerichts München I
8. unter Nr. 910a-436/2010
9. Siegel
10. Unterschrift
    In Vertretung:

Thomas Spielbauer
Vizepräsident

COMO NOTARIA SEXTA DEL CIRCULO DE BOGOTA D.C., HAGO CONSTAR QUE LA FOTOCOPIA COINCIDE CON EL ORIGINAL QUE HE TENIDO A LA VISTA
BOGOTA D.C. REPUBLICA DE COLOMBIA
- 1 MAR. 2010
AMPARO QUINTERO ARTURO
NOTARIA

TRADUCCIÓN OFICIAL No. 02.24/10f realizada por Diego Vargas, Traductor Oficial, Resolución No. 0001 de 1999 del Ministerio de Justicia y registrado ante el Ministerio de Relaciones Exteriores de Colombia.

A continuación se traducen los sellos y legalizaciones de un documento mediante el cual **U3 PHARMA GMBH**, domiciliada en FRAUNHOFERSTR. 22 82152 MARTINSRIED, ALEMANIA, nombra a **CAVELIER ABOGADOS**, una sociedad colectiva debidamente constituida de conformidad con las leyes de la República de Colombia, con Matrícula Mercantil No. 00820237 y NIT 860041367-3, domiciliada en la Carrera 4 No. 72-35, de Bogotá, Colombia, como su representante en todos los asuntos de Propiedad Intelectual.

Dado y firmado el 22 de diciembre de 2009.

Firma *Firma Ilegible* *Firma Ilegible*

URNr. S3546/2009

Por el presente certifico que las anteriores son las firmas auténticas, suscritas en mí presencia, de

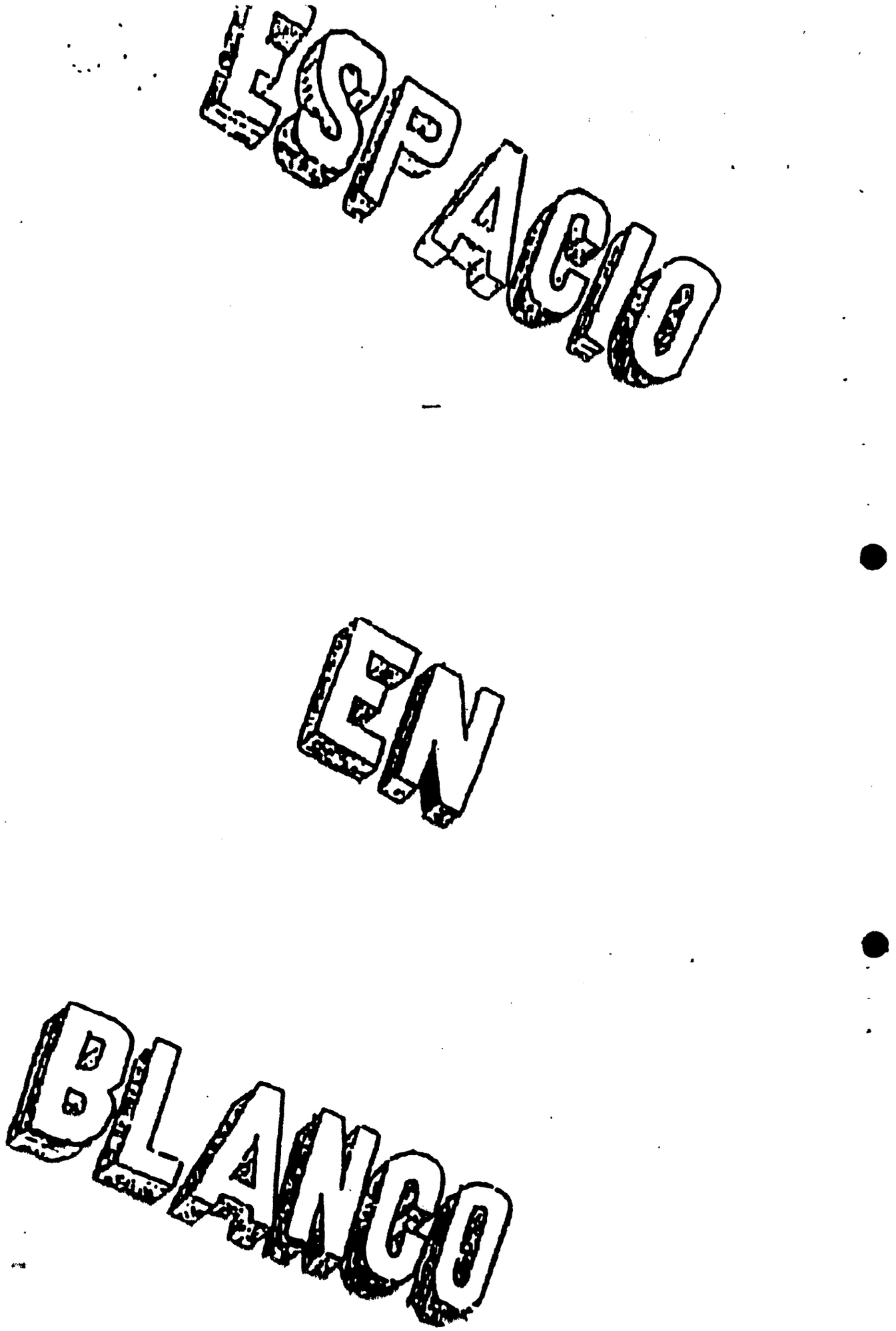
1. El Sr. Dr. Johannes Albrecht Bange, domiciliado en Fraunhoferstr. 22, 82152 Planegg OT Martinsried,
   nacido el 06.12.1969,
   a quien conozco personalmente
2. El Sr. Dr. Koichi Akahane, domiciliado en Fraunhoferstr. 22, 82152 Planegg OT Martinsried,
   nacido el 12.05.1955,
   a quien conozco personalmente

quienes actúan a nombre de "U3 Pharma GmbH" una compañía limitada privada domiciliada en Planegg OT Martinsried/Munich, Alemania.

NOTARIA SEXTA DEL CIRCULO DE BOGOTA D.C. HAGO CONSTAR QUE LA FOTOCOPIA COINCIDE CON EL ORIGINAL QUE HE TENIDO A LA VISTA BOGOTA D.C. REPUBLICA DE COLOMBIA
- 1 MAR. 2010
ARTURO QUINTERO ARTURO
NOTARIA

DIEGO F. VARGAS Z.
TRADUCTOR E INTERPRETE OFICIAL
ESPAÑOL - INGLES - INGLES - ESPAÑOL
RES. 0001 DE ENERO 4 DE 1999

NOTARIA SEXTA DE BOGOTA


ESPACIO
EN
BLANCO

De la revisión del Registro Mercantil del Tribunal de Distrito de Munich el 22 de noviembre de 2009, por el presente certifico que dicha firma "U3 Pharma GmbH", domicilada en Planegg OT Martinsried/Munich, Alemania, se encuentra inscrita en la Sección B de dicho Registro con el No. 177122 y que el señor Dr. Johannes Albrecht Bange, como director ejecutivo y el señor Dr. Koichi Akahane como director ejecutivo están autorizados para representarla conjuntamente.

Munich, 22 de diciembre de 2009

Firma Ilegible

Schmitt, Notario

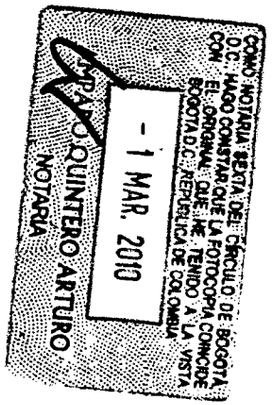
Sello de Apostille expedido en la República Federal de Alemania y certificado en Munich el 21 de enero de 2010 con el **Nr. 910 a-436/2010**, firmado por Thomas Spielbauer.

Es traducción fiel y completa de la cual se deja copia en esta oficina para su confrontación.
DVZ\DVZ\ID-166371\WPCL002H\COLO 17559-845-001-3

DIEGO F. VARGAS E.
TRADUCTOR E INTERPRETE OFICIAL
ESPAÑOL - INGLES – INGLES - ESPAÑOL
RES. 0001 DE ENERO 4 DE 1999
MINISTERIO DE JUSTICIA

COMO NOTARIA SEXTA DEL CIRCULO DE BOGOTA D.C. HAGO CONSTAR QUE LA FOTOCOPIA COINCIDE CON EL ORIGINAL QUE HE TENIDO A LA VISTA
BOGOTA D.C. REPUBLICA DE COLOMBIA
- 1 MAR. 2010
AMPARO QUINTERO ARTURO
NOTARIA

NOTARIA SEXTA DE BOGOTA



MINISTERIO DE
RELACIONES EXTERIORES

2010 FEB 25 A 10:25

JEFE DE LEGALIZACIONES
BOGOTA D.C.

NO SE ASUME
RESPONSABILIDAD
DEL TEXTO

010088

Diego Vargas
CUYA FIRMA APARECE EN EL
DOCUMENTO DESEMPEÑA
LAS FUNCIONES INDICADAS

La presente traducción oficial **No. 0018/10** *fue elaborada por Hernando Torres Barrera, Traductor e Intérprete Oficial, según Resolución 01305 de 1998 del Ministerio de Justicia y del Derecho.*

A continuación se traduce una apostilla en alemán, que acompaña a la Certificación Notarial No. S3546 / 2009 en idioma inglés en un DOCUMENTO DE REPRESENTACIÓN.

APOSTILLA

(Convention de la Haye du 5 octobre 1961)

1. País: República Federal de Alemania

2. Este documento público está firmado por el Notario **Bernd Schmitt**

3. en su calidad de **Notario**

4. lleva el sello del **Notario Bernd Schmitt en Munich**

Certificado

5. en Munich 6. el 21 de enero de 2010

7. por el Presidente del Tribunal Regional de Munich I

8. bajo el No. 910a - 436/2010

9. Sello/timbre 10. Firma
En representación:

Thomas Spielbauer
Vicepresidente

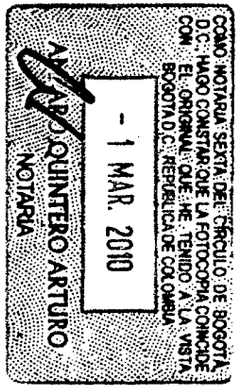
SELLO: EL PRESIDENTE DEL TRIBUNAL REGIONAL MUNICH I * BAVIERA *

Bogotá, D.C., 24 de febrero de 2010

HERNANDO TORRES BARRERA
TRADUCTOR E INTÉRPRETE OFICIAL
RES. No. 1305 MINJUSTICIA 1998

COMO NOTARIA SEXTA DEL CIRCULO DE BOGOTA D.C. HAGO CONSTAR QUE LA FOTOCOPIA COINCIDE CON EL ORIGINAL QUE HE TENIDO A LA VISTA
BOGOTA D.C. REPÚBLICA DE COLOMBIA
- 1 MAR. 2010
AMPARO QUI[illegible]O ARTURO
NOTA[illegible]

NOTARÍA SEXTA DE BOGOTÁ



MINISTERIO DE
RELACIONES EXTERIORES

2010 FEB 25 A 10: 25

JEFE DE LEGALIZACIONES
BOGOTA D.C.

NO SE ASUME
RESPONSABILIDAD
DEL TEXTO

010089

Hernando Torres
CUYA FIRMA APARECE EN EL
DOCUMENTO DESEMPEÑA
LAS FUNCIONES INDICADAS

01

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CAMARA DE COMERCIO DE BOGOTA

SEDE CHAPINERO

24 DE FEBRERO DE 2010 HORA 15:29:39

R027619924 PAGINA: 1 de 3

* *

****
* EN JUNIO DE ESTE AÑO SE ELEGIRAN JUNTA DIRECTIVA Y REVISOR FISCAL *
* DE LA CAMARA DE COMERCIO DE BOGOTA. LAS INSCRIPCIONES DE *
* CANDIDATOS DEBEN HACERSE EN LA PRIMERA QUINCENA DE MAYO. *
* PARA INFORMACION DETALLADA DIRIGIRSE A LA SEDE PRINCIPAL, QUINTO *
* PISO, O COMUNICARSE AL SIGUIENTE TELEFONO: 5941000 EXTENSION 2899.*
****

CERTIFICADO DE EXISTENCIA Y REPRESENTACION LEGAL O INSCRIPCION DE DOCUMENTOS

CERTIFICA:

NOMBRE : CAVELIER ABOGADOS
N.I.T. : 860041367-3
DOMICILIO : BOGOTA D.C.

CERTIFICA:

NO: 00820237

CERTIFICA:

CONSTITUCION : QUE POR ESCRITURA PUBLICA NO. 0006233 DE NOTARIA SEXTA DE BOGOTA D.C. DEL 10 DE SEPTIEMBRE DE 1974 , INSCRITA EL 26 DE SEPTIEMBRE DE 1974 BAJO EL NUMERO 00021234 DEL LIBRO IX, SE CONSTITUYO LA SOCIEDAD CIVIL DENOMINADA: CAVELIER PERDOMO Y CAVELIER.

CERTIFICA :

QUE POR ESCRITURA PUBLICA NO. 0001000 DE NOTARIA SEXTA DE BOGOTA D.C. DEL 10 DE MARZO DE 1983 , INSCRITA EL 5 DE ABRIL DE 1983 BAJO EL NUMERO 00130769 DEL LIBRO IX, LA SOCIEDAD CAMBIO SU NOMBRE DE : CAVELIER PERDOMO Y CAVELIER. POR EL DE : CAVELIER ABOGADOS

CERTIFICA:

QUE POR ESCRITURA PUBLICA NUMERO 1.000 OTORGADA EN LA NOTARIA 6A. DE BOGOTA EL 10 DE MARZO DE 1.983, INSCRITA EN ESTA CAMARA DE COMERCIO EL 5 DE ABRIL DE 1.983 BAJO EL NUMERO 130769 DEL LIBRO IX, LA SOCIEDAD CAMBIO SU NOMBRE DE: CAVELIER PERDOMO Y CAVELIER, POR EL DE: CAVELIER ABOGADOS, E INTRODUJO OTRAS REFORMAS.

CERTIFICA:

CERTIFICA

QUE POR E.P.NO. 2.034 DE LA NOTARIA 6 DE SANTAFE DE BOGOTA DEL 18 DE ABRIL DE 1.995, INSCRITA EL 27 DE ABRIL DE 1.995 BAJO EL NO. 5.937 DEL LIBRO XIII,LA SOCIEDAD TRASLADO SU DOMICILIO DE LA CIUDAD DE SANTAFE DE BOGOTA D.C. AL MUNICIPIO DE TABIO (CUNDINAMARCA).-.

CERTIFICA:

QUE POR ESCRITURA PUBLICA NO. 7710 DE LA NOTARIA SEXTA DE BOGOTA DEL 10 DE OCTUBRE DE 1984, INSCRITA EL 15 DE NOVIEMBRE DE 1984 BAJO EL NO. 1559 DEL LIBRO XIII, LA SOCIEDAD CAMBIO SU

COMO NOTARIA SEXTA DEL CIRCULO DE BOGOTA D.C., HAGO CONSTAR QUE LA FOTOCOPIA COINCIDE CON EL ORIGINAL QUE HE TENIDO A LA VISTA
BOGOTA D.C., REPUBLICA DE COLOMBIA
- 1 MAR. 2010
QUINTERO ARTURO
NOTARIA

NOTARIA SEXTA DE BOGOTA

NATURALEZA JURIDICA DE SOCIEDAD COMERCIAL A SOCIEDAD CIVIL.

CERTIFICA:

REFORMAS:

ESCRITURAS NO.	FECHA	NOTARIA	INSCRIPCION
842	10-V-1.977	18. BTA.	27-V-1.977-NO. 46.204
3.430	1-VII-1.980	6A. BTA.	3-IX-1.980-NO. 89.582
4.844	10-IX-1.980	6A. BTA.	8-X-1.980-NO. 91.261
432	10-II-1.983	6A. BTA.	1-III-1.983-NO.129.337
7.710	10-X-1.984	6A. BTA.	15-XI-1.984-NO. 1.559
7.305	21-X-1.985	6A. BTA.	18-XI-1.985-NO. 1.906
2.567	29-IV-1.987	6A. BTA.	7-V- 1.987-NO. 2.386
4.278	3-VII-1.987	6A. BTA.	23-VII-1987 NO.215.652
2.657	25- IV-1.988	6A. BTA.	19- V -1988-NO. 2,740
9.033	21-XII-1.990	6A. BTA.	10- I - 1991-NO. 3.786
25	3- I -1.991	6A. BTA.	10- I - 1991-NO. 3.787
1.608	8-III-1.991	6A. BTA.	14-III- 1991-NO. 3.841
2.155	2-IV- 1.991	6A. BTA.	8-IV - 1991-NO. 3.862
797	7-II -1.991	6A. BTA.	7- V -1991-NO. 3.882
1.739	14-III-1.991	6A. BTA.	7- V -1991-NO. 3.881
5.886	21-VIII-1.991	6A. BTA	27-VIII-1991 NO. 4.019
8.596	4-XII -1.991	6A. BTA	16-III -1992 NO. 4.430
1.494	10-III -1.992	6A. BTA.	19-III -1992 NO. 4.436
4.205	8 -VII -1.992	6A. BTA.	15-VII -1992 NO. 4.554
8.829	16-XII -1.992	6A. BTA.	24-XII -1992 NO. 4.819
12	5-I -1.993	6 STAFE BTA	13-I -1993 NO. 4.850
4.877	29-VI -1.993	6 STAFE BTA	7-VII -1993 NO. 5.065
5.216	12-VII -1.993	6 STAFE BTA	16-VII -1993 NO. 5.077
ACTA NO.71	2-IX- 1.993	JUNTA DE SOCIOS	29-IX- 1993 NO. 5.174
2.034	18-IV- 1.995	6 STAFE BTA	27- IV -1995 NO. 5.937
2.227	25-IV-1.995	6 STAFE BTA	18-VIII-1.995 NO. 6.092
7.594	12-XII-1.995	6 STAFE BTA	19- XII-1.995 NO. 6.294
676	11- II-1.997	6 STAFE BTA	14- II -1.997 NO. 6.873

CERTIFICA:

REFORMAS:

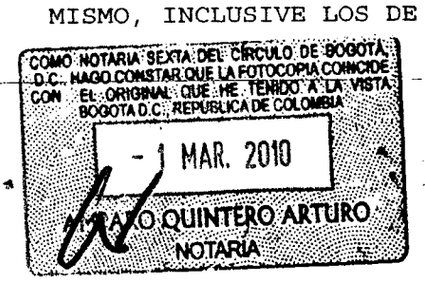
E.P. NO.	FECHA	NOTARIA	CIUDAD	FECHA	NO.INSC.
0004506	1997/07/28	0006	BOGOTA D.C.	1997/09/02	00007115
0002103	1998/04/08	0006	BOGOTA D.C.	1998/04/21	00007426
0005326	1998/08/06	0006	BOGOTA D.C.	1998/08/13	00007544
0005538	1998/08/14	0006	BOGOTA D.C.	1998/08/27	00007564
0007760	1998/11/10	0006	BOGOTA D.C.	1998/11/12	00007644
0006709	1997/11/04	0006	BOGOTA D.C.	2000/12/04	00008481
0003034	2003/05/30	0006	BOGOTA D.C.	2003/06/04	00882729
0003786	2004/07/16	0006	BOGOTA D.C.	2004/07/28	00009703
0001432	2005/03/18	0006	BOGOTA D.C.	2005/04/07	00009917
0004818	2005/08/22	0006	BOGOTA D.C.	2005/08/26	00010008
0005506	2007/07/17	0006	BOGOTA D.C.	2007/07/24	00010841
5453	2009/10/19	0006	BOGOTA D.C.	2009/10/21	00012243

CERTIFICA:

VIGENCIA: QUE LA SOCIEDAD NO SE HALLA DISUELTA. DURACION HASTA EL 10 DE SEPTIEMBRE DE 2024 .

CERTIFICA:

OBJETO SOCIAL: LA SOCIEDAD TENDRA POR OBJETO : EL EJERCICIO DE LA ACTIVIDAD PROFESIONAL DE ABOGADOS. EN DESARROLLO DE ESTE OBJETO LA SOCIEDAD PODRA ADQUIRIR, CONTRAER OBLIGACIONES Y CELEBRAR TODA CLASE DE CONTRATOS DIRECTAMENTE RELACIONADOS Y SUBORDINADOS AL MISMO, INCLUSIVE LOS DE ARRENDAMIENTO, HIPOTECA, MUTUO CON O SIN



INTERES, MANDATO CIVIL Y COMERCIAL, Y SOCIEDAD, ASI COMO PARTICIPAR EN ASOCIACIONES CIENTIFICAS, GREMIALES O PROFESIONALES SIN ANIMO DE LUCRO.

CERTIFICA:

CAPITAL Y SOCIOS: $10,000.00 DIVIDIDO EN 10,000.00 CUOTAS CON VALOR NOMINAL DE $1.00 CADA UNA, DISTRIBUIDO ASI :

- SOCIO CAPITALISTA (S)

ASOCIACION CAVELIER DEL DERECHO N.I.T. 000008001722568
NO. CUOTAS: 8,800.00 VALOR: $8,800.00
GAUDEBERT DE CAVELIER AGNES JEANNE C.E. 000000000131100
NO. CUOTAS: 1,200.00 VALOR: $1,200.00

- SOCIO INDUSTRIAL (S)

CHAVARRO JORGE C.C. 000000016209380
NO. CUOTAS: 0.00 VALOR: $0.00
SUAREZ DE PAEZ LUZ CLEMENCIA C.C. 000000035456344
NO. CUOTAS: 0.00 VALOR: $0.00
PEÑA VALENZUELA DANIEL C.C. 000000079518915
NO. CUOTAS: 0.00 VALOR: $0.00
MARIN RUALES GERMAN HUMBERTO C.C. 000000079155665
NO. CUOTAS: 0.00 VALOR: $0.00
TOTALES
NO. CUOTAS: 10,000.00 VALOR: $10,000.00

CERTIFICA:

QUE POR ESCRITURAS PUBLICAS NO. 001431 Y 001432 DEL 18 DE MARZO DE 2005 DE LA NOTARIA 06 DE BOGOTA D.C., INSCRITA EL 07 DE ABRIL DE 2005 BAJO EL NO. 0009918 Y 0009917, RESPECTIVAMENTE DEL LIBRO XIII, DE LAS MIL DOSCIENTAS (1200) PARTES DE INTERES SOCIAL RADICADAS EN CABEZA DE AGNES GAUDEBERT DE CAVELIER, SEISCIENTAS (600) PARTES ESTAN GRAVADAS O AFECTADAS EN PROPIEDAD FIDUCIARIA A FAVOR DE LAS SIGUIENTES PERSONAS : GERMAN CAVELIER FRANCO, ERNESTO CAVELIER FRANCO, JORGE CAVELIER FRANCO, INES CAVELIER FRANCO, GUILLERMO CAVELIER FRANCO, ELENA CAVELIER FRANCO, ALEJANDRO CAVELIER FRANCO, BEATRIZ CAVELIER FRANCO, Y LUCIA CAVELIER FRANCO.

CERTIFICA:

REPRESENTACION LEGAL: EL REPRESENTANTE LEGAL ES EL DIRECTOR. EL SOCIO FUNDADOR GERMAN CAVELIER GAVIRIA TENDRA EL CARACTER DE PRESIDENTE DIRECTOR VITALICIO, PARTICIPARA POR DERECHO PROPIO EN EL CONSEJO SUPERIOR Y EN EL CONSEJO DIRECTIVO Y LLEVARA LA REPRESENTACION LEGAL DE LA SOCIEDAD CUANDO LO ESTIME PERTINENTE SIN LIMITACION ALGUNA. IGUAL PARTICIPACION Y ATRIBUCIONES TENDRA SU SUPLENTE AGNES GAUDEBERT DE CAVELIER CUANDO OCUPE EL CARGO, EN CASO DE FALTA ABSOLUTA DE GERMAN CAVELIER GAVIRIA. LOS SOCIOS COLECTIVOS ESTÁN AUTORIZADOS PARA EJERCER LA REPRESENTACIÓN DE LA SOCIEDAD EN CUALQUIER TIEMPO, SIN PERJUICIO DE LAS DELEGACIONS CONFERIDAS A LOS ORGANOS CREADOS POR LOS PRESENTES

COMO NOTARIA SEXTA DEL CIRCULO DE BOGOTA D.C., HAGO CONSTAR QUE LA FOTOCOPIA COINCIDE CON EL ORIGINAL QUE HE TENIDO A LA VISTA
BOGOTA D.C., REPUBLICA DE COLOMBIA
- 1 MAR. 2010
AMPARO QUINTERO ARTURO
NOTARIA

NOTARIA SEXTA DE BOGOTA

ESTATUTOS

CERTIFICA:

** NOMBRAMIENTOS **

QUE POR NO. 12 DE JUNTA DE SOCIOS DEL 14 DE AGOSTO DE 2009, INSCRITA EL 24 DE SEPTIEMBRE DE 2009 BAJO EL NUMERO 00012200 DEL LIBRO XIII, FUE (RON) NOMBRADO (S):

NOMBRE IDENTIFICACION

DIRECTOR (REPRESENTANTE LEGAL DE LA ASOCIACIÓN CAVELIER DEL DERECHO)

GALLON GIRALDO CARLOS C.C. 000000019066425

QUE POR ESCRITURA PUBLICA NO. 0004818 DE NOTARIA 6 DE BOGOTA D.C. DEL 22 DE AGOSTO DE 2005, INSCRITA EL 26 DE AGOSTO DE 2005 BAJO EL NUMERO 00010008 DEL LIBRO XIII, FUE (RON) NOMBRADO (S):

NOMBRE IDENTIFICACION

PRESIDENTE DIRECTOR VITALICIO

CAVELIER GAVIRIA GERMAN C.C. 000000002877924

SUPLENTE DEL PRESIDENTE DIRECTOR VITALICIO

GAUDEBERT DE CAVELIER AGNES JEANNE C.E. 000000000131100

CERTIFICA:

FACULTADES DEL REPRESENTANTE LEGAL: APARTE DE LAS FACULTADES Y DEBERES QUE DE TIEMPO EN TIEMPO SE LE ASIGNEN POR EL CONSEJO SUPERIOR, EL DIRECTOR TENDRA LAS SIGUIENTES FUNCIONES : A) LA DE REPRESENTAR LEGALMENTE A LA SOCIEDAD ANTE LAS AUTORIDADES DE CUALQUIER ORDEN O NATURALEZA Y ANTE OTRAS PERSONAS NATURALES O JURIDICAS, CON FACULTADES PARA NOVAR, TRANSIGIR, COMPROMETER Y DESISTIR Y PARA COMPARECER EN JUICIOS INCLUSIVE EN AQUELLOS EN DONDE SE DISPUTE LA PROPIEDAD DE BIENES INMUEBLES; B) CUMPLIR Y HACER CUMPLIR LOS ESTATUTOS Y REGLAMENTOS DE LA SOCIEDAD; Y C) CREAR O SUPRIMIR TODOS LOS EMPLEOS QUE SEAN NECESARIOS DE ACUERDO CON EL CONSEJO SUPERIOR PARA EL BUEN FUNCIONAMIENTO DE LA SOCIEDAD, ASIGNARLES FUNCIONES, FIJAR SUS SALARIOS Y NOMBRAR LAS PERSONAS QUE DEBAN DESEMPEÑARLOS, ASI COMO RETIRARLOS Y REEMPLAZARLOS CUANDO HAYA LUGAR. CUANDO CUALQUIERA DE LOS ACTOS INDICADOS EN LA CLAUSULA ANTERIOR SE REFIERA A OPERACIONES CUYO MONTO EXCEDA DE LA SUMA EQUIVALENTE A CIENTO OCHENTA (180) SALARIOS MINIMOS MENSUALES, SU CELEBRACION REQUERIRA LA APROBACION PREVIA DEL CONSEJO SUPERIOR.

CERTIFICA:

** REVISOR FISCAL **

QUE POR ACTA NO. 0000071 DEL 2 DE SEPTIEMBRE DE 1993, INSCRITA EL 29 DE SEPTIEMBRE DE 1993 BAJO EL NUMERO 00005175 DEL LIBRO XIII, FUE (RON) NOMBRADO (S):

NOMBRE IDENTIFICACION

REVISOR FISCAL

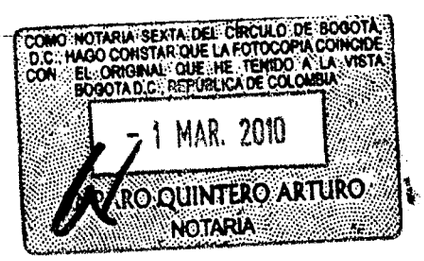
RINCON FANDIÑO MIGUEL ALFONSO C.C. 000000002877024

CERTIFICA:

DE CONFORMIDAD CON LO ESTABLECIDO POR LA LEY 962 DE 2005, LOS ACTOS DE REGISTRO AQUI CERTIFICADOS QUEDAN EN FIRME CINCO (5) DIAS HABILES DESPUES DE LA FECHA DE INSCRIPCION, SIEMPRE QUE NO SEAN OBJETO DE RECURSOS EN LA VIA GUBERNATIVA.

* * * EL PRESENTE CERTIFICADO NO CONSTITUYE PERMISO DE * * *
* * * FUNCIONAMIENTO EN NINGUN CASO * * *

SEÑOR EMPRESARIO, SI SU EMPRESA TIENE ACTIVOS INFERIORES A 30.000 SMLMV Y UNA PLANTA DE PERSONAL DE MENOS DE 200 TRABAJADORES, USTED TIENE DERECHO A RECIBIR UN DESCUENTO EN EL PAGO DE LOS PARAFISCALES DE



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CAMARA DE COMERCIO DE BOGOTA

SEDE CHAPINERO

24 DE FEBRERO DE 2010 HORA 15:29:39

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* *

75% EN EL PRIMER AÑO DE CONSTITUCION DE SU EMPRESA, DE 50% EN EL SEGUNDO AÑO Y DE 25% EN EL TERCER AÑO. LEY 590 DE 2000 Y DECRETO 525 DE 2009.

EL SECRETARIO DE LA CAMARA DE COMERCIO,
VALOR : $ 3,600
DE CONFORMIDAD CON EL DECRETO 2150 DE 1995 Y LA AUTORIZACION IMPARTIDA POR LA SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO, MEDIANTE EL OFICIO DEL 18 DE NOVIEMBRE DE 1996, LA FIRMA MECANICA QUE APARECE A CONTINUACION TIENE PLENA VALIDEZ PARA TODOS LOS EFECTOS LEGALES

Benjamin Esteban R

COMO NOTARIA SEXTA DEL CIRCULO DE BOGOTA, D.C., HAGO CONSTAR QUE LA FOTOCOPIA COINCIDE CON EL ORIGINAL QUE HE TENIDO A LA VISTA BOGOTA D.C., REPUBLICA DE COLOMBIA

- 1 MAR. 2010

AMPARO QUINTERO ARTURO
NOTARIA

NOTARIA SEXTA DE BOGOTA

legalizado ----------

Presente el señor **CARLOS ALBERTO GALLÓN GIRALDO**, domiciliado en Bogotá, identificado como aparece al pie de su firma y manifestó que está conforme con el contenido de esta escritura pública ----------

---------- **HASTA AQUÍ LA MINUTA PRESENTADA** ----------

OTORGAMIENTO Y AUTORIZACION: LEIDA la presente escritura por los comparecientes y habiéndoseles hecho las advertencias sobre los trámites y formalidades de rigor le impartieron su aprobación y para constancia la firman ante mí el NOTARIO QUE AUTORIZA ----------

DERECHOS NOTARIALES: $ 42.860.oo -- - - - - - - - - - -

IVA 16% $ 17.365.oo - - - - - - - - - - - - - - - - - -

PAPEL NOTARIAL: esta escritura ha quedado extendida en las hojas de papel sellado notarial números: ----------

7-700004-342153 - 7-700004-342146 - - - - - - - - - - - - -

EN BLANCO... EN BLANCO

OTORGANTE

CARLOS ALBERTO GALLÓN GIRALDO

C.C. 19066424 Bta.

TEL 3373611

REPRESENTANTE LEGAL DE **CAVELIER ABOGADOS**

REPÚBLICA DE COLOMBIA
Amparo Quintero Arturo
NOTARIA
NOTARIA SEXTA DE BOGOTA

AMPARO QUINTERO ARTURO

NOTARIA SEXTA (6a) DE BOGOTA D.C.

NOTARIA SEXTA DE BOGOTA

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IMPRESO EN DICIEMBRE 1º DE 2009 POR POLYPRINT EDITORIAL LTDA. - NIT 830.029.959-5

PAPEL DE USO EXCLUSIVO DEL PROTOCOLO NOTARIAL . NO TIENE COSTO PARA EL USUARIO

ES FIEL Y TERCERA COPIA (FOTOCOPIA) TOMADA DE LA ESCRITURA PUBLICA NUMERO 1098 DE FECHA 1 DE MARZO DE 2010.

COPIA QUE EXPIDO EN 10 HOJAS RUBRICADAS EN SUS MARGENES , LA CUAL CARECE DE NOTAS DE REVOCATORIA, MODIFICACION O SUSTITUCION, POR TANTO SE PRESUME VIGENTE EL PODER EN ELLA CONTENIDO.

BOGOTA, D.C. 22 DE ABRIL DE 2010

RESOLUCION 01 DE 2008

AMPARO [illegible] RO
NOTARIA [illegible] TA.

REPÚBLICA DE COLOMBIA
Mabel Andrea Rodriguez D.
NOTARIA (E)
NOTARIA SEXTA DE BOGOTA

CAVELIER
ABOGADOS
EDIFICIO SISKI
CARRERA 4a N° 72-35
BOGOTA, 8 – COLOMBIA

193

Representación, Ratificación y Poder con autenticación notarial y Apostille para patentes, modelos de utilidad diseños industriales, marcas de fábrica, nombres comerciales, enseñas, nombres de dominio, lemas comerciales, licencias.

Representation, ratification and Power-of-Attorney with notarial authentication and Apostille for patents, utility models, industrial designs, trademarks, commercial names, trade emblems, domain names, slogans, licenses.

REPRESENTACION, RATIFICACION Y PODER

REPRESENTATION, RATIFICATION AND POWER-OF-ATTORNEY

15193
12203

Yo (nosotros), abajo firmado (s)/I (we), the undersigned

AMGEN INC.

domiciliado (s) en/of

One Amgen Center Drive
Thousand Oaks, California 91320
United States of América

por el presente ratificamos las solicitudes de patente Nos. 06.014.624 y 06.047.666 presentadas por Emilio Ferrero

como agente oficioso ante Superintendencia de Industria y Comercio

en Bogotá

el 14 de febrero de 2006 y el 18 de mayo de 2006 respectivamente

por el presente nombramos a EMILIO FERRERO, tpa. 31929; GONZALO PERDOMO, tpa. 831; LUZ CLEMENCIA DE PAEZ, tpa. 23555 y DANIEL PEÑA, tpa. 65620 domiciliados en la Carrera 4ª N° 72-35, Bogotá, Colombia, en obedecimiento a lo dispuesto en el parágrafo 1o del Artículo 543 del Código de Comercio, el primero como principal y los demás como suplentes, en su orden, como mis (nuestros) representantes en todos los asuntos de propiedad industrial con facultad para recibir notificaciones y nombrar apoderados judiciales o extrajudiciales. El primer representante suplente reemplazará al principal en caso de ausencia o impedimento temporal o definitivo de aquél. La misma regla se aplicará cuando el segundo representante suplente haya de reemplazar al primero, o el tercero al segundo. En tales casos, el representante principal, o el primero, o segundo suplente, en su caso, o ambos, declararán su intención de no ejercer la representación mediante declaración autenticada por Notario Público en Colombia, o por Notario u otro Funcionario Público, o Cónsul de Colombia, en el extranjero; y si se tratare de impedimento, con el certificado respectivo. Si alguno de los nombrados faltare definitivamente, el siguiente tomará su lugar. Cuando cesare la ausencia o impedimento del representante principal, o de su primero o segundo suplentes, en su caso, podrán ejercer la representación, en su orden, uno u otros según el caso, asumiéndola por el solo hecho de ejercerla, cesando en ese momento el ejercicio de la representación por el primero, segundo o tercer suplente en su caso.

Además, confiero (conferimos) poder a los abogados arriba nombrados, para obtener la protección de mi (nuestra) propiedad industrial y contra la competencia desleal, a cuyo efecto autorizo (amos) a los dichos

Hereby ratify the Patent Applications Nos. 06.014.624 and 06.047.666

filed without a Power of Attorney by Emilio Ferrero

before Patent Office

in Bogotá

on February 14, 2006 and May 18, 2006 respectively

and do hereby appoint EMILIO FERRERO, tpa. 31929; GONZALO PERDOMO, tpa. 831; LUZ CLEMENCIA DE PAEZ, tpa. 23555 and DANIEL PEÑA, tpa. 65620, domiciled at Carrera 4ª N° 72-35, Bogotá, Colombia, in due compliance with the terms of Paragraph 1st. of Article 543 of the Commercial Code, the first as principal and the others as alternates, in the order of their appointment, as our representatives for all industrial property matters with faculty to receive notifications and to appoint attorneys in and out of Court. The first alternate shall replace the principal in case of his absence or of temporal or definitive impediment. The same rule will apply when the second alternate representative is to replace the first one, or when the third is to replace the first or second alternates in their turn, or both of them, second. In such cases, the principal representative, or the shall state their intention not to act as representatives through a declaration given before a Notary Public in Colombia, or before a Notary or another Public Official or a Colombian Consul abroad; and in case of impediment, the appropriate certificate shall suffice. If any of the appointees were to be definitively absent, the following alternate shall take its place. When the absence or impediment of the principal representative, or of the first or second alternate in their turn ceases, the representation can be taken again in their sequence, by the principal, the first or second alternate depending on case, and the mere exercise will suffice. The exercise of the representation by the alternates in their turn shall end at such time.

COPIA AUTENTICADO
COMO NOTARIA SEXTA DEL CIRCULO DE BOGOTA
CON EL ORIGINAL QUE SE TUVO A LA VISTA
22 ABR 2010

REPÚBLICA DE COLOMBIA
Mabel Andrea Rodríguez D.
NOTARIA (E)
NOTARIA SEXTA DE BOGOTÁ

Power of Attorney in favor of the above-named they may obtain the protection of my (our) against the unfair competition, for which purpose

apoderados para que me (nos) representen ante cualesquiera entidades o personas, ejerzan o no jurisdicción, especialmente ante las del orden administrativo, contencioso-administrativo y judicial, así como los tribunales de arbitramento, en todo lo concerniente a los siguientes asuntos: a) Obtención de patentes de invención, modelos de utilidad y diseños industriales; el registro de marcas de fábrica, colectivas, defensivas, de servicio, lemas comerciales, nombres comerciales, enseñas, nombres de dominio, variedades vegetales y denominaciones de origen; su renovación, traspaso, cambio de nombre o domicilio, cancelación voluntaria; y el registro de licencias de uso de esos derechos; b) Las acciones de competencia desleal, protección del consumidor, oposiciones u observaciones, cancelación administrativa o judicial, nulidad, medidas cautelares, concesión de licencias, la tutela, la protección de secretos industriales, y en general los juicios civiles, penales, administrativos o contencioso-administrativos relacionados con estos derechos; acciones y procesos que promovamos o se nos promuevan. Y para que en todos los asuntos arriba determinados, puedan sustituir este mandato, transigir, conciliar, admitir los hechos del proceso, desistir, cancelar, recibir, renunciar, y ratificar los actos de agentes oficiosos.

(we) authorize the said attorneys to represent me (us) before any authorities or persons, with or without jurisdiction, specially those administrative, administrative contentious and judicial, as well as before Arbitration Court, in all matters concerning the following: a) Obtainment of patents, utility models and industrial designs; ~~the registration of trademarks, collective, defensive and service marks, slogans, commercial names, trade emblems, domain names~~, vegetal varieties and denominations of origin; its renewal, assignment, change of name or domicile, voluntary cancellation; and the registration of licenses of use of the above rights; b) Actions of unfair competition, protection to the consumer, oppositions or observations, administrative or Court cancellation, nullity, infringement, granting of licenses, the action for writ mandamus, the protection of trade secrets, and in general the civil, penal, and administrative suits relating to those rights; actions and suits instituted by me (us) or against me (us). And that in all the above matters they may substitute this Power of Attorney, compromise, conciliate, admit the facts of the case, desist, cancel, receive, resign, and ratify acts done by representatives without a power of attorney.

RE: Patent Applicaction
PCTUS2004/022876

Dado y firmado hoy/Given and signed this 24 February 2006

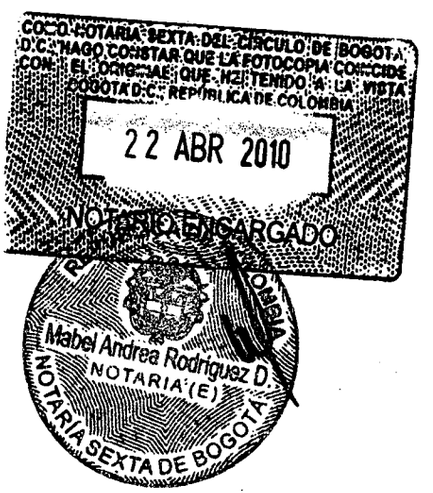
Stuart L. Watt

en/in _____

por/by Stuart L. Watt, Vice President, Law

Signed in Thousand Oaks, Ventura County, CA, US

Firma Signature



A-860 (CO)

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19

State of California

SECRETARY OF STATE

APOSTILLE

(Convention de La Haye du 5 octobre 1961)

1. *Country: United States of America*
   This public document
2. *has been signed by L. Holtke*
3. *acting in the capacity of Notary Public, State of California*
4. *bears the seal/stamp of L. Holtke, Notary Public, State of California*

CERTIFIED

5. *At Sacramento, California*
6. *the 8th day of April 2006*
7. *by Deputy Secretary of State, State of California*
8. *No. 281687*
9. *Seal/Stamp:*

10. *Signature*

COMO NOTARIA SEXTA DEL CIRCULO DE BOGOTA D.C. HAGO CONSTAR QUE LA FOTOCOPIA COINCIDE CON EL ORIGINAL QUE HE TENIDO A LA VISTA
BOGOTA D.C., REPUBLICA DE COLOMBIA
22 ABR 2010
NOTARIO ENCARGADO

REPUBLICA DE COLOMBIA
Maibel Andrea Rodriguez D.
NOTARIA (E)
NOTARIA SEXTA DE BOGOTA

Secretary of State

NP-24 A (REV. 4-05)

BY Cacha

OSP 05 90772

CALIFORNIA ALL-PURPOSE ACKNOWLEDGMENT

State of California
County of VENTURA } ss.

On 24 FEBRUARY 2006 (Date), before me, L. HOLTKE (Name and Title of Officer (e.g., "Jane Doe, Notary Public")),
personally appeared STUART L. WATT (Name(s) of Signer(s)),

☒ personally known to me
☐ proved to me on the basis of satisfactory evidence

to be the person(s) whose name(s) is/~~are~~ subscribed to the within instrument and acknowledged to me that he/she/~~they~~ executed the same in his/her/~~their~~ authorized capacity(ies), and that by his/her/~~their~~ signature(s) on the instrument the person(s), or the entity upon behalf of which the person(s) acted, executed the instrument.

WITNESS my hand and official seal.

L. HOLTKE
Comm. # 1399086
NOTARY PUBLIC - CALIFORNIA
Los Angeles County
My Comm. Expires Feb. 8, 2007

Place Notary Seal Above

Signature of Notary Public

OPTIONAL

Though the information below is not required by law, it may prove valuable to persons relying on the document and could prevent fraudulent removal and reattachment of this form to another document.

Description of Attached Document
Title or Type of Document: REPRESENTATION, RATIFICATION & POWER OF ATTORNEY
Document Date: _____ Number of Pages: 2
Signer(s) Other Than Named Above: _____

Capacity(ies) Claimed by Signer
Signer's Name: STUART L. WATT
☐ Individual
☒ Corporate Officer — Title(s): VICE PRESIDENT, LAW
☐ Partner — ☐ Limited ☐ General
☐ Attorney in Fact
☐ Trustee
☐ Guardian or Conservator
☐ Other: _____

Signer Is Representing: AMGEN INC.

RIGHT THUMBPRINT OF SIGNER
Top of thumb here

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CONSULADO DE COLOMBIA
D.C.: NADO CONSTAR QUE LA FOTOCOPIA COINCIDE
CO... EL ORIGINAL QUE HE TENIDO A LA VISTA
BOGOTA D.C., REPUBLICA DE COLOMBIA
22 ABR 2010
NOTARIO ENCARGADO
Mabel Andrea Rodriguez D.
NOTARIA (E)
NOTARIA SEXTA DE BOGOTA

A-860(CO)

21

CORPORATE CERTIFICATE

State of California)
) SS:
County of Ventura)

I, Stuart L. Watt, am the person who signed the foregoing instrument as Vice President, Law, of Amgen Inc., and I hereby certify the following:

1. That Amgen is a corporation duly organized and legally existing under the laws of the State of Delaware and is domiciled at One Amgen Center Drive, Thousand Oaks, California 91320-1799 USA.

2. That I am its legitimate Vice President in accordance with the appointment issued in the City of Los Angeles, California on June 27, 2000, by the Board of Directors of said corporation, which was duly elected by the General Meeting of Stockholders held in Los Angeles, California on May 11, 2000, as evidenced by the minutes, which I have seen, and I have the competence of representing same, including faculties to grant powers.

3. That I am duly authorized to sign the foregoing instrument in the name of said corporation in accordance with my above-mentioned position and/or with a resolution of the Board of Directors of said corporation, which I have seen, taken on June 27, 2000, in the City of Los Angeles, California.

4. That the purposes for which said instrument is granted are within the scope of the objects or activities of said corporation, in accordance with the Act of Incorporation issued in the City of Dover, Delaware and dated October 31, 1986, and/or the Amended and Restated By-Laws issued in the City of Thousand Oaks, California and dated April 11, 1996, both of which I have seen.

Karen Podgorny
Witness (Karen Podgorny)

Stuart L. Watt
Stuart L. Watt
Vice President, Law

Debbie L. Merrill
Witness (Debbie Merrill)

State of California)
) SS:
County of Ventura)

On this 22 day of February, 2006, before me, L. HOLTKE, Notary Public, personally appeared Stuart L. Watt, Vice President, Law, and Associate General Counsel, personally known to me to be the person, whose name is subscribed to the within instrument and acknowledged to me that he executed the same in his authorized capacity, and that by his signature on the instrument the person, or the entity upon behalf of which the person acted, executed the instrument.

Witness my hand and seal.

L. Holtke
Notary Public

L. HOLTKE
Comm. # 1399086
NOTARY PUBLIC - CALIFORNIA
Los Angeles County
My Comm. Expires Feb. 8, 2007

A 860 (CO)
COPIA NOTARIA SEXTA DEL CIRCULO DE BOGOTA D.C. HAGO CONSTAR QUE LA FOTOCOPIA COINCIDE CON EL ORIGINAL QUE ME FUE PRESENTADO A LA VISTA BOGOTA D.C., REPUBLICA DE COLOMBIA
22 ABR 2010
NOTARIO ENCARGADO
REPUBLICA DE COLOMBIA
Mabel Andrea Rodriguez
NOTARIA (E)
NOTARIA SEXTA DE BOGOTA

TRADUCCIÓN OFICIAL 161/2006 DE UN DOCUMENTO ESCRITO EN INGLÉS Y EN ESPAÑOL DE ACUERDO CON EL CUAL **AMGEN INC.,** EMPRESA DOMICILIADA EN ONE AMGEN CENTER DRIVE THOUSAND OAKS, CALIFORNIA 91320 ESTADOS UNIDOS DE AMÉRICA RATIFICAN LAS SOLICITUDES DE PATENTE NOS. 06.014.624 Y 06.047.666 PRESENTADAS POR EMILIO FERRERO EL 14 DE FEBRERO DE 2006 Y EL 18 DE MAYO DE 2006 RESPECTIVAMENTE, COMO AGENTE OFICIOSO ANTE LA SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO EN BOGOTÁ Y OTORGA PODER A EMILIO FERRERO, TPA 31929, GONZALO PERDOMO, TPA 831; LUZ CLEMENCIA DE PAEZ, TPA 23555 Y A DANIEL PEÑA, TPA 65620.

EXPEDIDO Y FIRMADO HOY 24 DE FEBRERO DE 2006 POR STUART L. WATT, VICEPRESIDENTE ASUNTOS JURÍDICOS. FIRMADO EN THOUSAND OAKS, VENTURA COUNTY, CA, US.

RE: SOLICITUD DE PATENTE PCTUS2004/022876

RECONOCIMIENTO MULTIPROPÓSITO DE CALIFORNIA

ESTADO DE CALIFORNIA

CONDADO DE VENTURA

DECLARACIÓN JURADA

El 24 de febrero de 2006, ante mi L. HOLTKE, compareció personalmente STUART WATT, conocido personalmente por mí como la persona cuyo nombre aparece firmado en el documento adjunto y reconoció ante mi haber firmado el mismo en su calidad autorizada y que mediante su firma en el documento la persona o entidad a nombre de la cual la persona actuaba, firmó el

Atestiguo mediante mi firma y sello oficial

Firma ilegible

DESCRIPCIÓN DEL DOCUMENTO ADJUNTO:

Tipo de documento o título: REPRESENTACIÓN, RATIFI

CALIDAD RECLAMADA POR EL FIRMANTE:

COMO NOTARIA SEXTA DEL CIRCULO DE BOGOTA D.C. HAGO CONSTAR QUE LA FOTOCOPIA COINCIDE CON EL ORIGINAL QUE HE TENIDO A LA VISTA BOGOTA D.C. REPUBLICA DE COLOMBIA
22 ABR 2010
NOTARIO ENCARGADO
REPUBLICA DE COLOMBIA
Mabel Andrea Rodriguez
NOTARIA (E)
NOTARIA SEXTA DE BOGOTA

NOMBRE DEL FIRMANTE:

STUART L. WATT, VICEPRESIDENTE ASUNTOS JURÍDICOS

EL FIRMANTE REPRESENTA A AMGEN, INC.

CERTIFICADO SOCIETARIO

ESTADO DE CALIFORNIA, CONDADO DE VENTURA

DECLARACIÓN JURAMENTADA

Yo, Stuart L. Watt, soy la persona que firmó el documento precedente en mi calidad de vicepresidente de asuntos jurídicos de Amgen Inc. y por la presente verifico lo siguiente:

1. Que Amgen es una sociedad debidamente constituida y legalmente existente de acuerdo con las leyes del estado de Delaware y se encuentra domiciliada en ONE AMGEN CENTER DRIVE, THOUSAND OAKS, CALIFORNIA 91320-1799, USA (Estados Unidos de América).

2. Que soy su vicepresidente legítimo de acuerdo con el nombramiento realizado en la ciudad de Los Angeles, California el 27 de junio de 2000 por la junta directiva de dicha empresa, que fue debidamente elegida por la reunión general de accionistas realizada en Los Angeles, California el 11 de mayo de 2000, tal como se evidencia por las actas que he visto y que tengo competencia para representarla, incluyendo con facultades para otorgar poderes.

3. Que estoy debidamente autorizado para firmar el documento precedente a nombre de dicha sociedad en concordancia con mi cargo arriba mencionado y/con una resolución de la junta directiva de dicha sociedad, que he visto, tomada el 27 de junio de 2000 en la ciudad de Los Angeles, California.

4. Que los objetos por los cuales se otorg[illegible] están bajo el alcance del objeto social d[illegible] empresa, concordancia con el acta de constitución expe[illegible] en la ciudad [illegible]

NOTARIA SEXTA DEL CIRCULO DE BOGOTA D.C. HAGO CONSTAR QUE LA FOTOCOPIA COINCIDE CON EL ORIGINAL QUE HE TENIDO A LA VISTA BOGOTA D.C. REPUBLICA DE COLOMBIA

22 ABR 2010

NOTARIA ENCARGADO

Mabel Andrea Rodriguez D.
NOTARIA (E)

NOTARIA SEXTA DE BOGOTA

24

Dover, Delaware y de fecha 31 de octubre de 1986 y con los estatutos reformados y reestructurados emitidos en la ciudad de Thousand Oaks, California y de fecha 11 de abril de 1986, los cuales ambos he visto.

FIRMADO: STUART L. WATT, vicepresidente asuntos jurídicos.

Firmado: dos testigos, Karen Podgorny y Debbie Merrill

ESTADO DE CALIFORNIA

CONDADO DE VENTURA

DECLARACION JURADA

Hoy 22 de febrero de 2006, ante mí, L HOCTKE, notario público, compareció personalmente STUART L. WATT, vicepresidente asuntos jurídicos, y abogado general asociado, de quien me consta es la persona cuyo nombre aparece escrito en el documento adjunto y reconoció ante mí haber firmado el mismo en su calidad autorizada, y que mediante su firma en el documento la persona o la entidad a nombre de la cual actuaba la persona, firmó el documento.

Atestiguo mediante mi firma y sello.

Firmado: (ilegible) notario público

SELLO: L HOLTKE, Nombramiento #139086, notario público, California. Condado de Los Angeles. Mi cargo vence el 8 de febrero de 2007.

ESTADO DE CALIFORNIA

SECRETARÍA DE ESTADO

APOSTILLA

(CONVENCIÓN DE LA HAYA DEL 5 DE OCT[illegible] DE 1961)

1. PAIS: ESTADOS UNIDOS DE AMÉRICA

Este documento público

2. ha sido firmado por L. HOLTKE

COTEJO: NOTARIA SEXTA DEL CIRCULO DE BOGOTA D.C. HAGO CONSTAR QUE LA FOTOCOPIA COINCIDE CON EL ORIGINAL QUE HE TENIDO A LA VISTA BOGOTA D.C. REPUBLICA DE COLOMBIA
22 ABR 2010
NOTARIO ENCARGADO
REPÚBLICA DE COLOMBIA
Mabel Andrea Rodrigu[illegible]
NOTARIA (E)
NOTARIA SEXTA DE BOGOTA

3. quien actúa en su calidad de NOTARIO PÚBLICO, ESTADO DE CALIFORNIA

4. y lleva el sello/estampilla de L. HOLTKE, notario público, estado de California.

CERTIFICADO

5. en Sacramento, California 6. el 8 de abril de 2006

7. por el Secretario de estado suplente del estado de California

8. Certificado número 281687

9. Sello: EL GRAN SELLO DEL ESTADO DE CALIFORNIA

10. Firma: (ILEGIBLE)

COLO- 15193-841-001-7

WPCL002G ID 7879

Bogotá, 22 de junio de 2006.

Eduardo Calado

Eduardo Calado Nogueira
"TRADUCTOR OFICIAL"
INGLES - ESPAÑOL INGLES
Res. 541 Febrero de 1979

COMO NOTARIA SEXTA DEL CIRCULO DE BOGOTA D.C. HAGO CONSTAR QUE LA FOTOCOPIA COINCIDE CON EL ORIGINAL QUE HE TENIDO A LA VISTA
BOGOTA D.C., REPUBLICA DE COLOMBIA
22 ABR 2010
NOTARIO ENCARGADO

REPÚBLICA DE COLOMBIA
Mabel Andrea Rodriguez
NOTARIA (E)
NOTARIA SEXTA DE BOGOTA

COMO NOTARIO SEXTO DEL CIRCULO DE SANTAFE DE BOGOTA, HAGO CONSTAR QUE LA(S) FIRMA(S) DE

Eduardo Calado Noguera

COINCIDE(N) CON LA FIRMA REGISTRADA POR EL (ELLOS) EN ESTA NOTARIA

SANTAFE DE BOGOTA 23 JUN 2006

CODEX JUDIS CIVILIS

REPUBLICA DE COLOMBIA
Juan Manuel Botero Medina
Notario Sexto
SANTAFE DE BOGOTA, D.C.

NO SE ASUME RESPONSABILIDAD DEL TEXTO

2006 JUN 23 P 2:32

JEFE DE LEGALIZACIONES
SANTAFE DE BOGOTA D.C.

MINISTERIO DE RELACIONES EXTERIORES

07119

Eduardo Calado

CUYA FIRMA APARECE EN EL DOCUMENTO DESEMPEÑA LAS FUNCIONES INDICADAS

COMO NOTARIA SEXTA DEL CIRCULO DE BOGOTA D.C. HAGO CONSTAR QUE LA FOTOCOPIA COINCIDE CON EL ORIGINAL QUE HE TENIDO A LA VISTA
BOGOTA D.C., REPUBLICA DE COLOMBIA

22 ABR 2010

NOTARIO ENCARGADO

REPUBLICA DE COLOMBIA
Mabel Andrea Rodríguez D.
NOTARIA (E)
NOTARIA SEXTA DE BOGOTA

CAVELIER
ABOGADOS

EDIFICIO SISKI
CARRERA 4 No. 72 - 35
BOGOTA 8, COLOMBIA

WEB SITE: www.cavelier.com
E-MAIL: cavelier@cavelier.com

TELEFONO: (57) (1) 347-3611
TELEFAX: (57) (1) 217-9211 (57) (1) 310-4995

Señores

SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO

E. S. D.

Poderdante : AMGEN INC.

Poder conferido el : 24/02/2006

Yo, EMILIO FERRERO, obrando como apoderado principal del poderdante arriba mencionado, mediante el presente escrito sustituyo el poder a mi otorgado a la doctora LUZ CLEMENCIA DE PAEZ, identificada con cédula de ciudadanía No. 35.456.344 y Tarjeta Profesional N°23.555, con todas las facultades que me fueron conferidas.

Hago la anterior sustitución conforme al artículo 66 del Código de Procedimiento Civil.

EMILIO FERRERO
T.P.A. N° 31.929
C.C. N° 438.019 de Usaquén

Acepto:

LUZ CLEMENCIA DE PAEZ
T.P.A. N° 23.555
C.C. No. 35.456.344 de Usaquén

COMO NOTARIA SEXTA DEL CIRCULO DE BOGOT. D.C. HAGO CONSTAR QUE LA FOTOCOPIA COINCIDE CON EL ORIGINAL QUE HE TENIDO A LA VISTA
BOGOTA D.C. REPUBLICA DE COLOMBIA
22 ABR 2010
NOTARIO ENCARGADO
NOTARIA SEXTA DE BOGOTA D.C. REPUBLICA DE COLOMBIA
Mabel Andrea Rodrigu
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NOTARIA SEXTA DE BOGOTA

15193

NOTARIA SEXTA DE BOGOTA

RECONOCIMIENTO Y PRESENTACION PERSONAL

Bogotá, D.C. 03 NOV 2009

Ante mi **AMPARO QUINTERO ARTURO,**

NOTARIA SEXTA DEL CÍRCULO DE

BOGOTÁ, D.C.

Comparecio(eron) Emilio Ferrero Williamson

Luz Clemencia de Paez

Quien(es) exhibió(eron) la(s) C.C.

CC# 438.019 TP# 31929

CC# 35.456.344 TP# 23555

Y declaró(aron) que la(s) firma(s) que aparece(n) en el presente documento es(son) la(s) suya(s) y que el contenido del mismo es cierto.

En constancia se firma esta diligencia.

Emilio Ferrero

Luz Clemencia Sotelo Paez

REPÚBLICA DE COLOMBIA
Amparo Quintero Arturo
NOTARIA
NOTARÍA SEXTA DE BOGOTÁ

COMO NOTARIA SEXTA DEL CÍRCULO DE BOGOTÁ D.C. HAGO CONSTAR QUE LA FOTOCOPIA COINCIDE CON EL ORIGINAL QUE HE TENIDO A LA VISTA
BOGOTA D.C., REPÚBLICA DE COLOMBIA

22 ABR 2010

NOTARIO ENCARGADO

REPÚBLICA DE COLOMBIA
Mabel Andrea Rodríguez D.
NOTARIA (E)
NOTARÍA SEXTA DE BOGOTÁ

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International Bureau

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2 April 2009 (02.04.2009)

PCT

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A61K 39/395 (2006.01) *C07K 16/28* (2006.01)
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(71) Applicants *(for all designated States except US)*: **U3 PHARMA AG** [DE/DE]; Bunsenstrasse 1, 82152 Martinsried (DE). **AMGEN INC.** [US/US]; One Center Drive, Thousand Oaks, CA 91320-1799 (US).

(71) Applicant *(for US only)*: **ZWICK-WALLASCH, Esther** [DE/DE]; Frühlingsstrasse 112, 82131 Gauting (DE).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **ROTHE, Mike** [DE/DE]; Elisenstrasse 4, 82152 Krailing (DE). **PRENZEL, Norbert** [DE/DE]; Pentenriedderstr. 32, 82152 Krailing (DE). **BORGES, Eric** [DE/AT]; Roseggergasse 25, A-2344 Maria Enzersdorf (AT). **HETTMANN, Thore** [DE/DE]; Am Stadtpark 38D, 81243 München (DE).

(74) Agent: **WEICKMANN & WEICKMANN**; Postfach 860 820, 81635 Munich (DE).

(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

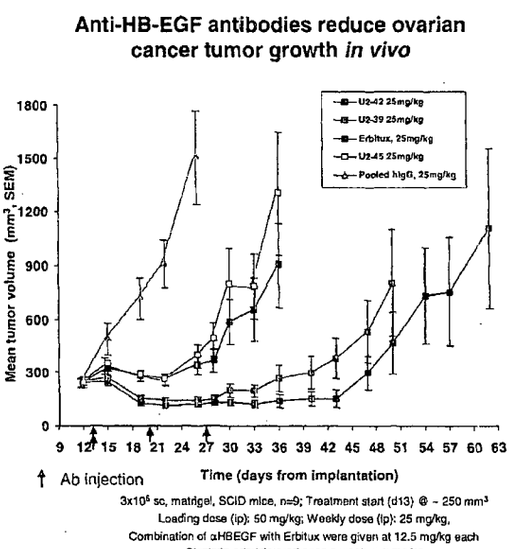
(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MT, NL, NO, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— *with international search report*

[Continued on next page]

(54) Title: HEPARIN-BINDING EPIDERMAL GROWTH FACTOR-LIKE GROWTH FACTOR ANTIGEN BINDING PROTEINS

Fig 38A



(57) Abstract: Provided herein are antigen binding proteins, e.g.,human and/or monoclonal antibodies that have affinity for heparin-binding epidermal growth factor-like growth factor (HB-EGF) and neutralize the biological functions of this growth factor.

WO 2009/040134 A1

— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments*

HEPARIN-BINDING EPIDERMAL GROWTH FACTOR-LIKE GROWTH FACTOR ANTIGEN BINDING PROTEINS

BACKGROUND

[0001]The human epidermal growth factor receptor (HER) family comprises four distinct receptor tyrosine kinases referred to as HER1 (or erbB1), HER2 (or erbB2), HER3 (or erbB3), and HER4 (or erbB4). HER1 is also commonly referred to as epidermal growth factor receptor (EGFR). With the exception of HER3, these receptors have phospho-acceptor target specific intrinsic protein tyrosine kinase activities. Members of the HER family are expressed in most epithelial cells as well as in a number of different tumor cell types. For example, receptors of the HER family are expressed in tumor cells of epithelial origin, and of mesenchymal origin. Moreover, HER receptor tyrosine kinases are involved in cell proliferation and angiogenesis, which are associated with diseases such as cancer. For example, EGFR is frequently over-expressed or aberrantly activated in breast cancers, liver cancers, kidney cancers, leukemia, bronchial cancers, pancreatic cancers and gastrointestinal cancers such as colon, rectal or stomach cancers. High levels of the EGF receptor also correlate with poor prognosis and response to treatment (Wright *et al.*, 1992, *Br. J. Cancer* 65:118-121). Thus, disruption of signal transduction from and to these kinases would have an anti-proliferative, and as such, therapeutic effect upon a number of cancer and tumor cell types.

[0002]The enzymatic activity of receptor tyrosine kinases can be stimulated by over-expression and/or by ligand-mediated dimerization (Heldin, 1995, *Cell* 80:213-223). Activation of receptor homodimers and heterodimers results in phosphorylation of tyrosine residues on the receptors, which in turn phosphorylate tyrosine residues of other molecules, including intracellular proteins. (Ullrich *et al.*, 1990, *Cell* 61:203-212). This is followed by the activation of intracellular signaling pathways such as those involving the mitogen-activated protein kinase (MAP kinase) (Dhillon et al., 2007, *Oncogene* 26: 3279-3290) and the phosphatidylinositol 3-kinase (PI3 kinase). While activation of these pathways has been shown to increase cell proliferation and inhibit apoptosis, inhibition of signaling mediated by HER family members by either small molecule inhibitors or monoclonal antibodies has been shown to inhibit cell proliferation and promote apoptosis (Prenzel *et al.*, 2001, *Endocr. Relat. Cancer* 8: 11-31)

[0003]Heparin-binding epidermal growth factor-like growth factor (HB-EGF) is a 22 kDa, O-glycosylated protein (Higahiyama *et al.*, 1992, *J Biol Chem* 267: 6205-6212). In its mature form, HB-EGF binds to and activates the EGF receptor and HER4 (Elenius et al., 1997, EMBO 16:1268-1278). HB-EGF is the key mediator of G-protein coupled receptor (GPCR) induced cell proliferation *via* a process called triple-membrane passing signaling (TMPS) (Prenzel *et al.*,

1999, *Nature* 402:884-888, review in Fischer *et al.* 2003, *Biochem. Soc. Trans.* 31:1203-1208). It has been shown that HB-EGF promotes cellular proliferation as well as angiogenesis (Zushi *et al.*, 1997, *Int J Cancer* 73:917-923; Abramovitch *et al.*, 1998, *FEBS letters* 425:441-447). HB-EGF also has been demonstrated to play a key role in a number of cancers, *i.e.*, it has been linked to the aggressive behavior of ovarian tumors (Tanaka *et al.*, 2005, *Clin. Cancer Res.* 11:4783-4792). Moreover, HB-EGF is essential for xenograft tumor formation by ovarian cancer cell lines. Over-expression of HB-EGF (*wild type* or a secreted form) accelerates tumor formation in SKOV3 and RMG-1 cells. Knockdown of endogenous HB-EGF using siRNA, yet, abolished or delayed tumor formation by SKOV3 and RMG-1 cells. Miyamoto, 2004, *Cancer Res.* 64:5720. As suggested by the above evidence, inhibition of HB-EGF expression or activity may inhibit tumor formation.

[0004]Similarly, HB-EGF is a marker of poor prognosis in some cancers, including human bladder cancers (Thogersen *et al.*, 2001, *Cancer Res.* 61:6227-6233). *In vitro* studies indicate that human EJ bladder cells that were engineered to express HB-EGF (*wild type*, soluble or non-cleavable) exhibit an increase in growth, anchorage independent growth, and production of VEGF, and enhanced migration. When these HB-EGF-expressing EJ bladder cells were transplanted into nude mice, an increase in tumor formation, size and density of blood vessels was observed in those tumors. (Ongusaha, 2004, *Cancer Res.* 64:5283-5290).

SUMMARY

[0005]Provided herein are isolated antigen binding proteins that bind HB-EGF. Some of these antigen binding proteins comprise A) one or more light chain complementary determining regions (CDRLs) consisting of: (i) a CDRL1 selected from SEQ ID NOs:**189-217**; (ii) a CDRL2 selected from from SEQ ID NOs:**218-233**; (iii) a CDRL3 selected from SEQ ID NO:**234-274**; or (iv) a CDRL of (i), (ii) or (iii) that contains one or more amino acid substitutions, deletions or insertions of no more than four amino acids. Alternatively, the HB-EGF antigen binding protein may comprise B) one or more heavy chain complementary determining regions (CDRHs) consisting of: (i) a CDRH1 selected from SEQ ID NO:**275-299**; (ii) a CDRH2 selected from SEQ ID NO:**300-331**; (iii) a CDRH3 selected from SEQ ID NO:**332-372**; or (iv) a CDRH of (i), (ii) or (iii) that contains one or more amino acid substitutions, deletions or insertions of no more than four amino acids.

[0006]In one embodiment, the isolated antigen binding protein may comprise one, two or more of the aforementioned light chain CDRLs and one, two or more of the aforementioned heavy chain CDRHs. In one aspect, the isolated antigen binding protein comprises CDRH1, CDRH2, CDRH3, CDRL1, CDRL2 and CDRL3. In another aspect, the isolated antigen binding protein of A), *supra*, is selected from the group consisting of: a CDRL1 from SEQ ID NOs:**189-217**; a CDRL2 from SEQ ID NOs:**218-233**; a CDRL3 from SEQ ID NOs:**234-274**; and a CDRL of the

any of the aforementioned (i), (ii) or (ii) that contains one or more amino acid substitutions, deletions or insertions of no more than two amino acids. In addition, said heavy chain CDRH of B), *supra*, is selected from a CDRH1 from SEQ ID NOs:**275-299**; a CDRH2 from SEQ ID NOs:**300-331**; a CDRH3 amino acid sequence from SEQ ID NOs:**332-372** and a CDRH of the aforementioned that contains one or more amino acid substitutions, deletions or insertions of no more than two amino acids. Furthermore, the isolated antigen binding protein may comprise or one or more light chain CDRLs of A), *supra*; and one or more heavy chain CDRHs of B), *supra*.

[0007]In another embodiment, the antigen binding protein comprises a CDRL selected from the following: a CDRL1 from SEQ ID NOs:**189-217**; a CDRL2 from SEQ ID NOs:**218-233**; and a CDRL3 from SEQ ID NOs:**234-274**. The antigen binding protein may also comprise a CDRH selected from one of the following: a CDRH1 from SEQ ID NOs:**275-299**; a CDRH2 from SEQ ID NOs:**300-331**; and a CDRH3 selected from SEQ ID NOs:**332-372**. Alternatively, the isolated antigen binding protein may comprise one or more light chain CDRLs listed in A), *supra*, and one or more heavy chain CDRHs of B), *supra*. In particular, the isolated antigen binding protein may comprise a CDRL1 of SEQ ID NOs:**189-217**, a CDRL2 of SEQ ID NOs:**218-233**, and a CDRL3 of SEQ ID NOs:**234-274** and/or a CDRH1 of SEQ ID NOs:**275-299**, a CDRH2 of SEQ ID NOs:**300-331**, and a CDRH3 of SEQ ID NO:**332-372**.

[0008]In one aspect, the isolated antigen binding protein comprises a light chain variable region (V_L) having at least 80%, 90% or 100% sequence identity with an amino acid sequence selected from SEQ ID NOs:**94-141**. In another aspect, the isolated antigen binding protein comprises a heavy chain variable region (V_H) having at least 80%, 90% or 100% sequence identity with an amino acid sequence from SEQ ID NOs:**142-186**.

[0009]In another embodiment, the isolated antigen binding protein specifically recognizes at least an IHGE containing epitope and/or an EGF-like domain of HB-EGF.

[00010]Provided herein, in addition, is an isolated antigen binding protein that competes for binding with the isolated antigen binding protein that binds HB-EGF, as described above.

[00011]Also provided herein is an isolated antigen binding protein which binds HB-EGF and comprises A) one or more light chain CDRs (CDRLs) from the group consisting of: (i) a CDRL1 with at least 80%, or at least 90% sequence identity to SEQ ID NOs:**189-217**; (ii) a CDRL2 with at least 80%, or at least 90% sequence identity to SEQ ID NOs:**218-233**; and (iii) a CDRL3 with at least 80%, or at least 90% sequence identity to SEQ ID NOs:**234-274**. Alternatively, the isolated antigen binding protein which binds HB-EGF, comprises B) one or more heavy chain CDRs (CDRHs) from the group consisting of (i) a CDRH1 with at least 80%, or at least 90% sequence identity to SEQ ID NOs:**275-299**; (ii) a CDRH2 with at least 80%, or at least 90% sequence identity to SEQ ID NOs:**300-331**; and (iii) a CDRH3 with at least 80%, or at least 90%

sequence identity to SEQ ID NOs:**332-372**. The isolated antigen binding protein may also comprise C) one or more light chain CDRLs of A) and one or more heavy chain CDRHs of B).

[00012]In another embodiment, the isolated antigen binding protein binds HB-EGF and comprises: A) a light chain complementary determining region (CDRL) selected from: (i) a CDRL3 selected from the group consisting of SEQ ID NOs:**234-274**; (ii) a CDRL3 that differs in amino acid sequence from the CDRL3 of (i) by an amino acid addition, deletion or substitution of not more than two amino acids; and (iii) a CDRL3 amino acid sequence selected from the following:

$X_1QX_2X_3X_4X_5PX_6X_7$ (SEQ ID NO:1046), wherein

X_1 is I or M,

X_2 is A, G or S,

X_3 is I or T,

X_4 is H or Q,

X_5 is F, L or W,

X_6 is C, I, H, L or T,

X_7 is S or T;

$QQX_1X_2X_3X_4X_5IT$ (SEQ ID NO:1047), wherein

X_1 is I or S,

X_2 is F or Y,

X_3 is F, I, S or Y,

X_4 is A, S or T,

X_5 is P or S;

$X_1X_2X_3X_4X_5X_6X_7X_8T$ (SEQ ID NO:1048), wherein

X_1 is L or Q,

X_2 is K, N or Q,

X_3 is A, H, S or Y,

X_4 is H, N or Y,

X_5 is N, S or T,

X_6 is A, F, I, T, V or Y,

X_7 is P or no amino acid,

X_8 is F, L or P;

$QX_1X_2DX_3LPX_4X_5$ (SEQ ID NO:1049), wherein

X_1 is H or Q,

X_2 is C or Y,

X_3 is D, I, N, S or Y,

X_4 is F, I or L,

X_5 is A, S or T;

$QQX_1X_2X_3X_4PX_5X_6X_7$ (SEQ ID NO:1050), wherein

X_1 is H or Y,

X_2 is G or N,

X_3 is N or S,

X_4 is S or W,

X_5 is P or no amino acid,

X_6 is R or W,

X_7 is S or T; or

$X_1QYX_2X_3X_4X_5X_6X_7F$ (SEQ ID NO:1051), wherein

X_1 is H or Q,

X_2 is F or Y,

X_3 is G, I or S,

X_4 is F, I or T,

X_5 is M, P, S or T,

X_6 is F, L, R or W,

X_7 is S or T.

[00013]The isolated antigen binding protein may also comprise B) a heavy chain complementary determining region (CDRH) selected from the group consisting of: (i) a CDRH3 selected from the group consisting of SEQ ID NOs:**332-372**; (ii) a CDRH3 that differs in amino acid sequence from the CDRH3 of (i) by an amino acid addition, deletion or substitution of not more than two amino acids; and iii) a CDRH3 amino acid sequence selected from the following:

$X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}DX_{12}$ (SEQ ID NO:1065), wherein

X_1 is E or S,

X_2 is D, G or no amino acid,

X_3 is D, N or no amino acid,

X_4 is G or no amino acid,

X_5 is G or no amino acid,

X_6 is W, Y or no amino acid,

X_7 is I, N or Y,

X_8 is A or Y,

X_9 is G, V or Y,

X_{10} is A, F or G,

X_{11} is F, L or M,

X_{12} is V or Y;

$QX_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}YX_{12}X_{13}X_{14}DX_{15}$ (SEQ ID NO:1066), wherein

X_1 is G or no amino acid,
X_2 is K, L or Y,
X_3 is A, G or S,
X_4 is S, V or Y,
X_5 is A or G,
X_6 is G or no amino acid,
X_7 is T or no amino acid,
X_8 is S or no amino acid,
X_9 is Y or no amino acid,
X_{10} is W or Y,
X_{11} is G, S or Y,
X_{12} is F or Y,
X_{13} is G or no amino acid,
X_{14} is M or no amino acid,
X_{15} is V or Y;

$X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}$ (SEQ ID NO:1067), wherein
X_1 is D, G, L, S or no amino acid,
X_2 is G, H, W, Y or no amino acid,
X_3 is A, F, W, Y or no amino acid,
X_4 is D, G, Q, T or no amino acid,
X_5 is G, I, Q, S or no amino acid,
X_6 is A, D, N, Q, S or no amino acid,
X_7 is G, Y or no amino acid,
X_8 is D, Y or no amino acid,
X_9 is Y or no amino acid,
X_{10} is A, E, N or Y,
X_{11} is G, P, T, V or Y,
X_{12} is F or I,
X_{13} is D or Q,
X_{14} is C, H, V or Y;

$X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}DX_{18}$ (SEQ ID NO:1068), wherein
X_1 is E, D or no amino acid,
X_2 is G, R or no amino acid,
X_3 is I, V, Y or no amino acid,
X_4 is A, G, L or N,
X_5 is A, G, V or W,

X_6 is A, N, R or T,

X_7 is G, N, P or no amino acid,

X_8 is G, T or no amino acid,

X_9 is A or no amino acid,

X_{10} is D, E or no amino acid,

X_{11} is S, Y or no amino acid,

X_{12} is G, Y or no amino acid,

X_{13} is N, Y or no amino acid,

X_{14} is Y or no amino acid,

X_{15} is D, Y or no amino acid,

X_{16} is A, G or no amino acid,

X_{17} is F or M,

X_{18} is I, V or Y;

$X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}X_{18}X_{19}X_{20}X_{21}X_{22}X_{23}$ (SEQ ID NO:1069), wherein

X_1 is A, D, G, S or T,

X_2 is A, E, G, L, N, R, Y or no amino acid,

X_3 is A, G, L, N, R, T, Y or no amino acid,

X_4 is D, G, R, S, V, Y or no amino acid,

X_5 is A, G, I, S, V, Y or no amino acid,

X_6 is F, G, L, R, V or no amino acid,

X_7 is L, T, Y or no amino acid,

X_8 is Y or no amino acid,

X_9 is Y or no amino acid,

X_{10} is D or no amino acid,

X_{11} is S or no amino acid,

X_{12} is S or no amino acid,

X_{13} is G or no amino acid,

X_{14} is D, L, M, S, Y or no amino acid,

X_{15} is H, I, P, V, W or no amino acid,

X_{16} is F, G, L, R, S, Y or no amino acid,

X_{17} is D, F, V, W, Y or no amino acid,

X_{18} is C, F, L, P, S or Y,

X_{19} is D, F, G or Y,

X_{20} is A, C, G, P, R, V or Y,

X_{21} is F, L, M, S or no amino acid,

X_{22} is A, D or no amino acid,

X_{23} is I, L, V, Y or no amino acid;

$X_1YSSGWX_2X_3YGX_4X_5DX_6$ (SEQ ID NO:1070), wherein

X_1 is M or V,

X_2 is S or no amino acid,

X_3 is F or no amino acid,

X_4 is V or no amino acid,

X_5 is F or M,

X_6 is V or Y; or

$RX_1X_2X_3PFX_4Y$ (SEQ ID NO:1071), wherein

X_1 is G, H, L, N or R,

X_2 is E, T or W,

X_3 is L, N, T or V,

X_4 is D or E.

[00014]In another aspect, the isolated antigen binding protein may further comprise A) a CDRL selected from: (i) a CDRL1 selected from SEQ ID NOs:**189-217**; (ii) a CDRL1 that differs in amino acid sequence from the CDRH1 of (i) by an amino acid addition, deletion or substitution of not more than two amino acids; or (iii) a CDRL1 amino acid sequence from the following:

$X_1SSQSLX_2X_3SDGX_4TYLX_5$ (SEQ ID NO:1035), wherein

X_1 is K or R,

X_2 is L or V,

X_3 is H or Y,

X_4 is K or N,

X_5 is N, S or Y;

$RASQX_1ISX_2YLN$ (SEQ ID NO:1036), wherein

X_1 is R, S or T,

X_2 is R or S;

$RASQX_1IX_2X_3X_4LX_5$ (SEQ ID NO:1037), wherein

X_1 is D, G, S or T,

X_2 is A, R or S,

X_3 is H, I, N, R, S or T,

X_4 is D, W or Y,

X_5 is A, G or N;

$QASQDIX_1X_2X_3LN$ (SEQ ID NO:1038), wherein

X_1 is S or T,

X_2 is D or N,

X_3 is S or Y;

$RASQX_1VX_2X_3X_4X_5LA$ (SEQ ID NO:1039), wherein

X_1 is S or T,

X_2 is I or S,

X_3 is R or S,

X_4 is S, N or no amino acid,

X_5 is Y or no amino acid; or

$KSSQX_1X_2LX_3X_4SNNKNYLX_5$ (SEQ ID NO:1040), wherein

X_1 is N or S,

X_2 is I or V,

X_3 is D or Y,

X_4 is N, R or S,

X_5 is A or V;

(iv) a CDRL2 from the group consisting of SEQ ID NOs:**218-233**; (v) a CDRL2 that differs in amino acid sequence from the CDRL2 of (iv) by an amino acid addition, deletion or substitution of not more than two amino acids; or (vi) a CDRL2 amino acid sequence from the following:

$X_1X_2SNX_3X_4S$ (SEQ ID NO:1041), wherein

X_1 is E or K,

X_2 is I or V,

X_3 is R or W,

X_4 is D or F;

$X_1X_2SX_3LQS$ (SEQ ID NO:1042), wherein

X_1 is A or T,

X_2 is A, E or V,

X_3 is S or T;

X_1ASX_2LQS (SEQ ID NO:1043), wherein

X_1 is A or V,

X_2 is S or T;

$DASX_1LET$ (SEQ ID NO:1044), wherein

X_1 is I or N;

GASSRAT (SEQ ID NO:223); or

$WASX_1RES$ (SEQ ID NO:1045), wherein

X_1 is A or T.

[00015]The isolated antigen binding proteins may further comprise B) a CDRH from the group consisting of: (i) a CDRH1 from the group consisting of SEQ ID NOs:**275-299**; (ii) a CDRH1 that differs in amino acid sequence from the CDRH1 of (i) by an amino acid addition, deletion or substitution of not more than two amino acids; (iii) a CDRH1 amino acid sequence selected from:

$GYTX_1TX_2X_3X_4X_5X_6$ (SEQ ID NO:1052), wherein

X_1 is F or L,

X_2 is E, G or S,

X_3 is H, L or Y,

X_4 is G, S or Y,

X_5 is I or M,

X_6 is H or S;

$GYX_1FTSYWIG$ (SEQ ID NO:1053), wherein

X_1 is R or S;

$GFTFX_1SX_2X_3MH$ (SEQ ID NO:1054), wherein

X_1 is R or S,

X_2 is H or Y,

X_3 is D or G;

$GFX_1FSX_2YX_3MX_4$ (SEQ ID NO:1055), wherein

X_1 is P or T,

X_2 is A, R or S,

X_3 is A or S,

X_4 is N or S;

$GX_1SX_2SX_3X_4X_5X_6X_7WX_8$ (SEQ ID NO:1056), wherein

X_1 is D or G,

X_2 is F, I or V,

X_3 is R, S or no amino acid,

X_4 is G, Y or no amino acid,

X_5 is D, G, S or no amino acid,

X_6 is A, S or Y,

X_7 is A or Y,

X_8 is N or S;

GFSLSNARMGVS (SEQ ID NO:279); or

$GFSLX_1TGGVGVG$ (SEQ ID NO:1057), wherein

X_1 is S or N;

[00016](iv) a CDRH2 selected from the group consisting of SEQ ID NOs:**300-331**; (v) a CDRH2 that differs in amino acid sequence from the CDRH2 of (iv) by an amino acid addition, deletion or substitution of not more than two amino acids; or (vi) a CDRH2 amino acid sequence from the following:

$X_1X_2X_3X_4X_5X_6GX_7TX_8X_9X_{10}QKX_{11}X_{12}$ (SEQ ID NO:1058), wherein

X_1 is S or W,

X_2 is F or I,

X_3 is D, N or S,

X_4 is A or P,

X_5 is E, N or S,

X_6 is D, N or S,

X_7 is E, G or N,

X_8 is I or N,

X_9 is C, H or Y,

X_{10} is A or T,

X_{11} is F or L,

X_{12} is D or G;

IIYPX_1DSDX_2RYSPSFQG (SEQ ID NO:1059), wherein

X_1 is D or G,

X_2 is A, I or T;

X_1IX_2X_3DGS$X_4X_5X_6$YX_7DSVX_8G (SEQ ID NO:1060), wherein

X_1 is F or V,

X_2 is S or W,

X_3 is D, S or Y,

X_4 is I, N or T,

X_5 is K or Q,

X_6 is N, R or Y,

X_7 is A, T or V,

X_8 is K or R;

X_1ISX_2S$X_3X_4X_5X_6$YYADSVKG (SEQ ID NO:1061), wherein

X_1 is A, H or Y,

X_2 is G, R or S,

X_3 is G or S,

X_4 is G, R or S,

X_5 is S, T or Y,

X_6 is I or T;

$X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}YX_{12}X_{13}SX_{14}KS$ (SEQ ID NO:1062), wherein

X_1 is E, R or Y,

X_2 is I or T,

X_3 is H, N or Y,

X_4 is C, H, S, T or Y,

X_5 is S or R,

X_6 is G or S,

X_7 is G, K, S or T,

X_8 is T or W,

X_9 is N or Y,

X_{10} is N or no amino acid,

X_{11} is D or no amino acid,

X_{12} is A or N,

X_{13} is P or V,

X_{14} is L or V;

X_1IFSNDEKSYSTSLKS (SEQ ID NO:1063), wherein

X_1 is H or LI; or

LIYWNX_1X_2KRYSPSLX_3S (SEQ ID NO:1064), wherein

X_1 is D or V,

X_2 is D or E,

X_3 is K or R.

[00017]In yet another embodiment, the isolated antigen binding protein described hereinabove comprises the first amino acid sequence and the second amino acid sequence, both sequences of which are covalently bonded to each other. The first amino acid sequence also comprises CDRL3 of SEQ ID NOs:**234-274**, CDRL2 of SEQ ID NOs:**218-233**, and CDRL1 of SEQ ID NOs:**189-217**, and the second amino acid sequence comprises said CDRH3 of SEQ ID NOs:**332-372**, CDRH2 of SEQ ID NOs:**300-331**, and CDRH1 of SEQ ID NOs:**275-299**.

[00018]In one aspect, the isolated antigen binding proteins can be a monoclonal antibody, a polyclonal antibody, a recombinant antibody, a human antibody, a humanized antibody, a chimeric antibody, a multispecific antibody, or an antibody fragment thereof. The antibody fragment may be a Fab fragment, a Fab' fragment, a $F(ab')_2$ fragment, a Fv fragment, a diabody, or a single chain antibody molecule. In one embodiment, the isolated antigen binding protein of the present invention is a human antibody. In another embodiment, the isolated antigen binding protein is a monoclonal antibody.

[00019]The isolated antigen binding proteins as described herein, may be of any of the following types: IgG1-, IgG2- IgG3- or IgG4-type. In one embodiment, the antigen binding protein is of

the IgG2- or IgG4- type. Furthermore, the antigen binding protein may be coupled to a labeling group. These labeling groups may be, for example, a radioisotope, radionuclide, a fluorescent group, an enzymatic group, a chemiluminescent group, a biotinyl group, or a predetermined polypeptide group.

[00020]In another embodiment, the isolated antigen binding protein is coupled to an effector group such as, for example, a radioisotope, a radionuclide, a toxin, a therapeutic group, or a chemotherapeutic group. The chemotherapeutic groups may be, for example, calicheamicin, auristatin-PE, geldanamycin, maytanasine, or derivatives thereof.

[00021]In yet another embodiment, the isolated antigen binding protein competes for binding to human HB-EGF with a antigen binding protein as described and claimed herein. This competing antigen binding protein may be, for example, a monoclonal antibody, a polyclonal antibody, a recombinant antibody, a human antibody, a humanized antibody, a chimeric antibody, a multispecific antibody, or an antibody fragment thereof. The antibody fragment may be, for example, a Fab fragment, a Fab' fragment, a $F(ab')_2$ fragment, a Fv fragment, a diabody, or a single chain antibody molecule. In one embodiment, the isolated binding protein is a human antibody. In another embodiment, the isolated antigen binding protein is a monoclonal antibody. In another embodiment, this isolated antigen binding protein is of the IgG1-, IgG2- IgG3- or IgG4-type. In one embodiment, the antigen binding protein is of the IgG2- or IgG4- type. In another embodiment, the antigen binding proteins as described herein can be coupled to a labeling group. Examples of labeling groups are: a radioisotope, radionuclide, a fluorescent group, an enzymatic group, a chemiluminescent group, a biotinyl group, or a predetermined polypeptide group. In another embodiment, the isolated antigen binding protein is coupled to an effector group such as, for example, a radioisotope, a radionuclide, a toxin, a therapeutic group, or a chemotherapeutic group. Examples of the therapeutic or chemotherapeutic groups include, for example, calicheamicin, auristatin-PE, geldanamycin, maytanasine, or derivatives thereof.

[00022]In one aspect, an isolated antigen binding protein is provided that reduces, at least partially, HB-EGF-mediated signal transduction.

[00023]Also presented herein is a nucleic acid molecule encoding the isolated antigen binding protein previously described, wherein the nucleic acid molecule is operably linked to a control sequence. In one aspect, a vector comprising the aforementioned nucleic acid molecule is provided. In another aspect, a host cell is provided that comprises the aforementioned nucleic acid molecule and/or vector.

[00024]In one embodiment, a method for making the antigen binding protein is provided that includes the step of preparing said antigen binding protein from a host cell that secretes said antigen binding protein.

[00025]In yet another embodiment, a pharmaceutical composition is provided comprising at least one of the aforementioned antigen binding proteins of the present invention and a pharmaceutically acceptable carrier, diluent or adjuvant. In one embodiment, the pharmaceutical composition may comprise an additional active agent, such as an anti-neoplastic agent. The anti-neoplastic agent may be, for example, an anti-tumor antibody. Examples of an anti-tumor antibody may be, for example, antibodies directed against receptor tyrosine kinase or EGFR.

[00026]In one aspect, the pharmaceutical composition is used for diagnosis, prevention or treatment of a hyperproliferative disease. In a further aspect, the hyperproliferative disease is associated with HB-EGF expression. In another aspect, the hyperproliferative disease is associated with or accompanied by a disturbed, (*e.g.*pathologically enhanced), growth factor receptor activation, wherein said pathologically enhanced growth factor receptor activation is associated with or caused by a pathological increase in the activity of a G protein and/or a G protein coupled receptor.

[00027]In one embodiment, the pharmaceutical composition comprises at least one antigen binding protein and pharmaceutically acceptable carrier, diluents and/or adjuvants for the diagnosis, prevention or treatment of cancer, such as, for example, breast cancer, gastrointestinal cancer, pancreas cancer, prostate cancer, ovarian cancer, stomach cancer, endometrial cancer, salivary gland cancer, lung cancer, kidney cancer, colon cancer, colorectal cancer, thyroid cancer, bladder cancer, glioma, melanoma, other HB-EGF expressing or overexpressing cancers, and formation of tumor metastases.

[00028]In another embodiment, antigen binding proteins as described herein are used for the manufacture of a pharmaceutical composition for the diagnosis, prevention or treatment of a hyperproliferative disease. In a further embodiment, the hyperproliferative disease is associated with HB-EGF expression.

[00029]One embodiment describes a method for diagnosing a condition associated with the expression of HB-EGF, the method comprising the step of contacting a sample an isolated antigen binding proteins as described herein, and determining the presence of HB-EGF in said sample. In a further embodiment, the condition is a hyperproliferative disease associated with HB-EGF expression.

[00030]Another aspect describes a method for preventing or treating a condition associated with the expression of HB-EGF in a patient, comprising administering to a patient in need thereof an effective amount of a antigen binding protein as described herein. In a further aspect, the condition is a hyperproliferative disease associated with HB-EGF expression. In yet another aspect, the patient is a mammalian patient.

[00031]In one embodiment, a kit is provided that comprises a antigen binding protein, a nucleic acid molecule, or a vector as described above. In a further embodiment, the kit comprises at least one further active agent, wherein the further active agent is an anti-neoplastic agent.

[00032]These and other aspects of the invention will be described in greater detail herein. Each of the aspects of the invention can encompass various embodiment of the present invention. It is therefore anticipated that each of the embodiments of the invention involving one element or combinations of elements can be included in each aspect of the invention. Other features, objects, and advantages of the present invention are apparent in the detailed description that follows.

DESCRIPTION OF THE FIGURES

[00033]FIGURES 1A-1P depict various light chain variable regions of the antigen binding proteins. The CDR1, CDR2 and CDR3 regions are indicated in boxes.

[00034]FIGURES 2A-2O depict various heavy chain variable regions of the antigen binding proteins. The CDR1, CDR2 and CDR3 regions are indicated in boxes.

[00035]FIGURES 3A-3K depict the amino acid sequences of various light chains of the antigen binding proteins.

[00036]FIGURES 4A-4O depict the amino acid sequences of various heavy chains of the antigen binding proteins.

[00037]FIGURE 5A depicts the amino acid sequence of an exemplary light chain constant region of the antigen binding proteins.

[00038]FIGURE 5B depicts the amino acid sequence of an exemplary heavy chain constant region of the antigen binding proteins.

[00039]FIGURES 6A-6F depict the amino acid sequences for various CDR regions of the light chain variable regions of the antigen binding proteins.

[00040]FIGURES 7A-7E depict the amino acid sequences for various CDR regions of the heavy chain variable regions of the antigen binding proteins.

[00041]FIGURES 8A-8H depict the amino acid sequences for various FR regions of the light chain variable regions of the antigen binding proteins.

[00042]FIGURES 9A-9F depict the amino acid sequences for various FR regions of the heavy chain variable regions of the antigen binding proteins.

[00043]FIGURES 10A and 10B depict an alignment of the amino acid sequences of the light chain variable sequences of the antigen binding proteins. The CDR1, CDR2 and CDR3 regions are shown in boxes.

[00044]FIGURES 11A and 11B depict an alignment of the amino acid sequences of the heavy chain variable sequences of the antigen binding proteins. The CDR1, CDR2 and CDR3 regions are shown in boxes.

[00045]FIGURE 12A depicts a cladogram showing the relatedness of the light chain variable regions of the antigen binding proteins.

[00046]FIGURE 12B depicts a cladogram showing the relatedness of the light chain CDRL3 regions of the antigen binding proteins.

[00047]FIGURE 12C depicts a cladogram showing the relatedness of the heavy chain variable regions of the antigen binding proteins.

[00048]FIGURES 13A-13V depict the nucleotide sequences of various light chain variable regions of the antigen binding proteins.

[00049]FIGURES 14A-14AC depict the nucleotide sequences of various heavy chain variable regions of the antigen binding proteins.

[00050]FIGURES 15A-15M depict the nucleotide sequences of the various light chains of the antigen binding proteins.

[00051]FIGURES 16A-16L depict the nucleotide sequences of the various heavy chains of the antigen binding proteins.

[00052]FIGURE 17A depicts the nucleotide sequence of the light chain constant region of the antigen binding proteins.

[00053]FIGURE 17B depicts the nucleotide sequence of the heavy chain constant region of the antigen binding proteins.

[00054]FIGURES 18A-18F depict the nucleotide sequences for various CDR regions of the light chain variable regions of the antigen binding proteins.

[00055]FIGURES 19A-19G depict the nucleotide sequences for various CDR regions of the heavy chain variable regions of the antigen binding proteins.

[00056]FIGURES 20A-20K depict the nucleotide sequences for various FR regions of the light chain variable regions of the antigen binding proteins.

[00057]FIGURES 21A-21K depict the nucleotide sequences for various FR regions of the heavy chain variable regions of the antigen binding proteins.

[00058]FIGURE 22A graphically illustrates the degree to which different anti-HB-EGF IgG2 antibody preparations provided herein inhibit HB-EGF-induced epidermal growth factor receptor (EGFR) tyrosine phosphorylation. The results for preparations of antibodies U2-1 to U2-68 are provided. As illustrated, monoclonal antibody preparations U2-18, U2-24, U2-19 and U2-42 strongly inhibit EGFR tyrosine phosphorylation.

[00059]FIGURE 22B graphically illustrates the degree to which different anti-HB-EGF IgG4 antibody preparations provided herein inhibit HB-EGF-induced epidermal growth factor receptor (EGFR) tyrosine phosphorylation. The results for preparations of antibodies U2-2 to U2-66 are provided. As illustrated, monoclonal antibody preparations U2-39, U2-34, U2-45 and U2-6 strongly inhibit EGFR tyrosine phosphorylation.

[00060]FIGURE 23 illustrates that the antibodies inhibit lysophosphatidic acid (LPA)-induced EGFR tyrosine phosphorylation in COS-7 cells. LPA is a GPCR ligand that activates the TMPS pathway, resulting in release of HB-EGF with consequent EGFR tyrosine phosphorylation. COS-7 cells were pretreated with antibodies as indicated and stimulated with LPA, then cell lysates were prepared and lysate proteins were separated by polyacrylamide gel electrophoresis. After preparation of the blot, an anti-phosphotyrosine antibody was used to detect phosphorylated EGFR. As a control, total EGFR was detected as shown at the bottom, using a WB anti-EGFR antibody. As illustrated, anti-HB-EGF antibody preparations U2-24, U2-19 and U2-42 strongly inhibit LPA-induced EGFR phosphorylation.

[00061]FIGURE 24 graphically illustrates dose-dependent inhibition of HB-EGF-induced EGF receptor tyrosine phosphorylation by various antibodies provided herein. Different concentrations of the candidate U2-39, U2-42 and U2-45 antibody preparations were preincubated with HB-EGF prior to stimulation of SCC9 squamous cancer cells and the amount of EGFR tyrosine phosphorylation was detected. As shown, antibody U2-42 and U2-39 achieved up to 111% inhibition. IC50 values determined for the antibodies were 0.167 nM (U2-39), 1 nM (U2-42) and 2 nM (U2-45), respectively.

[00062]FIGURE 25 graphically illustrates dose-dependent inhibition of thrombin-induced EGFR phosphorylation *via* TMPS in MDA-MB231 cells by anti-HB-EGF antibody preparations. MDA-MB231 cells were incubated with candidate U2-42, U2-39 and U2-45 antibody preparations in the presence of thrombin and the amount of EGFR tyrosine phosphorylation was detected using a procedure described in Example 6. As shown, antibodies U2-42 and U2-39 achieving 100% inhibition.

[00063]FIGURE 26 illustrates dose-dependent inhibition of LPA-induced EGFR tyrosine phosphorylation *via* TMPS in PPC-1 cells by anti-HB-EGF antibody preparations. PPC-1 cells were incubated with candidate U2-42, U2-39 and U2-45 antibody preparations and the amount of EGFR tyrosine phosphorylation following LPA stimulation was detected using a procedure described in Example 4. As shown, antibodies U2-42, U2-39 and U2-45 achieved 100% inhibition.

[00064]FIGURE 27 illustrates that anti-HB-EGF antibody preparations inhibited by up to 100% the induction of MDA-MB231 breast cancer cell migration by sphingosine-1-phosphate. Candidate anti-HB-EGF antibody preparations U2-42, U2-39 and U2-45 were tested for cell migration inhibition using of collagen I-coated transwells (BD Falcon, 8 μm pores). As shown, anti-HB-EGF antibody preparation U2-42 inhibited sphingosine-1-phosphate-induced MDA-MB231 cell migration by about 70% while the U2-39 and U2-45 anti-HB-EGF antibody preparations inhibited MDA-MB231 cell migration by about 100%. Thus, the anti-HB-EGF antibodies provided herein strongly inhibit MDA-MB231 cell migration.

[00065]FIGURE 28 graphically illustrates that HB-EGF-induced migration of MCF-7 breast cancer cells is inhibited by three anti-HB-EGF antibody preparations (the U2-42, the U2-39 and the U2-45 monoclonal antibody preparations).

[00066]FIGURE 29 illustrates the dose-dependent inhibition of HB-EGF-induced tyrosine phosphorylation of HER4 by anti-HB-EGF antibody preparations. U2-42.1 or U2-39.1 anti-HB-EGF antibody preparations were incubated with HB-EGF prior to stimulation and detection of HER4 tyrosine phosphorylation. As shown, 100% inhibition of HER4 tyrosine phosphorylation was observed. Note that the amount of antibody shown on the x-axis decreases logarithmically.

[00067]FIGURE 30A shows that monoclonal antibody preparations cross-react with HB-EGF from cynomolgus monkeys as assessed by flow cytometry (FACS) using HEK-293 cells transfected with a DNA vector expressing cynomolgus HB-EGF. As shown, very low X-mean values (1-2) are observed for HEK-293 control cells that were transfected with an empty vector control. In contrast, X-mean values of 250 or more were observed when HEK-293 cells were transfected with an expression cassette encoding cynomolgus monkey HB-EGF.

[00068]FIGURE 30B shows that monoclonal antibody U2-45 preparation cross-reacts with HB-EGF from mouse as assessed by flow cytometry (FACS) using HEK-293 cells transfected with a DNA vector expressing mouse HB-EGF. X-mean values of 33.7 were observed when HEK-293 cells were transfected with an expression cassette encoding mouse HB-EGF.

[00069]FIGURE 30C shows the degree of cross-reactivity of HB-EGF antibodies with amphiregulin.

[00070]FIGURE 31 shows that HB-EGF is expressed on human vascular endothelial cells (HUVECs), as detected by FACS analysis.

[00071]FIGURES 32A - 32B show that while HB-EGF stimulates HUVEC cellular proliferation, anti-HB-EGF antibody preparations inhibited basal proliferation by about 8% to 14%. HB-EGF stimulates HUVEC cellular proliferation by about 38% (FIGURE 32A). However, upon addition of anti-HB-EGF antibody preparations U2-42, U2-39 or U2-45, basal cellular proliferation is inhibited by about 8% to 14% (FIGURE 32B).

[00072]FIGURES 33A-33L illustrate that anti-HB-EGF antibodies accelerate HUVEC tube regression. HUVEC tube formation is a model system for endothelial cell angiogenesis. FIGURES 33A-33C provide control assays that were performed without anti-HB-EGF antibodies. As shown, HUVEC cells join to form many circular structures or "tubes." FIGURES 33D-33F illustrate the effects of adding the anti-HB-EGF U2-39 antibody preparation upon tube formation. FIGURES 33G-33I illustrate the effects of adding the anti-HB-EGF U2-42 antibody preparation upon tube formation. FIGURES 33J-33L illustrate the effects of adding the anti-HB-EGF U2-45 antibody preparation upon tube formation. As shown, fewer HUVEC tubes are visible and the

network is diminished when the U2-42, U2-39 and U2-45 anti-HB-EGF antibody preparations are present.

[00073]FIGURE 33M graphically illustrates a quantitative evaluation of HUVEC tube formation after adding the anti-HB-EGF antibody preparations provided herein, supporting the utility of HB-EGF antibodies for inhibiting angiogenesis. The number of tubes or closed cell structures per microscopic field is plotted for the U2-42, U2-39 or U2-45 anti-HB-EGF antibody preparations. As shown, while approximately 10 HUVEC tubes were visible per field when no anti-HB-EGF antibodies were present, only about 4 HUVEC tubes were observed per microscopic field when the U2-39 anti-HB-EGF antibody preparation was added. In the presence of the U2-42 anti-HB-EGF antibody preparation only about 1 HUVEC tube was observed. When the U2-45 anti-HB-EGF antibody preparation was present only 6 HUVEC tubes were observed.

[00074]FIGURE 34A illustrates that anti-HB-EGF antibodies inhibit HB-EGF-stimulated colony formation of OVCAR-8 ovarian cancer cells. As shown, HB-EGF stimulated OVCAR-8 cells to form a significantly larger mean colony size than control OVCAR-8 cells cultured without HB-EGF. However, when OVCAR-8 cells were cultured with anti-HB-EGF U2-39 antibodies in the presence of HB-EGF, mean colony size was reduced to the baseline size observed for control cells without HB-EGF treatment.

[00075]FIGURE 34B illustrates that anti-HB-EGF antibodies inhibit HB-EGF-stimulated colony formation of BM1604 prostate cancer cells in soft agar. As shown, HB-EGF stimulated BM1604 cells to form a larger number of colonies per well than control BM1604 cells cultured without HB-EGF. However, when BM1604 cells were cultured with anti-HB-EGF U2-39 antibodies in the presence of HB-EGF, mean colony size was reduced to a size similar to that observed for control cells without HB-EGF treatment. Anti-HB-EGF U2-45 and U2-42 antibodies partially inhibited colony formation, while, in this assay, the U2-39 anti-HB-EGF antibody completely inhibited colony formation.

[00076]FIGURE 34C illustrates that anti-HB-EGF antibodies inhibit HB-EGF-stimulated colony formation of NCI-H226 lung carcinoma cells. As shown, HB-EGF stimulated NCI-H226 cells to form a significantly larger mean colony size than control NCI-H226 cells cultured without HB-EGF. However, when NCI-H226 cells were cultured with anti-HB-EGF U2-39 antibodies in the presence of HB-EGF, mean colony size was reduced to the baseline size observed for control cells without HB-EGF treatment.

[00077]FIGURE 34D illustrates that anti-HB-EGF antibodies inhibit basal colony formation of SkOV-3 HB-EGF clone 71 cells, derived from SkOV-3 ovarian cancer cells transfected with an HB-EGF expression vector to cause constitutive over-expression of HB-EGF. As shown, control SkOV-3 HB-EGF clone 71 cells formed large numbers of colonies. However, when SkOV-3 HB-

EGF cl. 71 cells were cultured with either anti-HB-EGF U2-42 or U2-39 antibodies, the number of colonies was dramatically reduced.

[00078]FIGURE 34E illustrates that anti-HB-EGF antibodies inhibit basal colony formation of SkOV-3 HB-EGFclone 74 cells, derived from SkOV-3 ovarian cancer cells transfected with an HB-EGF expression vector to cause constitutive over-expression of HB-EGF. As shown, control SkOV-3 HB-EGF clone 74 cells formed large numbers of colonies. However, when SkOV-3 HB-EGF clone 74 cells were cultured with anti-HB-EGF U2-39 antibodies, the number of colonies was dramatically reduced.

[00079]FIGURE 34F illustrates that anti-HB-EGF antibodies inhibit basal colony formation of BxPC3 pancreatic adenocarcinoma cells grown in soft agar. As shown, control BxPC3 cells formed large numbers of colonies. However, when BxPC3 cells were cultured with either anti-HB-EGF U2-42 or U2-39 antibodies in the presence of HB-EGF, the number of colonies was dramatically reduced.

[00080]FIGURE 35 illustrates that anti-HB-EGF antibodies inhibit basal colony formation of EFO-27 HB-EGF clone 58 ovarian cancer cells overexpressing HB-EGF grown in soft agar. As shown, control cells formed large numbers of colonies. However, when EFO-27 HB-EGF cl. 58 cells were cultured with either anti-HB-EGF U2-42, U2-39 or U2-45 antibodies the number of colonies was dramatically reduced. Moreover, combination therapy of anti-HB-EGF antibodies with the anti-EGFR antibody Erbitux completely inhibited the colony formation.

[00081]FIGURE 36 shows that anti-HB-EGF antibodies inhibit HB-EGF induced angiogenesis *in vivo*. Angiogenic network formation in a mouse matrigel plug assay could be blocked in a dose-dependent manner by antibodies U2-42, U2-39 and U2-45.

[00082]FIGURE 37 illustrates inhibition of the growth of established BxPC3 tumors in mouse xenograft models by antibodies U2-42 and U2-39.

[00083]FIGURES 38A-38C illustrate inhibition of the growth of established EFO-27 HB-EGF clone 58 tumors in mouse xenograft models by antibodies U2-42, U2-39 and U2-45 (FIGURE 38A). As shown in FIGURE 38B, efficacy of inhibition of the xenograft tumor growth by antibodies U2-42 and U2-39 was shown to be dose dependent. Moreover, combination treatment with the anti-EGFR antibody Erbitux leads to complete regression of tumor growth and shows the potent synergistic activity of the anti-HB-EGF antibodies as agents for combination therapy (FIGURE 38C).

[00084]FIGURES 39A-39B illustrate the use of the human anti-HB-EGF antibodies for detection of HB-EGF in human tissue by immunohistochemistry (FIGURE 39A) and by ELISA (FIGURE 39B).

[00085]FIGURE 40A illustrates a scratch assay indicating the inhibition of HB-EGF-induced migration of CLS354 epithelial squamous carcinoma cells (mouth).

[00086]FIGURE 40B illustrates a transmigration assay indicating the inhibition of HB-EGF-induced migration of Detroit 562 epithelial carcinoma cells (pharynx).

[00087]FIGURE 41 illustrates a spheroid-based cellular angiogenesis assay indicating the inhibition of VEGF-stimulated endothelial cell sprouting.

[00088]FIGURE 42 illustrates immunohistochemistry (IHC) analysis of human tumor xenograft samples indicating the inhibition of CD31 staining of tumor in vivo.

[00089]FIGURE 43 illustrates in vivo ovarian tumor xenograft model indicating combination treatment of U2-39 with Cisplatin and Avastin.

DETAILED DESCRIPTION

[00090]The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described.

[00091]Unless otherwise defined herein, scientific and technical terms used in connection with the present application shall have the meanings that are commonly understood by those of ordinary skill in the art. Further, unless otherwise required by context, singular terms shall include pluralities and plural terms shall include the singular.

[00092]Generally, nomenclatures used in connection with, and techniques of, cell and tissue culture, molecular biology, immunology, microbiology, genetics and protein and nucleic acid chemistry and hybridization described herein are those well known and commonly used in the art. The methods and techniques of the present application are generally performed according to conventional methods well known in the art and as described in various general and more specific references that are cited and discussed throughout the present specification unless otherwise indicated. *See, e.g.,* Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 3rd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (2001) and Ausubel *et al.*, Current Protocols in Molecular Biology, Greene Publishing Associates (1992), and Harlow and Lane Antibodies: A Laboratory Manual Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1990), which are incorporated herein by reference. Enzymatic reactions and purification techniques are performed according to manufacturer's specifications, as commonly accomplished in the art or as described herein. The terminology used in connection with, and the laboratory procedures and techniques of, analytical chemistry, synthetic organic chemistry, and medicinal and pharmaceutical chemistry described herein are those well known and commonly used in the art. Standard techniques can be used for chemical syntheses, chemical analyses, pharmaceutical preparation, formulation, and delivery, and treatment of patients.

[00093]It should be understood that this invention is not limited to the particular methodology, protocols, and reagents, etc., described herein and as such may vary. The terminology used

herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the disclosed, which is defined solely by the claims.

[00094]Other than in the operating examples, or where otherwise indicated, all numbers expressing quantities of ingredients or reaction conditions used herein should be understood as modified in all instances by the term "about." The term "about" when used in connection with percentages may mean ±1%.

[00095]

A. General Overview

[00096]Antigen binding proteins that bind HB-EGF protein, in particular human HB-EGF (hHB-EGF) protein are provided herein. The antigen binding proteins provided are polypeptides into which one or more complementary determining regions (CDRs), as described herein, are embedded and/or joined. In some antigen binding proteins, the CDRs are embedded into a "framework" region, which orients the CDR(s) such that the proper antigen binding properties of the CDR(s) is achieved. In general, antigen binding proteins that are provided can interfere with, block, reduce or modulate the interaction between HB-EGF and its cognate receptors, including EGF-R and HER4.

[00097]Certain antigen binding proteins described herein are antibodies or are derived from antibodies. In certain embodiments, the polypeptide structure of the antigen binding proteins is based on antibodies, including, but not limited to, monoclonal antibodies, bispecific antibodies, minibodies, domain antibodies, synthetic antibodies (sometimes referred to herein as "antibody mimetics"), chimeric antibodies, humanized antibodies, human antibodies, antibody fusions (sometimes referred to herein as "antibody conjugates"), and fragments thereof, respectively. The various structures are further described herein below.

[00098]The antigen binding proteins provided herein have been demonstrated to bind to several epitopes of HB-EGF, in particular human HB-EGF. As demonstrated in the examples, the ability of HB-EGF to bind to its cognate receptors is reduced or inhibited. As a consequence, the antigen binding proteins provided herein are capable of inhibiting the activity of HB-EGF. In particular, antigen binding proteins binding to these epitopes can have one or more of the following activities: inhibiting, *inter alia*, EGF-R and HER4 autophosphorylation, induction of EGF-R and HER4 signal transduction pathway, EGF-R and HER4 induced cell growth, and other physiological effects induced by EGF-R and HER4 upon HB-EGF binding.

[00099]The antigen binding proteins that are disclosed herein have a variety of utilities. Some of the antigen binding proteins, for instance, are useful in specific binding assays, affinity purification of HB-EGF, in particular hHB-EGF and in screening assays to identify pof such receptors. In additiojn, the disclosed antigen binding proteins may be used for the diagnosis

and/or treatment of disease, such as proliferative disorders. These include, but are not limited to, various types of cancer.

B. Heparin-Binding Epidermal Growth Factor-like Growth Factor (HB-EGF)

[000100]HB-EGF is produced by various tumor cells and acts as an autocrine tumor growth factor. Davis-Fleischer *et al.*, 1998, *Front Biosci.* 3:288-299; Iwamoto & Mekada, 2000, *Cytokine Growth Factor Rev.* 11:335-344. HB-EGF has a strong affinity for heparin which can increase the biological activity of HB-EGF. HB-EGF is produced as a transmembrane protein which is proteolytically cleaved by metalloproteinases to yield the mature soluble form of the growth factor.

[000101]HB-EGF was first identified from supernatants of cultured human macrophages in a soluble, secreted form. On human cells, the precursor proHB-EGF, acts as the diphtheria toxin receptor. Various cell types, including epithelial cells, keratinocytes, monocytes, mesangial cells, lymphoid cells, and skeletal muscle cells, produce HB-EGF. It is a potent mitogen and chemotactic factor for epithelial cells, fibroblasts, smooth muscle cells and various human cancer cells.

[000102]The transmembrane form of HB-EGF is synthesized by many cell types as a 208-amino acid transmembrane precursor (tm-HB-EGF) containing EGF, heparin-binding, transmembrane, and cytoplasmic domains. The extracellular domain can be released as a 12- to 22-kDa soluble form of HB-EGF (sol-HB-EGF) through the action of metalloproteinases, which is regulated by different G protein-coupled receptors (GPCRs) or tumor promoters such as tetradecanoyl phorbol acetate (TPA). Typically, a substantial amount of transmembrane HB-EGF precursor remains uncleaved on the cell surface.

[000103]Both tm-HB-EGF and sol-HB-EGF are biologically active. The biological functions of both sol- and tm-HB-EGF are mediated by the EGF receptor (EGFR; HER1) and ErbB4 (HER4). Activation of these types of these receptors is believed to occur as a consequence of ligand-induced receptor homo- or hetero-dimerization. Upon activation, the EGF receptor has been demonstrated to increase cell growth, increase cell motility, inhibit apoptosis and increase cellular transformation.

[000104]EGFR-dependent signaling pathways can be transactivated upon stimulation of G-protein-coupled receptors (GPCR). Ligand activation of heterotrimeric G proteins by interaction with a GPCR results in an intracellular signal that induces the extracellular activity of a transmembrane metalloproteinase. Ligands that activate the GPCR pathway include LPA (lysophosphatidic acid), thrombin, carbachol, bombesin, and endothelin. Such activation leads to extracellular processing of a transmembrane growth factor precursor and release of the mature factor which, directly or through the proteoglycan matrix, interacts with the ectodomain of

EGFR and activates it through tyrosine phosphorylation. *See*, Prenzel *et al.*, 1999, *Nature* 402:884-888. Thus, HB-EGF is a component of a triple membrane-passing signal (TMPS) mechanism whereby a GPCR activates a membrane-bound metalloproteinase, which cleaves proHB-EGF to release the soluble growth factor, which subsequently activates the EGF receptor. EGFR transactivation has been linked to various disease states such as cardiac hypertrophy (reviewed in Shah BH, Catt KJ. Trends Pharmacol Sci. 2003 May;24(5):239-244), vascular remodeling (reviewed in Eguchi *et al.*, 2003, *Biochem Soc Trans. 2003 Dec;31(Pt 6):1198-202.*) and cancer (reviewed in Fischer *et al.*, 2003, *supra*).

[000105]Sequences for HB-EGF proteins and nucleic acids encoding those proteins are available to one of skill in the art. For example, such HB-EGF sequences can be found in the database provided by the National Center for Biotechnology Information (NCBI) (*see*, http://www.ncbi.nlm.nih.gov/). One example of a sequence for a HB-EGF is the amino acid sequence at NCBI accession numbers NM 001945 and NP_001936 (gi:4503413). This sequence is provided below for easy reference (SEQ ID NO:1072):

[000106]MKLLPSVVLKLFLAAVLSALVTGESLERLRRGLAAGTSNPDPPTVSTDQLLPLGGGRD RKVRDLQEADLDLLRVTLSSKPQALATPNKEEHGKRKKKGKGLGKKRDPCLRKYKDFCIHGEC KYVKELRAPSCICHPGYHGERCHGLSLPVENRLYTYDHTTILAVVAVVLSSVCLLVIVG LLMFRYHRRG GYDVENEEKVKLGMTNSH.

[000107]Note that the HB-EGF sequence shown above (SEQ ID NO:1072) has the nineteen amino acid signal peptide (MKLLPSVVLK LFLAAVLSA, SEQ ID NO:1073).

[000108]The soluble extracellular domain consists of amino acids 1-149 of the above HB-EGF sequence. This sequence for the HB-EGF soluble extracellular domain is provided below as SEQ ID NO:1074:

[000109]MKLLPSVVLKLFLAAVLSALVTGESLERLRRGLAAGTSNPDPPTVSTDQLLPLGGGRD RKVRDLQEADLDLLRVTLSSKPQALATPNKEEHGKRKKKGKGLGKKRDPCLR KYKDFCIHGECKYVKELRAPSCICHPGYHGERCHGLSLP.

[000110]Upon cleavage, a mature HB-EGF is generated that consists of amino acids 63-149 (87 amino acids). This sequence for the mature HB-EGF is provided below as SEQ ID NO:1075:

[000111]DLQEADLDLLRVTLSSKPQALATPNKEEHGKRKKKGKGLGKKRDPCLRKYKDFCIHG ECKYVKELRAPSCICHPGYHGERCHGLSLP.

[000112]HB-EGF interacts with and activates the.. epidermal growth factor receptor (EGFR). EGFR is a 170 kDa transmembrane glycoprotein consisting of an extracellular ligand-binding domain, a transmembrane region and an intracellular domain with tyrosine kinase activity. Binding of growth factors to the EGFR results in internalization of the ligand-receptor complex, autophosphorylation of the receptor and other protein substrates, leading ultimately to DNA

synthesis and cell division. The external ligand binding domain is not only stimulated by HB-EGF, but also by EGF, TGFα and amphiregulin (AR).

[000113]Overexpression of the EGFR is often accompanied by the co-expression of EGF-like growth factors, suggesting that an autocrine pathway for control of growth may play a major part in the progression of tumors. It is now widely believed that this is a mechanism by which tumor cells can escape normal physiological control.

C. HB-EGF Receptor Antigen Binding Proteins

[000114]A variety of selective binding agents useful for regulating the activity of HB-EGF are provided. These agents include, for instance, antigen binding proteins that contain an antigen binding domain (*e.g.*, single chain antibodies, domain antibodies, inmmunoadhesions, and polypeptides with an antigen binding region) and specifically bind to a HB-EGF polypeptide, in particular human HB-EGF. Some of the agents, for example, are useful in inhibiting the binding of HB-EGF to its receptors, and can thus be used to inhibit, interfere with, or modulate one or more activities associated with HB-EGF-mediated signaling.

[000115]In general, the antigen binding proteins that are provided typically comprise one or more CDRs as described herein (*e.g.*, 1, 2, 3, 4, 5 or 6). In some instances, the antigen binding protein comprises (a) a polypeptide structure and (b) one or more CDRs that are inserted into and/or joined to the polypeptide structure. The polypeptide structure can take a variety of different forms. For example, it can be, or comprise, the framework of a naturally occurring antibody, or fragment or variant thereof, or may be completely synthetic in nature. Examples of various polypeptide structures are further described below.

[000116]In certain embodiments, the polypeptide structure of the antigen binding proteins is an antibody or is derived from an antibody, including, but not limited to, monoclonal antibodies, bispecific antibodies, minibodies, domain antibodies, synthetic antibodies (sometimes referred to herein as "antibody mimetics"), chimeric antibodies, humanized antibodies, antibody fusions (sometimes referred to as "antibody conjugates"), and portions or fragments of each, respectively. In some instances, the antigen binding protein is an immunological fragment of an antibody (*e.g.*, a Fab, a Fab', a $F(ab')_2$, or a scFv). The various structures are further described and defined herein.

[000117]Certain of the antigen binding proteins as provided herein specifically bind to human HB-EGF. In a specific embodiment, the antigen binding protein specifically binds to human HB-EGF protein having the amino acid sequence of SEQ ID NO:1072.

[000118]In embodiments where the antigen binding protein is used for therapeutic applications, an antigen binding protein can inhibit, interfere with or modulate one or more biological activities of HB-EGF. In this case, an antigen binding protein binds specifically to and/or substantially

inhibits binding of human HB-EGF to its receptor when an excess of antibody reduces the quantity of human HB-EGF bound to its receptor, or *vice versa*, by at least about 20%, 40%, 60%, 80%, 85%, or more (for example by measuring binding in an *in vitro* competitive binding assay). HB-EGF has many distinct biological effects, which can be measured in many different assays in different cell types; examples of such assays are provided herein.

1. Naturally Occurring Antibody Structure

[000119]Some of the antigen binding proteins that are provided have the structure typically associated with naturally occurring antibodies. The structural units of these antibodies typically comprise one or more tetramers, each composed of two identical couplets of polypeptide chains, though some species of mammals also produce antibodies having only a single heavy chain. In a typical antibody, each pair or couplet includes one full-length "light" chain (in certain embodiments, about 25 kDa) and one full-length "heavy" chain (in certain embodiments, about 50-70 kDa). Each individual immunoglobulin chain is composed of several "immunoglobulin domains", each consisting of roughly 90 to 110 amino acids and expressing a characteristic folding pattern. These domains are the basic units of which antibody polypeptides are composed. The amino-terminal portion of each chain typically includes a variable domain that is responsible for antigen recognition. The carboxy-terminal portion is more conserved evolutionarily than the other end of the chain and is referred to as the "constant region" or "C region". Human light chains generally are classified as kappa and lambda light chains, and each of these contains one variable domain and one constant domain. Heavy chains are typically classified as mu, delta, gamma, alpha, or epsilon chains, and these define the antibody's isotype as IgM, IgD, IgG, IgA, and IgE, respectively. IgG has several subtypes, including, but not limited to, IgG1, IgG2, IgG3, and IgG4. IgM subtypes include IgM1, and IgM2. IgA subtypes include IgA1 and IgA2. In humans, the IgA and IgD isotypes contain four heavy chains and four light chains; the IgG and IgE isotypes contain two heavy chains and two light chains; and the IgM isotype contains five heavy chains and five light chains. The heavy chain C region typically comprises one or more domains that may be responsible for effector function. The number of heavy chain constant region domains will depend on the isotype. IgG heavy chains, for example, contain three C region domains known as C_H1, C_H2 and C_H3. The antibodies that are provided can have any of these isotypes and subtypes. In certain embodiments, the HB-EGF antibody is of the IgG1, IgG2, or IgG4 subtype.

[000120]In full-length light and heavy chains, the variable and constant regions are joined by a "J" region of about twelve or more amino acids, with the heavy chain also including a "D" region of about ten more amino acids. *See, e.g.*, Fundamental Immunology, 2nd ed., Ch. 7 (Paul, W., ed.) 1989, New York: Raven Press (hereby incorporated by reference in its entirety for all

purposes). The variable regions of each light/heavy chain pair typically form the antigen binding site.

[000121]One example of a kappa Light Constant domain of an exemplary HB-EGF monoclonal antibody has the amino acid sequence:

[000122]RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC. (SEQ ID NO:187).

[000123]One example of an IgG2 heavy constant domain of an exemplary HB-EGF monoclonal antibody has the amino acid sequence:

[000124]ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRT PEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKG LPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPML DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:188).

[000125]Variable regions of immunoglobulin chains generally exhibit the same overall structure, comprising relatively conserved framework regions (FR) joined by three hypervariable regions, more often called "complementarity determining regions" or CDRs. The CDRs from the two chains of each heavy chain/light chain pair mentioned above typically are aligned by the framework regions to form a structure that binds specifically to a specific epitope on the target protein (*e.g.*, HB-EGF). From N-terminal to C-terminal, naturally-occurring light and heavy chain variable regions both typically conform with the following order of these elements: FR1, CDR1, FR2, CDR2, FR3, CDR3 and FR4. A numbering system has been devised for assigning numbers to amino acids that occupy positions in each of these domains. This numbering system is defined in Kabat Sequences of Proteins of Immunological Interest (1987 and 1991, NIH, Bethesda, MD), or Chothia & Lesk, 1987, *J. Mol. Biol.* 196:901-917; Chothia *et al.*, 1989, *Nature* 342:878-883.

[000126]The various light chain and heavy chain variable regions provided herein are depicted in FIGURES 1A-1P, and FIGURES 2A-2O, respectively. Each of these variable regions may be attached to the above heavy and light chain constant regions to form a complete antibody heavy and light chain, respectively. Further, each of the so generated heavy and light chain sequences may be combined to form a complete antibody structure.

[000127]Specific examples of some of the full length light and heavy chains of the antibodies that are provided and their corresponding amino acid sequences are summarized in FIGURES 3A-3K and FIGURES 4A-4O, respectively.

[000128]Again, each of the exemplary light chains (U_L-1, U_L-2, U_L-3 etc.) listed in FIGURES 3A-3K can be combined with any of the exemplary heavy chains shown in FIGURES 4A-4O to form an antibody. Examples of such combinations include U_L-1 combined with any of U_H-1 through

U_H-58; U_L-2 combined with any of U_H-1 through U_H-58; or U_L-3 combined with any of U_H-1 through U_H-58, and so on. In some instances, the antibodies include at least one light chain and one heavy chain from those listed in FIGURES 3A-3K and FIGURES 4A-4O, respectively. In other instances, the antibodies contain two identical light chains and two identical heavy chains. As an example, an antibody or immunologically functional fragment may include two U_L-1 light chains and two U_H-1 heavy chains, or two U_L-2 light chains and two U_H-2 heavy chains, or two U_L-3 light chains and two U_H-3 heavy chains and other similar combinations of pairs of light chains and pairs of heavy chains as listed in FIGURES 3A-3K and FIGURES 4A-4O, respectively.

[000129]Other antibodies that are provided are variants of antibodies formed by combination of the heavy and light chains shown in FIGURES 3A-3K and FIGURES 4A-4O, respectively, and comprise light and/or heavy chains that each have at least 70%, 75%, 80%, 85%, 90%, 95%, 97% or 99% identity to the amino acid sequences of these chains. In some instances, such antibodies include at least one light chain and one heavy chain, whereas in other instances the variant forms contain two identical light chains and two identical heavy chains.

2. Variable Domains of Antibodies

[000130]Also provided are antigen binding proteins that contain an antibody light chain variable region selected from the group consisting of U-V_L1, U-V_L2, U-V_L3, U-V_L4, U-V_L5, U-V_L6, U-V_L7, U-V_L8, U-V_L9, U-V_L10, U-V_L11, U-V_L12, U-V_L13, U-V_L14, U-V_L15, U-V_L16, U-V_L17, U-V_L18, U-V_L19, U-V_L20, U-V_L21, U-V_L22, U-V_L23, U-V_L24, U-V_L25, U-V_L26, U-V_L27, U-V_L28, U-V_L29, U-V_L30, U-V_L31, U-V_L32, U-V_L33, U-V_L34, U-V_L35, U-V_L36, U-V_L37, U-V_L38, U-V_L39, U-V_L40, U-V_L41, U-V_L42, U-V_L43, U-V_L44, U-V_L45, U-V_L46, U-V_L47, U-V_L48, U-V_L49, U-V_L50, U-V_L51, U-V_L52, U-V_L54, U-V_L55, U-V_L56, U-V_L57, U-V_L58, U-V_L59, U-V_L60, U-V_L61, U-V_L62, U-V_L64, and U-V_L65; and/or an antibody light chain variable region selected from the group consisting of U-V_H1, U-V_H2, U-V_H3, U-V_H4, U-V_H5, U-V_H6, U-V_H7, U-V_H8, U-V_H9, U-V_H10, U-V_H11, U-V_H12, U-V_H13, U-V_H14, U-V_H15, U-V_H16, U-V_H17, U-V_H18, U-V_H19, U-V_H20, U-V_H21, U-V_H22, U-V_H23, U-V_H24, U-V_H25, U-V_H26, U-V_H27, U-V_H28, U-V_H29, U-V_H30, U-V_H31, U-V_H32, U-V_H33, U-V_H34, U-V_H35, U-V_H36, U-V_H37, U-V_H38, U-V_H39, U-V_H40, U-V_H41, U-V_H42, U-V_H43, U-V_H44, U-V_H45, U-V_H46, U-V_H47, U-V_H48, U-V_H49, U-V_H50, U-V_H51, U-V_H52, U-V_H53, U-V_H54, U-V_H55, U-V_H56, U-V_H57, and U-V_H58, as shown in FIGURES 1A-1P, and FIGURES 2A-2O, respectively, and immunologically functional fragments, derivatives, muteins and variants of these light chain and heavy chain variable regions.

[000131]Sequence alignments of the various light and heavy chain variable regions, respectively, are provided in FIGURES 10A and 10B, and FIGURES 11 A and 11B, respectively.

[000132]Antigen binding proteins of this type can generally be designated by the formula " V_Hx/ V_Ly," where "x" corresponds to the number of heavy chain variable regions and "y" corresponds to the number of the light chain variable regions (in general, x and y are each 1 or 2).

[000133]Each of the light chain variable regions listed in FIGURES 1A-1P may be combined with any of the light chain variable regions shown in FIGURES 2A-2O to form an antigen binding protein. Examples of such combinations include U-V_L1 combined with any of U-V_H1, U-V_H2, U-V_H3, U-V_H4, U-V_H5, U-V_H6, U-V_H7, U-V_H8, U-V_H9, U-V_H10, U-V_H11, U-V_H12, U-V_H13, U-V_H14, U-V_H15, U-V_H16, U-V_H17, U-V_H18, U-V_H19, U-V_H20, U-V_H21, U-V_H22, U-V_H23, U-V_H24, U-V_H25, U-V_H26, U-V_H27, U-V_H28, U-V_H29, U-V_H30, U-V_H31, U-V_H32, U-V_H33, U-V_H34, U-V_H35, U-V_H36, U-V_H37, U-V_H38, U-V_H39, U-V_H40, U-V_H41, U-V_H42, U-V_H43, U-V_H44, U-V_H45, U-V_H46, U-V_H47, U-V_H48, U-V_H49, U-V_H50, U-V_H51, U-V_H52, U-V_H53, U-V_H54, U-V_H55, U-V_H56, U-V_H57, or U-V_H58, or U-V_L2 combined with any of U-V_H1, U-V_H2, U-V_H3, U-V_H4, U-V_H5, U-V_H6, U-V_H7, U-V_H8, U-V_H9, U-V_H10, U-V_H11, U-V_H12, U-V_H13, U-V_H14, U-V_H15, U-V_H16, U-V_H17, U-V_H18, U-V_H19, U-V_H20, U-V_H21, U-V_H22, U-V_H23, U-V_H24, U-V_H25, U-V_H26, U-V_H27, U-V_H28, U-V_H29, U-V_H30, U-V_H31, U-V_H32, U-V_H33, U-V_H34, U-V_H35, U-V_H36, U-V_H37, U-V_H38, U-V_H39, U-V_H40, U-V_H41, U-V_H42, U-V_H43, U-V_H44, U-V_H45, U-V_H46, U-V_H47, U-V_H48, U-V_H49, U-V_H50, U-V_H51, U-V_H52, U-V_H53, U-V_H54, U-V_H55, U-V_H56, U-V_H57, or U-V_H58, etc.

[000134]In some instances, the antigen binding protein includes at least one heavy chain variable region and/or one light chain variable region from those listed in FIGURES 1A-1P, and FIGURES 2A-2O, respectively. In some instances, the antigen binding protein includes at least two different heavy chain variable regions and/or light chain variable regions from those listed in FIGURES 1A-1P, and FIGURES 2A-2O, respectively. An example of such an antigen binding protein comprises (a) one U-V_L1, and (b) one of U-V_L2, U-V_L3, U-V_L4, U-V_L5, U-V_L6, U-V_L7, U-V_L8, U-V_L9, U-V_L10, U-V_L11, U-V_L12, U-V_L13, U-V_L14, U-V_L15, U-V_L16, U-V_L17, U-V_L18, U-V_L19, U-V_L20, U-V_L21, U-V_L22, U-V_L23, U-V_L24, U-V_L25, U-V_L26, U-V_L27, U-V_L28, U-V_L29, U-V_L30, U-V_L31, U-V_L32, U-V_L33, U-V_L34, U-V_L35, U-V_L36, U-V_L37, U-V_L38, U-V_L39, U-V_L40, U-V_L41, U-V_L42, U-V_L43, U-V_L44, U-V_L45, U-V_L46, U-V_L47, U-V_L48, U-V_L49, U-V_L50, U-V_L51, U-V_L52, U-V_L54, U-V_L55, U-V_L56, U-V_L57, U-V_L58, U-V_L59, U-V_L60, U-V_L61, U-V_L62, U-V_L64, and U-V_L65. Again another example of such an antigen binding protein comprises (a) one U-V_L2, and (b) one of U-V_L1, U-V_L3, U-V_L4, U-V_L5, U-V_L6, U-V_L7, U-V_L8, U-V_L9, U-V_L10, U-V_L11, U-V_L12, U-V_L13, U-V_L14, U-V_L15, U-V_L16, U-V_L17, U-V_L18, U-V_L19, U-V_L20, U-V_L21, U-V_L22, U-V_L23, U-V_L24, U-V_L25, U-V_L26, U-V_L27, U-V_L28, U-V_L29, U-V_L30, U-V_L31, U-V_L32, U-V_L33, U-V_L34, U-V_L35, U-V_L36, U-V_L37, U-V_L38, U-V_L39, U-V_L40, U-V_L41, U-V_L42, U-V_L43, U-V_L44, U-V_L45, U-V_L46, U-V_L47, U-V_L48, U-V_L49, U-V_L50, U-V_L51, U-V_L52, U-V_L54, U-V_L55, U-V_L56, U-V_L57, U-V_L58, U-V_L59, U-V_L60, U-V_L61, U-V_L62, U-V_L64, and U-V_L65. Again another example of such an antigen binding protein comprises (a) one U-V_L3, and (b) one of U-V_L1, U-V_L2, U-V_L4, U-V_L5, U-V_L6, U-

V_L7, U-V_L8, U-V_L9, U-V_L10, U-V_L11, U-V_L12, U-V_L13, U-V_L14, U-V_L15, U-V_L16, U-V_L17, U-V_L18, U-V_L19, U-V_L20, U-V_L21, U-V_L22, U-V_L23, U-V_L24, U-V_L25, U-V_L26, U-V_L27, U-V_L28, U-V_L29, U-V_L30, U-V_L31, U-V_L32, U-V_L33, U-V_L34, U-V_L35, U-V_L36, U-V_L37, U-V_L38, U-V_L39, U-V_L40, U-V_L41, U-V_L42, U-V_L43, U-V_L44, U-V_L45, U-V_L46, U-V_L47, U-V_L48, U-V_L49, U-V_L50, U-V_L51, U-V_L52, U-V_L54, U-V_L55, U-V_L56, U-V_L57, U-V_L58, U-V_L59, U-V_L60, U-V_L61, U-V_L62, U-V_L64, and U-V_L65, etc.

[000135]Again another example of such an antigen binding protein comprises (a) one U-V_H1, and (b) one of U-V_H2, U-V_H3, U-V_H4, U-V_H5, U-V_H6, U-V_H7, U-V_H8, U-V_H9, U-V_H10, U-V_H11, U-V_H12, U-V_H13, U-V_H14, U-V_H15, U-V_H16, U-V_H17, U-V_H18, U-V_H19, U-V_H20, U-V_H21, U-V_H22, U-V_H23, U-V_H24, U-V_H25, U-V_H26, U-V_H27, U-V_H28, U-V_H29, U-V_H30, U-V_H31, U-V_H32, U-V_H33, U-V_H34, U-V_H35, U-V_H36, U-V_H37, U-V_H38, U-V_H39, U-V_H40, U-V_H41, U-V_H42, U-V_H43, U-V_H44, U-V_H45, U-V_H46, U-V_H47, U-V_H48, U-V_H49, U-V_H50, U-V_H51, U-V_H52, U-V_H53, U-V_H54, U-V_H55, U-V_H56, U-V_H57, and U-V_H58. Another example comprises (a) one U-V_H2, and (b) one of U-V_H1, U-V_H3, U-V_H4, U-V_H5, U-V_H6, U-V_H7, U-V_H8, U-V_H9, U-V_H10, U-V_H11, U-V_H12, U-V_H13, U-V_H14, U-V_H15, U-V_H16, U-V_H17, U-V_H18, U-V_H19, U-V_H20, U-V_H21, U-V_H22, U-V_H23, U-V_H24, U-V_H25, U-V_H26, U-V_H27, U-V_H28, U-V_H29, U-V_H30, U-V_H31, U-V_H32, U-V_H33, U-V_H34, U-V_H35, U-V_H36, U-V_H37, U-V_H38, U-V_H39, U-V_H40, U-V_H41, U-V_H42, U-V_H43, U-V_H44, U-V_H45, U-V_H46, U-V_H47, U-V_H48, U-V_H49, U-V_H50, U-V_H51, U-V_H52, U-V_H53, U-V_H54, U-V_H55, U-V_H56, U-V_H57, and U-V_H58. Again another example comprises (a) one U-V_H3, and (b) one of U-V_H1, U-V_H2, U-V_H4, U-V_H5, U-V_H6, U-V_H7, U-V_H8, U-V_H9, U-V_H10, U-V_H11, U-V_H12, U-V_H13, U-V_H14, U-V_H15, U-V_H16, U-V_H17, U-V_H18, U-V_H19, U-V_H20, U-V_H21, U-V_H22, U-V_H23, U-V_H24, U-V_H25, U-V_H26, U-V_H27, U-V_H28, U-V_H29, U-V_H30, U-V_H31, U-V_H32, U-V_H33, U-V_H34, U-V_H35, U-V_H36, U-V_H37, U-V_H38, U-V_H39, U-V_H40, U-V_H41, U-V_H42, U-V_H43, U-V_H44, U-V_H45, U-V_H46, U-V_H47, U-V_H48, U-V_H49, U-V_H50, U-V_H51, U-V_H52, U-V_H53, U-V_H54, U-V_H55, U-V_H56, U-V_H57, and U-V_H58, etc.

[000136]The various combinations of heavy chain variable regions may be combined with any of the various combinations of light chain variable regions.

[000137]In other instances, the antigen binding protein contains two identical light chain variable regions and/or two identical heavy chain variable regions. As an example, the antigen binding protein may be an antibody or immunologically functional fragment that includes two light chain variable regions and two heavy chain variable regions in combinations of pairs of light chain variable regions and pairs of heavy chain variable regions as listed in FIGURES 1A-1P, and FIGURES 2A-2O, respectively.

[000138]Some antigen binding proteins that are provided comprise a light chain variable domain comprising a sequence of amino acids that differs from the sequence of a light chain variable domain selected from U-V_L1, U-V_L2, U-V_L3, U-V_L4, U-V_L5, U-V_L6, U-V_L7, U-V_L8, U-V_L9, U-V_L10, U-V_L11, U-V_L12, U-V_L13, U-V_L14, U-V_L15, U-V_L16, U-V_L17, U-V_L18, U-V_L19, U-V_L20, U-V_L21, U-

V_L22, U-V_L23, U-V_L24, U-V_L25, U-V_L26, U-V_L27, U-V_L28, U-V_L29, U-V_L30, U-V_L31, U-V_L32, U-V_L33, U-V_L34, U-V_L35, U-V_L36, U-V_L37, U-V_L38, U-V_L39, U-V_L40, U-V_L41, U-V_L42, U-V_L43, U-V_L44, U-V_L45, U-V_L46, U-V_L47, U-V_L48, U-V_L49, U-V_L50, U-V_L51, U-V_L52, U-V_L54, U-V_L55, U-V_L56, U-V_L57, U-V_L58, U-V_L59, U-V_L60, U-V_L61, U-V_L62, U-V_L64, or U-V_L65 at only 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acid residues, wherein each such sequence difference is independently either a deletion, insertion or substitution of one amino acid. The light chain variable region in some antigen binding proteins comprises a sequence of amino acids that has at least 70%, 75%, 80%, 85%, 90%, 95%, 97% or 99% sequence identity to the amino acid sequences of the light chain variable region of U-V_L1, U-V_L2, U-V_L3, U-V_L4, U-V_L5, U-V_L6, U-V_L7, U-V_L8, U-V_L9, U-V_L10, U-V_L11, U-V_L12, U-V_L13, U-V_L14, U-V_L15, U-V_L16, U-V_L17, U-V_L18, U-V_L19, U-V_L20, U-V_L21, U-V_L22, U-V_L23, U-V_L24, U-V_L25, U-V_L26, U-V_L27, U-V_L28, U-V_L29, U-V_L30, U-V_L31, U-V_L32, U-V_L33, U-V_L34, U-V_L35, U-V_L36, U-V_L37, U-V_L38, U-V_L39, U-V_L40, U-V_L41, U-V_L42, U-V_L43, U-V_L44, U-V_L45, U-V_L46, U-V_L47, U-V_L48, U-V_L49, U-V_L50, U-V_L51, U-V_L52, U-V_L54, U-V_L55, U-V_L56, U-V_L57, U-V_L58, U-V_L59, U-V_L60, U-V_L61, U-V_L62, U-V_L64, or U-V_L65.

[000139]Certain antibodies comprise a heavy chain variable domain comprising a sequence of amino acids that differs from the sequence of a heavy chain variable domain selected from U-V_H1, U-V_H2, U-V_H3, U-V_H4, U-V_H5, U-V_H6, U-V_H7, U-V_H8, U-V_H9, U-V_H10, U-V_H11, U-V_H12, U-V_H13, U-V_H14, U-V_H15, U-V_H16, U-V_H17, U-V_H18, U-V_H19, U-V_H20, U-V_H21, U-V_H22, U-V_H23, U-V_H24, U-V_H25, U-V_H26, U-V_H27, U-V_H28, U-V_H29, U-V_H30, U-V_H31, U-V_H32, U-V_H33, U-V_H34, U-V_H35, U-V_H36, U-V_H37, U-V_H38, U-V_H39, U-V_H40, U-V_H41, U-V_H42, U-V_H43, U-V_H44, U-V_H45, U-V_H46, U-V_H47, U-V_H48, U-V_H49, U-V_H50, U-V_H51, U-V_H52, U-V_H53, U-V_H54, U-V_H55, U-V_H56, U-V_H57, or U-V_H58 at only 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acid residues, wherein each such sequence difference is independently either a deletion, insertion or substitution of one amino acid. The heavy chain variable region in some antigen binding proteins comprises a sequence of amino acids that has at least 70%, 75%, 80%, 85%, 90%, 95%, 97% or 99% sequence identity to the amino acid sequences of the heavy chain variable region of U-V_H1, U-V_H2, U-V_H3, U-V_H4, U-V_H5, U-V_H6, U-V_H7, U-V_H8, U-V_H9, U-V_H10, U-V_H11, U-V_H12, U-V_H13, U-V_H14, U-V_H15, U-V_H16, U-V_H17, U-V_H18, U-V_H19, U-V_H20, U-V_H21, U-V_H22, U-V_H23, U-V_H24, U-V_H25, U-V_H26, U-V_H27, U-V_H28, U-V_H29, U-V_H30, U-V_H31, U-V_H32, U-V_H33, U-V_H34, U-V_H35, U-V_H36, U-V_H37, U-V_H38, U-V_H39, U-V_H40, U-V_H41, U-V_H42, U-V_H43, U-V_H44, U-V_H45, U-V_H46, U-V_H47, U-V_H48, U-V_H49, U-V_H50, U-V_H51, U-V_H52, U-V_H53, U-V_H54, U-V_H55, U-V_H56, U-V_H57, or U-V_H58.

[000140]Still other antigen binding proteins, *e.g.*, antibodies or immunologically functional fragments include variant forms of a variant light chain and a variant heavy chain as just described.

3. CDRs

[000141]The antigen binding proteins disclosed herein are polypeptides into which one or more CDRs are grafted, inserted and/or joined. An antigen binding protein can have 1, 2, 3, 4, 5 or 6 CDRs. An antigen binding protein thus can have, for example, one light chain CDR1 ("CDRL1"), and/or one light chain CDR2 ("CDRL2"), and/or one light chain CDR3 ("CDRL3"), and/or one heavy chain CDR1 ("CDRH1"), and/or one heavy chain CDR2 ("CDRH2"), and/or one heavy chain CDR3 ("CDRH3"). Some antigen binding proteins inlcude both a CDRL3 and a CDRH3. Specific CDRs are identified in FIGURES 6A-6F, and FIGURES 7A-7E.

[000142]Complementarity determining regions (CDRs) and framework regions (FR) (examples of light and heavy chain FR amino acid sequences are given in FIGURES 8A-8H and FIGURES 9A-9F, respectively) of a given antibody may be identified using the system described by Kabat *et al.* in Sequences of Proteins of Immunological Interest, 5th Ed., US Dept. of Health and Human Services, PHS, NIH, NIH Publication No. 91-3242, 1991. Certain antibodies that are disclosed herein comprise one or more amino acid sequences that are identical or have substantial sequence identity to the amino acid sequences of one or more of the CDRs presented in FIGURES 6A-6F (CDRLs) and FIGURES 7A-7E (CDRHs).

[000143]The structure and properties of CDRs within a naturally occurring antibody has been described, *supra*. Briefly, in a traditional antibody, the CDRs are embedded within a framework in the heavy and light chain variable region where they constitute the regions responsible for antigen binding and recognition. A variable region comprises at least three heavy or light chain CDRs, *see, supra* (Kabat *et al.*, 1991, *Sequences of Proteins of Immunological Interest*, Public Health Service N.I.H., Bethesda, MD; *see,* also Chothia and Lesk, 1987, *J. Mol. Biol.* 196:901-917; Chothia *et al.*, 1989, *Nature* 342: 877-883), within a framework region (designated framework regions 1-4, FR1, FR2, FR3, and FR4, by Kabat *et al.*, 1991, *supra*; *see,* also Chothia and Lesk, 1987, *supra*). The CDRs provided herein, however, may not only be used to define the antigen binding domain of a traditional antibody structure, but may be embedded in a variety of other polypeptide structures, as described herein.

[000144]In one aspect, the CDRs provided are a (a) a CDRL selected from the group consisting of (i) a CDRL1 selected from the group consisting of SEQ ID NOs:189-217; (ii) a CDRL2 selected from the group consisting of SEQ ID NO:218-233; (iii) a CDRL3 selected from the group consisting of SEQ ID NO:234-274; and (iv) a CDRL of (i), (ii) and (iii) that contains one or more amino acid substitutions, deletions or insertions of no more than five, four, three, two, or one amino acids; (B) a CDRH selected from the group consisting of (i) a CDRH1 selected from the group consisting of SEQ ID NO:275-299; (ii) a CDRH2 selected from the group consisting of SEQ ID NO:300-331; (iii) a CDRH3 selected from the group consisting of SEQ ID NO:332-372;

and (iv) a CDRLHof (i), (ii) and (iii) that contains one or more amino acid substitutions, deletions or insertions of no more than five, four, three, two, or one amino acids amino acids.

[000145]In yet another aspect, variant forms of the CDRs are provided that have at least 80%, 85%, 90% or 95% sequence identity to a CDR sequence listed in FIGURES 6A-6F and FIGURES 7A-7E.

[000146]

[000147]In yet another aspect, the CDRs disclosed herein include consensus sequences derived from groups of related monoclonal antibodies. As described herein, a "consensus sequence" refers to amino acid sequences having conserved amino acids common among a number of sequences and variable amino acids that vary within a given amino acid sequences. The CDR consensus sequences provided include CDRs corresponding to each of CDRL1, CDRL2, CDRL3, CDRH1, CDRH2 and CDRH3.

[000148]Consensus sequences were determined using a standard phylogenic analysis approach of the CDRs corresponding to the U-V_L and U-V_H of anti-HB-EGF antibodies. First, in this approach, amino acid sequences corresponding to the entire variable domains of either U-V_L or U-V_H were converted to FASTA formatting for ease in processing comparative alignments and inferring phylogenies. Based on this comparison, each the light and heavy chain variable regions, respectivey were divided in phylogenetically related groups, *i.e.*, the light chain variable regions were devided into six groups A, B, C, D, E, and F (*see*, FIGURE 12A and 12B), and the heavy chain variable regions were ddivided into seven groups A, B, C, D, E, F, and G (*see*, FIGURE 12C). Then, within each of these groups, comparison of each of the the CDRL1, CDRL2, CDRL3, CDRH1, CDRH2, CDRH3 regions was used to define consensus collections.

[000149]Group A of the light chain CDRs includes the following consensus collections:

a. a CDRL1 of the generic formula $X_1SSQSLX_2X_3SDGX_4TYLX_5$ (SEQ ID NO:1035), wherein

X_1 is K or R,

X_2 is L or V,

X_3 is H or Y,

X_4 is K or N,

X_5 is N, S or Y.

b. a CDRL2 of the generic formula $X_1X_2SNX_3X_4S$ (SEQ ID NO:1041), wherein

X_1 is E or K,

X_2 is I or V,

X_3 is R or W,

X_4 is D or F.

c. a CDRL3 of the generic formula $X_1QX_2X_3X_4X_5PX_6X_7$ (SEQ ID NO:1046), wherein

X_1 is I or M,

X_2 is A, G or S,

X_3 is I or T,

X_4 is H or Q,

X_5 is F, L or W,

X_6 is C, I, H, L or T,

X_7 is S or T.

[000150]Group B of the light chain CDRs includes the following consensus collections:

a. a CDRL1 of the generic formula $RASQX_1ISX_2YLN$ (SEQ ID NO:1036), wherein

X_1 is R, S or T,

X_2 is R or S.

b. a CDRL2 of the generic formula $X_1X_2SX_3LQS$ (SEQ ID NO:1042), wherein

X_1 is A or T,

X_2 is A, E or V,

X_3 is S or T.

c. a CDRL3 of the generic formula $QQX_1X_2X_3X_4X_5IT$ (SEQ ID NO:1047), wherein

X_1 is I or S,

X_2 is F or Y,

X_3 is F, I, S or Y,

X_4 is A, S or T,

X_5 is P or S.

[000151]Group C of the light chain CDRs includes the following consensus collections:

a. a CDRL1 of the generic formula $RASQX_1IX_2X_3X_4LX_5$ (SEQ ID NO:1037), wherein

X_1 is D, G, S or T,

X_2 is A, R or S,

X_3 is H, I, N, R, S or T,

X_4 is D, W or Y,

X_5 is A, G or N.

b. a CDRL2 of the generic formula X_1ASX_2LQS (SEQ ID NO:1043), wherein

X_1 is A or V,

X_2 is S or T.

c. a CDRL3 of the generic formula $X_1X_2X_3X_4X_5X_6X_7X_8T$ (SEQ ID NO:1048), wherein

X_1 is L or Q,

X_2 is K, N or Q,

X_3 is A, H, S or Y,

X_4 is H, N or Y,

X_5 is N, S or T,

X_6 is A, F, I, T, V or Y,

X_7 is P or no amino acid,

X_8 is F, L or P.

[000152]Group D of the light chain CDRs includes the following consensus collections:

a. a CDRL1 of the generic formula $QASQDIX_1X_2X_3LN$ (SEQ ID NO:1038), wherein

X_1 is S or T,

X_2 is D or N,

X_3 is S or Y.

b. a CDRL2 of the generic formula $DASX_1LET$ (SEQ ID NO:1044), wherein

X_1 is I or N.

c. a CDRL3 of the generic formula $QX_1X_2DX_3LPX_4X_5$ (SEQ ID NO:1049), wherein

X_1 is H or Q,

X_2 is C or Y,

X_3 is D, I, N, S or Y,

X_4 is F, I or L,

X_5 is A, S or T.

[000153]Group E of the light chain CDRs includes the following consensus collections:

a. a CDRL1 of the generic formula $RASQX_1VX_2X_3X_4X_5LA$ (SEQ ID NO:1039), wherein

X_1 is S or T,

X_2 is I or S,

X_3 is R or S,

X_4 is S, N or no amino acid,

X_5 is Y or no amino acid.

b. a CDRL2 of the generic formula GASSRAT (SEQ ID NO:223)

c. a CDRL3 of the generic formula $QQX_1X_2X_3X_4PX_5X_6X_7$ (SEQ ID NO:1050), wherein

X_1 is H or Y,

X_2 is G or N,

X_3 is N or S,

X_4 is S or W,

X_5 is P or no amino acid,

X_6 is R or W,

X_7 is S or T.

[000154]Group F of the light chain CDRs includes the following consensus collections:

a. a CDRL1 of the generic formula $KSSQX_1X_2LX_3X_4SNNKNYLX_5$ (SEQ ID NO:1040), wherein

X_1 is N or S,

X_2 is I or V,

X_3 is D or Y,

X_4 is N, R or S,

X_5 is A or V.

b. a CDRL2 of the generic formula $WASX_1RES$ (SEQ ID NO:1045), wherein

X_1 is A or T.

c. a CDRL3 of the generic formula $X_1QYX_2X_3X_4X_5X_6X_7F$ (SEQ ID NO:1051), wherein

X_1 is H or Q,

X_2 is F or Y,

X_3 is G, I or S,

X_4 is F, I or T,

X_5 is M, P, S or T,

X_6 is F, L, R or W,

X_7 is S or T

[000155]Group A of the heavy chain CDRs includes the following consensus collections:

a. a CDRH1 of the generic formula $GYTX_1TX_2X_3X_4X_5X_6$ (SEQ ID NO:1052), wherein

X_1 is F or L,

X_2 is E, G or S,

X_3 is H, L or Y,

X_4 is G, S or Y,

X_5 is I or M,

X_6 is H or S.

b. a CDRH2 of the generic formula $X_1X_2X_3X_4X_5X_6GX_7TX_8X_9X_{10}QKX_{11}X_{12}$ (SEQ ID NO:1058), wherein

X_1 is S or W,

X_2 is F or I,

X_3 is D, N or S,

X_4 is A, P,

X_5 is E, N or S,

X_6 is D, N or S,

X_7 is E, G or N,

X_8 is I or N,

X_9 is C, H or Y,

X_{10} is A or T,

X_{11} is F or L,

X_{12} is D or G.

c. a CDRH3 of the generic formula $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}DX_{12}$ (SEQ ID NO:1065), wherein

X_1 is E or S,

X_2 is D, G or no amino acid,

X_3 is D, N or no amino acid,

X_4 is G or no amino acid,

X_5 is G or no amino acid,

X_6 is W, Y or no amino acid,

X_7 is I, N or Y,

X_8 is A or Y,

X_9 is G, V or Y,

X_{10} is A, F or G,

X_{11} is F, L or M,

X_{12} is V or Y.

[000156]Group B of the heavy chain CDRs includes the following consensus collections:

a. a CDRH1 of the generic formula $GYX_1FTSYWIG$ (SEQ ID NO:1053), wherein

X_1 is R or S.

b. a CDRH2 of the generic formula $IIYPX_1DSDX_2RYSPSFQG$ (SEQ ID NO:1059), wherein

X_1 is D or G,

X_2 is A, I or T.

c. a CDRH3 of the generic formula $QX_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}YX_{12}X_{13}X_{14}DX_{15}$ (SEQ ID NO:1066), wherein

X_1 is G or no amino acid,

X_2 is K, L or Y,

X_3 is A, G or S,

X_4 is S, V or Y,

X_5 is A or G,

X_6 is G or no amino acid,

X_7 is T or no amino acid,

X_8 is S or no amino acid,

X_9 is Y or no amino acid,

X_{10} is W or Y,

X_{11} is G, S or Y,

X_{12} is F or Y,

X_{13} is G or no amino acid,

X_{14} is M or no amino acid,

X_{15} is V or Y.

[000157]Group C of the heavy chain CDRs includes the following consensus collections:

a. a CDRH1 of the generic formula $GFTFX_1SX_2X_3MH$ (SEQ ID NO:1054), wherein

X_1 is R or S,

X_2 is H or Y,

X_3 is D or G.

b. a CDRH2 of the generic formula $X_1IX_2X_3DGSX_4X_5X_6YX_7DSVX_8G$ (SEQ ID NO:1060), wherein

X_1 is F or V,

X_2 is S or W,

X_3 is D, S or Y,

X_4 is I, N or T,

X_5 is K or Q,

X_6 is N, R or Y,

X_7 is A, T or V,

X_8 is K or R.

c. a CDRH3 of the generic formula $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}$ (SEQ ID NO:1067), wherein

X_1 is D, G, L, S or no amino acid,

X_2 is G, H, W, Y or no amino acid,

X_3 is A, F, W, Y or no amino acid,

X_4 is D, G, Q, T or no amino acid,

X_5 is G, I, Q, S or no amino acid,

X_6 is A, D, N, Q, S or no amino acid,

X_7 is G, Y or no amino acid,

X_8 is D, Y or no amino acid,

X_9 is Y or no amino acid,

X_{10} is A, E, N or Y,

X_{11} is G, P, T, V or Y,

X_{12} is F or I,

X_{13} is D or Q,

X_{14} is C, H, V or Y.

[000158]Group D of the heavy chain CDRs includes the following consensus collections:

a. a CDRH1 of the generic formula $GFX_1FSX_2YX_3MX_4$ (SEQ ID NO:1055), wherein

X_1 is P or T,

X_2 is A, R or S,

X_3 is A or S,

X_4 is N or S.

b. a CDRH2 of the generic formula $X_1ISX_2SX_3X_4X_5X_6YYADSVKG$ (SEQ ID NO:1061), wherein

X_1 is A, H or Y,

X_2 is G, R or S,

X_3 is G or S,

X_4 is G, R or S,

X_5 is S, T or Y,

X_6 is I or T.

c. a CDRH3 of the generic formula $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}DX_{18}$ (SEQ ID NO:1068), wherein

X_1 is E, D or no amino acid,

X_2 is G, R or no amino acid,

X_3 is I, V, Y or no amino acid,

X_4 is A, G, L or N,

X_5 is A, G, V or W,

X_6 is A, N, R or T,

X_7 is G, N, P or no amino acid,

X_8 is G, T, no amino acid,

X_9 is A or no amino acid,

X_{10} is D, E or no amino acid,

X_{11} is S, Y or no amino acid,

X_{12} is G, Y or no amino acid,

X_{13} is N, Y or no amino acid,

X_{14} is Y or no amino acid,

X_{15} is D, Y or no amino acid,

X_{16} is A, G or no amino acid,

X_{17} is F or M,

X_{18} is I, V or Y.

[000159]Group E of the heavy chain CDRs includes the following consensus collections:

a. a CDRH1 of the generic formula $GX_1SX_2SX_3X_4X_5X_6X_7WX_8$ (SEQ ID NO:1056), wherein

X_1 is D or G,

X_2 is F, I or V,

X_3 is R, S or no amino acid,

X_4 is G, Y or no amino acid,

X_5 is D, G, S or no amino acid,

X_6 is A, S or Y,

X_7 is A or Y,

X_8 is N or S.

b. a CDRH2 of the generic formula $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}YX_{12}X_{13}SX_{14}KS$ (SEQ ID NO:1062), wherein

X_1 is E, R or Y,

X_2 is I or T,

X_3 is H, N or Y,

X_4 is C, H, S, T or Y,

X_5 is S or R,

X_6 is G or S,

X_7 is G, K, S or T,

X_8 is T or W,

X_9 is N or Y,

X_{10} is N or no amino acid,

X_{11} is D or no amino acid,

X_{12} is A or N,

X_{13} is P or V,

X_{14} is L or V.

c. a CDRH3 of the generic formula $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}X_{18}X_{19}X_{20}X_{21}X_{22}X_{23}$ (SEQ ID NO:1069), wherein

X_1 is A, D, G, S or T,

X_2 is A, E, G, L, N, R, Y or no amino acid,

X_3 is A, G, L, N, R, T, Y or no amino acid,

X_4 is D, G, R, S, V, Y or no amino acid,

X_5 is A, G, I, S, V, Y or no amino acid,

X_6 is F, G, L, R, V or no amino acid,

X_7 is L, T, Y or no amino acid,

X_8 is Y or no amino acid,

X_9 is Y or no amino acid,

X_{10} is D or no amino acid,

X_{11} is S or no amino acid,

X_{12} is S or no amino acid,

X_{13} is G or no amino acid,

X_{14} is D, L, M, S, Y or no amino acid,

X_{15} is H, I, P, V, W or no amino acid,

X_{16} is F, G, L, R, S, Y or no amino acid,

X_{17} is D, F, V, W, Y or no amino acid,

X_{18} is C, F, L, P, S or Y,

X_{19} is D, F, G or Y,

X_{20} is A, C, G, P, R, V or Y,

X_{21} is F, L, M, S or no amino acid,

X_{22} is A, D or no amino acid,

X_{23} is I, L, V, Y or no amino acid.

[000160]Group F of the heavy chain CDRs includes the following consensus collections:

a. a CDRH1 of the generic formula GFSLSNARMGVS (SEQ ID NO:279).

b. a CDRH2 of the generic formula X_1IFSNDEKSYSTSLKS (SEQ ID NO:1063), wherein

X_1 is H or L.

c. a CDRH3 of the generic formula X_1YSSGWX_2X_3YGX_4X_5DX_6 (SEQ ID NO:1070), wherein

X_1 is M or V,

X_2 is S or no amino acid,

X_3 is F or no amino acid,

X_4 is V or no amino acid,

X_5 is F or M,

X_6 is V or Y.

[000161]Group G of the heavy chain CDRs includes the following consensus collections:

a. a CDRH1 of the generic formula GFSLX_1TGGVGVG (SEQ ID NO:1057), wherein

X_1 is S or N.

b. a CDRH2 of the generic formula LIYWNX_1X_2KRYSPSLX_3S (SEQ ID NO:1064), wherein

X_1 is D or V,

X_2 is D or E,

X_3 is K or R.

c. a CDRH3 of the generic formula R$X_1X_2X_3$PFX_4Y (SEQ ID NO:1071), wherein

X_1 is G, H, L, N or R,

X_2 is E, T or W,

X_3 is L, N, T or V,

X_4 is D or E.

[000162] In another approach, consensus sequences may be determined by keeping the CDRs contiguous within the same sequence corresponding to a U-V_L or U-V_H. Briefly, in this approach, amino acid sequences corresponding to the entire variable domains of either U-V_L or U-V_H are converted to FASTA formatting for ease in processing comparative alignments and inferring phylogenies. Next, framework regions of these sequences are replaced with an artificial linker sequence so that examination of the CDRs alone is performed without introducing any amino acid position weighting bias due to coincident events (*e.g.*, such as unrelated antibodies that serendipitously share a common germline framework heritage) whilst still keeping CDRs contiguous within the same sequence corresponding to a U-V_l or U-V_H. U-V_L or U-V_H sequences of this format are then subjected to sequence similarity alignment interrogation using a program that employs a standard ClutalW-like algorithm (*see*, Thompson *et al.*, 1994, *Nucleic Acids Res.* 22:4673-4680). This program likewise generates phylograms (phylogenic tree illustrations) based on sequence similarity alignments using either UPGMA (unweighted pair group method using arithmetic averages) or Neighbor-Joining methods (*see*, Saitou and Nei, 1987, *Molecular Biology and Evolution* 4:406-425) to construct and illustrate similarity and distinction of sequence groups *via* branch length comparison and grouping. Both methods produce similar results to determine consensus sequence collections within the individual groups.

[000163] In some cases the antigen binding protein comprises at least one CDRL1, CDRL2, or CDRL3 having one of the above consensus sequences. In some cases, the antigen binding protein comprises at least one CDRH1, CDRH2, or CDRH3 having one of the above consensus sequences. In other cases, the antigen binding protein comprises at least two CDRLs according to the above consensus sequences, and/or at least two CDRHs according to the above consensus sequences. In one aspect, the CDRLs and/or CDRHs are derived from different groups. In other cases, the antigen binding protein comprises at least two CDRLs from the same group A, B, C, D, E, or F and/or at least two CDRHs from the same group A, B, C, D, E, F, or G. In other aspects, the antigen binding protein comprises all three CDRL1, CDRL2, and CDRL3 sequences from the same of the above groups A, B, C, D, E, or F, and/or all three CDRH1, CDRH2, and CDRH3 sequence from the same of the above groups A, B, C, D, E, F, or G.

[000164]

D. Exemplary Antigen Binding Proteins

[000165] According to one aspect, an isolated antigen binding protein is provided that binds HB-EGF comprising (A) one or more light chain complementary determining regions (CDRLs) selected from the group consisting of: (i) a CDRL1 selected from the group consisting of SEQ ID NO:189-217; (ii) a CDRL2 selected from the group consisting of SEQ ID NO:218-233; (iii) a

CDRL3 selected from the group consisting of SEQ ID NO:234-274; and (iv) a CDRL of (i), (ii) and (iii) that contains one or more amino acid substitutions, deletions or insertions of no more than five, four, three, four, two or one amino acids; (B) one or more heavy chain complementary determining regions (CDRHs) selected from the group consisting of: (i) a CDRH1 selected from the group consisting of SEQ ID NO:275-299; (ii) a CDRH2 selected from the group consisting of SEQ ID NO:300-331; (iii) a CDRH3 selected from the group consisting of SEQ ID NO:332-372; and (iv) a CDRH of (i), (ii) and (iii) that contains one or more amino acid substitutions, deletions or insertions of no more than five, four, three, four, two or one amino acids; or (C) one or more light chain CDRLs of (A); and (D) one or more heavy chain CDRHs of (B).

[000166]In yet another embodiment, the isolated antigen binding protein may comprise (A) a CDRL selected from the group consisting of (i) a CDRL1 selected from the group consisting of SEQ ID NO:189-217; (ii) a CDRL2 selected from the group consisting of SEQ ID NO:218-233; and (iii) a CDRL3 selected from the group consisting of SEQ ID NO:234-274; (B) a CDRH selected from the group consisting of (i) a CDRH1 selected from the group consisting of SEQ ID NO:275-299; (ii) a CDRH2 selected from the group consisting of SEQ ID NO:300-331; and (iii) a CDRH3 selected from the group consisting of SEQ ID NO:332-372; or (C) one or more light chain CDRLs of (A); and (D) one or more heavy chain CDRLs of (B). In one embodiment, the isolated antigen binding protein may include (A) a CDRL1 of SEQ ID NO:189-217, a CDRL2 of SEQ ID NO:218-233, and a CDRL3 of SEQ ID NO:234-274, and (B) a CDRH1 of SEQ ID NO:275-299, a CDRH2 of SEQ ID NO:300-331, and a CDRH3 of SEQ ID NO:332-372.

[000167]In another embodiment, the antigen binding protein comprises a variable light chain (V_L) has at least 80%, 85%, 90% or 95% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO:94-141, and/or the variable heavy chain (V_H) has at least 80%, 85%, 90% or 95% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NO:142-186. In a further embodiment, the V_L is selected from the group consisting of SEQ ID NO:94-141, and/or the V_H is selected from the group consisting of SEQ ID NO:142-186.

[000168]In another aspect, also provided is an isolated antigen binding protein that specifically binds to an epitope containing at least one IHGE-containing epitope and/or EGF-like epitope of HB-EGF.

[000169]In a further aspect, there is a provision of an isolated antigen binding protein that binds HB-EGF, the antigen binding protein including (A) a light chain complementary determining region (CDRL) selected from the group consisting of (i) a CDRL3 selected from the group consisting of SEQ ID NO:234-274, (ii) a CDRL3 that differs in amino acid sequence from the CDRL3 of (i) by an amino acid addition, deletion or substitution of not more than two amino acids; (iii) a CDRL3 amino acid sequence selected from the group consisting of

$X_1QX_2X_3X_4X_5PX_6X_7$ (SEQ ID NO:1046), wherein X_1 is selected from the group consisting of I and M, X_2 is selected from the group consisting of A, G and S, X_3 is selected from the group consisting of I and T, X_4 is selected from the group consisting of H and Q, X_5 is selected from the group consisting of F, L and W, X_6 is selected from the group consisting of C, I, H, L and T, X_7 is selected from the group consisting of S and T; $QQX_1X_2X_3X_4X_5IT$ (SEQ ID NO:1047), wherein X_1 is selected from the group consisting of I and S, X_2 is selected from the group consisting of F and Y, X_3 is selected from the group consisting of F, I, S and Y, X_4 is selected from the group consisting of A, S and T, X_5 is selected from the group consisting of P and S; $X_1X_2X_3X_4X_5X_6X_7X_8T$ (SEQ ID NO:1048), wherein X_1 is selected from the group consisting of L and Q, X_2 is selected from the group consisting of K, N and Q, X_3 is selected from the group consisting of A, H, S and Y, X_4 is selected from the group consisting of H, N and Y, X_5 is selected from the group consisting of N, S and T, X_6 is selected from the group consisting of A, F, I, T, V and Y, X_7 is selected from the group consisting of P and no amino acid, X_8 is selected from the group consisting of F, L and P; $QX_1X_2DX_3LPX_4X_5$ (SEQ ID NO:1049), wherein X_1 is selected from the group consisting of H and Q, X_2 is selected from the group consisting of C and Y, X_3 is selected from the group consisting of D, I, N, S and Y, X_4 is selected from the group consisting of F, I and L, X_5 is selected from the group consisting of A, S and T; $QQX_1X_2X_3X_4PX_5X_6X_7$ (SEQ ID NO:1050), wherein X_1 is selected from the group consisting of H and Y, X_2 is selected from the group consisting of G and N, X_3 is selected from the group consisting of N and S, X_4 is selected from the group consisting of S and W, X_5 is selected from the group consisting of P and no amino acid, X_6 is selected from the group consisting of R and W, X_7 is selected from the group consisting of S and T; and $X_1QYX_2X_3X_4X_5X_6X_7F$ (SEQ ID NO:1051), wherein X_1 is selected from the group consisting of H and Q, X_2 is selected from the group consisting of F and Y, X_3 is selected from the group consisting of G, I and S, X_4 is selected from the group consisting of F, I and T, X_5 is selected from the group consisting of M, P, S and T, X_6 is selected from the group consisting of F, L, R and W, X_7 is selected from the group consisting of S and T; and/or (B) a heavy chain complementary determining region (CDRH) selected from the group consisting of (i) a CDRH3 selected from the group consisting of SEQ ID NOs:332-372, (ii) a CDRH3 that differs in amino acid sequence from the CDRH3 of (i) by an amino acid addition, deletion or substitution of not more than two amino acids; and (iii) a CDRH3 amino acid sequence selected from the group consisting of $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}DX_{12}$ (SEQ ID NO:1065), wherein X_1 is selected from the group consisting of E and S, X_2 is selected from the group consisting of D, G and no amino acid, X_3 is selected from the group consisting of D, N and no amino acid, X_4 is selected from the group consisting of G and no amino acid, X_5 is selected from the group consisting of G and no amino acid, X_6 is selected from the group consisting of W, Y and no amino acid, X_7 is selected from the group consisting of I, N and Y, X_8

is selected from the group consisting of A and Y, X_9 is selected from the group consisting of G, V and Y, X_{10} is selected from the group consisting of A, F and G, X_{11} is selected from the group consisting of F, L and M, X_{12} is selected from the group consisting of V and Y; $QX_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}YX_{12}X_{13}X_{14}DX_{15}$ (SEQ ID NO:1066), wherein X_1 is selected from the group consisting of G and no amino acid, X_2 is selected from the group consisting of K, L and Y, X_3 is selected from the group consisting of A, G and S, X_4 is selected from the group consisting of S, V and Y, X_5 is selected from the group consisting of A and G, X_6 is selected from the group consisting of G and no amino acid, X_7 is selected from the group consisting of T and no amino acid, X_8 is selected from the group consisting of S and no amino acid, X_9 is selected from the group consisting of Y and no amino acid, X_{10} is selected from the group consisting of W and Y, X_{11} is selected from the group consisting of G, S and Y, X_{12} is selected from the group consisting of F and Y, X_{13} is selected from the group consisting of G and no amino acid, X_{14} is selected from the group consisting of M and no amino acid, X_{15} is selected from the group consisting of V and Y; $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}$ (SEQ ID NO:1067), wherein X_1 is selected from the group consisting of D, G, L, S and no amino acid, X_2 is selected from the group consisting of G, H, W, Y and no amino acid, X_3 is selected from the group consisting of A, F, W, Y and no amino acid, X_4 is selected from the group consisting of D, G, Q, T and no amino acid, X_5 is selected from the group consisting of G, I, Q, S and no amino acid, X_6 is selected from the group consisting of A, D, X_8 is selected from the group consisting of D, Y and no amino acid, X_9 is selected from the group consisting of Y and no amino acid, X_{10} is selected from the group consisting of A, E, N and Y, X_{11} is selected from the group consisting of G, P, T, V and Y, X_{12} is se X_{14} is selected from the group consisting of C, H, V and Y; $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}DX_{18}$ (SEQ ID NO:1068), wherein X_1 is selected from the group consisting of E, D and no amino acid, X_2 is selected from the group consisting of G, R and no amino acid, X_3 is selected from the group consisting of I, V, Y and no amino acid, X_4 is selected from the group consisting of A, G, L and N, X_5 is selected from the group consisting of A, G, V and W, X_6 is selected from the group consisting of A, N, R and T, X_7 is selected from the group consisting of G, N, P and no amino acid, X_8 is selected from the group consisting of G, T and no amino acid, X_9 is selected from the group consisting of A and no amino acid, X_{10} is selected from the group consisting of D, E and no amino acid, X_{11} is selected from the group consisting of S, Y and no amino acid, X_{12} is selected from the group consisting of G, Y and no amino acid, X_{13} is selected from the group consisting of N, Y and no amino acid, X_{14} is selected from the group consisting of Y and no amino acid, X_{15} is selected from the group consisting of D, Y and no amino acid, X_{16} is selected from the group consisting of A, G and no amino acid, X_{17} is selected from the group consisting of F and M, X_{18} is selected from the group consisting of I, V and Y; $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}X_{18}X_{19}X_{20}X_{21}X_{22}X_{23}$ (SEQ ID NO:1069),

wherein X_1 is selected from the group consisting of A, D, G, S and T, X_2 is selected from the group consisting of A, E, G, L, N, R, Y and no amino acid, X_3 is selected from the group consisting of A, G, L, N, R, T, Y and no amino acid, X_4 is selected from the group consisting of D, G, R, S, V, Y and no amino acid, X_5 is selected from the group consisting of A, G, I, S, V, Y and no amino acid, X_6 is selected from the group consisting of F, G, L, R, V and no amino acid, X_7 is selected from the group consisting of L, T, Y and no amino acid, X_8 is selected from the group consisting of Y and no amino acid, X_9 is selected from the group consisting of Y and no amino acid, X_{10} is selected from the group consisting of D and no amino acid, X_{11} is selected from the group consisting of S and no amino acid, X_{12} is selected from the group consisting of S and no amino acid, X_{13} is selected from the group consisting of G and no amino acid, X_{14} is selected from the group consisting of D, L, M, S, Y and no amino acid, X_{15} is selected from the group consisting of H, I, P, V, W and no amino acid, X_{16} is selected from the group consisting of F, G, L, R, S, Y and no amino acid, X_{17} is selected from the group consisting of D, F, V, W, Y and no amino acid, X_{18} is selected from the group consisting of C, F, L, P, S and Y, X_{19} is selected from the group consisting of D, F, G and Y, X_{20} is selected from the group consisting of A, C, G, P, R, V and Y, X_{21} is selected from the group consisting of F, L, M, S and no amino acid, X_{22} is selected from the group consisting of A, D and no amino acid, X_{23} is selected from the group consisting of I, L, V, Y and no amino acid; $X_1YSSGWX_2X_3YGX_4X_5DX_6$ (SEQ ID NO:1070), wherein X_1 is selected from the group consisting of M and V, X_2 is selected from the group consisting of S and no amino acid, X_3 is selected from the group consisting of F and no amino acid, X_4 is selected from the group consisting of V and no amino acid, X_5 is selected from the group consisting of F and M, X_6 is selected from the group consisting of V and Y; and $RX_1X_2X_3PFX_4Y$ (SEQ ID NO:1071), wherein X_1 is selected from the group consisting of G, H, L, N and R, X_2 is selected from the group consisting of E, T and W, X_3 is selected from the group consisting of L, N, T and V, X_4 is selected from the group consisting of D and E.

[000170]In one embodiment, the isolated antigen binding protein further comprises (A) a CDRL selected from the group consisting of: (i) a CDRL1 selected from the group consisting of SEQ ID NO:189-217; (ii) a CDRL1 that differs in amino acid sequence from the CDRL1 of (i) by an amino acid addition, deletion or substitution of not more than two amino acids; (iii) a CDRL1 amino acid sequence selected from the group consisting of $X_1SSQSLX_2X_3SDGX_4TYLX_5$ (SEQ ID NO:1035), wherein X_1 is selected from the group consisting of K and R, X_2 is selected from the group consisting of L and V, X_3 is selected from the group consisting of H and Y, X_4 is selected from the group consisting of K and N, X_5 is selected from the group consisting of N, S and Y; $RASQX_1ISX_2YLN$ (SEQ ID NO:1036), wherein X_1 is selected from the group consisting of R, S and T, X_2 is selected from the group consisting of R and S; $RASQX_1IX_2X_3X_4LX_5$ (SEQ ID NO:1037), wherein X_1 is selected from the group consisting of D, G, S and T, X_2 is selected from

the group consisting of A, R and S, X_3 is selected from the group consisting of H, I, N, R, S and T, X_4 is selected from the group consisting of D, W and Y, X_5 is selected from the group consisting of A, G and N; QASQDI$X_1X_2X_3$LN (SEQ ID NO:1038), wherein X_1 is selected from the group consisting of S and T, X_2 is selected from the group consisting of D and N, X_3 is selected from the group consisting of S and Y; RASQX_1V$X_2X_3X_4X_5$LA (SEQ ID NO:1039), wherein X_1 is selected from the group consisting of S and T, X_2 is selected from the group consisting of I and S, X_3 is selected from the group consisting of R and S, X_4 is selected from the group consisting of S, N and no amino acid, X_5 is selected from the group consisting of Y and no amino acid; and KSSQX_1X_2LX_3X_4SNNKNYLX_5 (SEQ ID NO:1040), wherein X_1 is selected from the group consisting of N and S, X_2 is selected from the group consisting of I and V, X_3 is selected from the group consisting of D and Y, X_4 is selected from the group consisting of N, R and S, X_5 is selected from the group consisting of A and V; or (iv) a CDRL2 selected from the group consisting of SEQ ID NO:218-233; (v) a CDRH2 that differs in amino acid sequence from the CDRL2 of (iv) by an amino acid addition, deletion or substitution of not more than two amino acids; or (vi) a CDRl2 amino acid sequence selected from the group consisting of X_1X_2SNX_3X_4S (SEQ ID NO:1041), wherein X_1 is selected from the group consisting of E and K, X_2 is selected from the group consisting of I and V, X_3 is selected from the group consisting of R and W, X_4 is selected from the group consisting of D and F; $X_1X_2SX_3$LQS (SEQ ID NO:1042), wherein X_1 is selected from the group consisting of A and T, X_2 is selected from the group consisting of A, E and V, X_3 is selected from the group consisting of S and T; X_1ASX_2LQS (SEQ ID NO:1043), wherein X_1 is selected from the group consisting of A and V, X_2 is selected from the group consisting of S and T; DASX_1LET (SEQ ID NO:1044), wherein X_1 is selected from the group consisting of I and N; GASSRAT (SEQ ID NO:223); and WASX_1RES (SEQ ID NO:1045), wherein X_1 is selected from the group consisting of A and T; or B) a CDRH selected from the group consisting of: (i) a CDRH1 selected from the group consisting of SEQ ID NO:275-299; (ii) a CDRH1 that differs in amino acid sequence from the CDRH1 of (i) by an amino acid addition, deletion or substitution of not more than two amino acids; (iii) a CDRH1 amino acid sequence selected from the group consisting of GYTX_1T$X_2X_3X_4X_5X_6$ (SEQ ID NO:1052), wherein X_1 is selected from the group consisting of F and L, X_2 is selected from the group consisting of E, G and S, X_3 is selected from the group consisting of H, L and Y, X_4 is selected from the group consisting of G, S and Y, X_5 is selected from the group consisting of I and M, X_6 is selected from the group consisting of H and S; GYX_1FTSYWIG (SEQ ID NO:1053), wherein X_1 is selected from the group consisting of R and S; GFTFX_1SX_2X_3MH (SEQ ID NO:1054), wherein X_1 is selected from the group consisting of R and S, X_2 is selected from the group consisting of H and Y, X_3 is selected from the group consisting of D and G; GFX_1FSX_2YX_3MX_4 (SEQ ID NO:1055), wherein X_1 is selected from the group consisting of P and T, X_2 is selected from the group

consisting of A, R and S, X_3 is selected from the group consisting of A and S, X_4 is selected from the group consisting of N and S; $GX_1SX_2SX_3X_4X_5X_6X_7WX_8$ (SEQ ID NO:1056), wherein X_1 is selected from the group consisting of D and G, X_2 is selected from the group consisting of F, I and V, X_3 is selected from the group consisting of R, S and no amino acid, X_4 is selected from the group consisting of G, Y and no amino acid, X_5 is selected from the group consisting of D, G, S and no amino acid, X_6 is selected from the group consisting of A, S and Y, X_7 is selected from the group consisting of A and Y, X_8 is selected from the group consisting of N and S; GFSLSNARMGVS (SEQ ID NO:279); and $GFSLX_1TGGVGVG$ (SEQ ID NO:1057), wherein X_1 is selected from the group consisting of S and N; (iv) a CDRH2 selected from the group consisting of SEQ ID NO:300-331; (v) a CDRH2 that differs in amino acid sequence from the CDRH2 of (iv) by an amino acid addition, deletion or substitution of not more than two amino acids; or (vi) a CDRH2 amino acid sequence selected from the group consisting of $X_1X_2X_3X_4X_5X_6GX_7TX_8X_9X_{10}QKX_{11}X_{12}$ (SEQ ID NO:1058), wherein X_1 is selected from the group consisting of S and W, X_2 is selected from the group consisting of F and I, X_3 is selected from the group consisting of D, N and S, X_4 is selected from the group consisting of A and P, X_5 is selected from the group consisting of E, N and S, X_6 is selected from the group consisting of D, N and S, X_7 is selected from the group consisting of E, G and N, X_8 is selected from the group consisting of I and N, X_9 is selected from the group consisting of C, H and Y, X_{10} is selected from the group consisting of A and T, X_{11} is selected from the group consisting of F and L, X_{12} is selected from the group consisting of D and G; $IIYPX_1DSDX_2RYSPSFQG$ (SEQ ID NO:1059), wherein X_1 is selected from the group consisting of D and G, X_2 is selected from the group consisting of A, I and T; $X_1IX_2X_3DGSX_4X_5X_6YX_7DSVX_8G$ (SEQ ID NO:1060), wherein X_1 is selected from the group consisting of F and V, X_2 is selected from the group consisting of S and W, X_3 is selected from the group consisting of D, S and Y, X_4 is selected from the group consisting of I, N and T, X_5 is selected from the group consisting of K and Q, X_6 is selected from the group consisting of N, R and Y, X_7 is selected from the group consisting of A, T and V, X_8 is selected from the group consisting of K and R; $X_1ISX_2SX_3X_4X_5X_6YYADSVKG$ (SEQ ID NO:1061), wherein X_1 is selected from the group consisting of A, H and Y, X_2 is selected from the group consisting of G, R and S, X_3 is selected from the group consisting of G and S, X_4 is selected from the group consisting of G, R and S, X_5 is selected from the group consisting of S, T and Y, X_6 is selected from the group consisting of I and T; $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}YX_{12}X_{13}SX_{14}KS$ (SEQ ID NO:1062), wherein X_1 is selected from the group consisting of E, R and Y, X_2 is selected from the group consisting of I and T, X_3 is selected from the group consisting of H, N and Y, X_4 is selected from the group consisting of C, H, S, T and Y, X_5 is selected from the group consisting of S and R, X_6 is selected from the group consisting of G and S, X_7 is selected from the group consisting of G, K, S and T, X_8 is selected

from the group consisting of T and W, X_9 is selected from the group consisting of N and Y, X_{10} is selected from the group consisting of N and no amino acid, X_{11} is selected from the group consisting of D and no amino acid, X_{12} is selected from the group consisting of A and N, X_{13} is selected from the group consisting of P and V, X_{14} is selected from the group consisting of L and V; X_1IFSNDEKSYSTSLKS (SEQ ID NO:1063), wherein X_1 is selected from the group consisting of H and LI; and LIYWNX_1X_2KRYSPSLX_3S (SEQ ID NO:1064), wherein X_1 is selected from the group consisting of D and V, X_2 is selected from the group consisting of D and E, X_3 is selected from the group consisting of K and R.

[000171]In some embodiments, at least two of, or all three of CDRL1, CDRL2, and CDRL3 sequences are derived from the same group A, B, C, D, E, or F of consensus sequences, and/or at least two, or all three of, CDRH1, CDRH2, and CDRH3 sequences are derived from the same group A, B, C, D, E, F, or G. In other cases CDRs from different consensus sequence groups are mixed and matched.

[000172]In yet another embodiment, the isolated antigen binding protein described hereinabove comprises the first amino acid sequence and the second amino acid sequence, both sequences of which are covalently bonded to each other. In a further embodiment, the first amino acid sequence of the isolated antigen binding protein includes the CDRL3 of SEQ ID NO:234-274, CDRL2 of SEQ ID NO:218-233, and CDRL1 of SEQ ID NO:189-217. On the other hand, the second amino acid sequence of the isolated antigen binding protein comprises the CDRH3 of SEQ ID NO:332-372, CDRH2 of SEQ ID NO:300-331, and CDRH1 of SEQ ID NO:275-299.

[000173]In one aspect, the isolated antigen binding proteins provided herein can be a monoclonal antibody, a polyclonal antibody, a recombinant antibody, a human antibody, a humanized antibody, a chimeric antibody, a multispecific antibody, or an antibody fragment thereof.

[000174]In another embodiment, the antibody fragment of the isolated antigen binding proteins provided herein can be a Fab fragment, a Fab' fragment, an $F(ab')_2$ fragment, an Fv fragment, a diabody, or a single chain antibody molecule.

[000175]In a further embodiment, the isolated antigen binding protein provided herein is a human antibody and can be of the IgG1-, IgG2- IgG3- or IgG4-type.

[000176]In yet another aspect, the isolated antigen binding protein provided herein can be coupled to a labeling group, such as radioisotope, radionuclide, a fluorescent group, an enzymatic group, a chemiluminescent group, a biotinyl group, or a predetermined polypeptide group, or an effector group, such as a radioisotope, a radionuclide, a toxin, a therapeutic group, or a chemotherapeutic group. Examples of a therapeutic or chemotherapeutic group are calicheamicin, auristatin-PE, geldanamycin, maytanasine, or derivatives thereof.

[000177]In yet other aspects, the invention includes antigen binding proteins competing with any of the above described antigen binding proteins.

[000178]As will be appreciated by those in the art, for any antigen binding protein with more than one CDR from the depicted sequences, any combination of CDRs independently selected from the depicted sequences is useful. Thus, antigen binding proteins with one, two, three, four, five or six of independently selected CDRs can be generated. However, as will be appreciated by those in the art, specific embodiments generally utilize combinations of CDRs that are non-repetitive, *e.g.*, antigen binding proteins are generally not made with two CDRH2 regions, etc.

[000179]Some of the antigen binding proteins provided are discussed in more detail below.

1. Antigen Binding Proteins And Binding Epitopes

[000180]When an antigen binding protein is said to bind an epitope within specified residues of a polypeptide, such as HB-EGF, for example, what is meant is that the antigen binding protein specifically binds to a polypeptide consisting of the specified residues (*e.g.*, a specified segment of HB-EGF). Such an antigen binding protein typically does not contact every residue within HB-EGF. Nor does every single amino acid substitution or deletion within HB-EGF, or the extracellular domain of HB-EGF, necessarily significantly affect binding affinity. Epitope specificity of an antigen binding protein can be determined in variety of ways. One approach, for example, involves testing a collection of overlapping peptides of about 15 amino acids spanning the sequence of the antigen and differing in increments of a small number of amino acids (*e.g.*, three amino acids). The peptides are immobilized within the wells of a microtiter dish. Immobilization can be effected by biotinylating one terminus of the peptides. Optionally, different samples of the same peptide can be biotinylated at the amino- and the carboxy-terminus and immobilized in separate wells for purposes of comparison. This is useful for identifying end-specific antigen binding proteins. Optionally, additional peptides can be included by terminating at a particular amino acid of interest. This approach is useful for identifying end-specific antigen binding proteins to internal fragments of HB-EGF. An antigen binding protein or immunologically functional fragment is screened for specific binding to each of the various peptides. The epitope is defined as occurring with a segment of amino acids that is common to all peptides to which the antigen binding protein shows specific binding. Details regarding a specific approach for defining an epitope are set forth in Example 23.

[000181]As demonstrated in Example 23, the antigen binding proteins provided herein are capable of binding at least one IHGE-containing epitope and/or an EGF-like domain of HB-EGF.

2. Competing Antigen Binding Proteins

[000182]In another aspect, antigen binding proteins are provided that compete with one of the exemplified antibodies or functional fragments binding to the epitope described above for specific binding to HB-EGF. Such antigen binding proteins may also bind to the same epitope as one of the herein exemplified antigen binding proteins, or an overlapping epitope. Antigen binding proteins and fragments that compete with or bind to the same epitope as the exemplified antigen binding proteins are expected to show similar functional properties. The exemplified antigen binding proteins and fragments include those described above, including those with the heavy and light chains, variable region domains and CDRs included in FIGURES 1, 2, 3, 4, 6, and 7.

3. Human Antibodies and Humanization of Antibodies

[000183]In one embodiment, the HB-EGF antigen binding proteins are human or humanized antibodies. Human antibodies avoid many of the problems associated with antibodies that possess murine or rat variable and/or constant regions. The presence of such murine or rat derived proteins can lead to the rapid clearance of the antibodies or can lead to the generation of an immune response against the antibody by a patient. In order to avoid the utilization of murine or rat derived antibodies, fully human antibodies have been generated through the introduction of functional human antibody genetic loci into a rodent, other mammal or animal so that the rodent, other mammal or animal produces fully human antibodies.

[000184]One method for generating fully human antibodies is through the use of XenoMouse® strains of mice that have been engineered to contain up to but less than 1000 kb-sized germline configured fragments of the human heavy chain locus and kappa light chain locus. *See,* Mendez *et al.*, 1997, *Nature Genetics* 15:146-156, and Green and Jakobovits, 1998, *J. Exp. Med.* 188:483-495. The XenoMouse® strains are available from Abgenix, Inc. (Fremont, CA).

[000185]The production of the XenoMouse® strains of mice is discussed and delineated in U.S. Patent Application Serial Nos. 07/466,008, filed January 12, 1990, 07/610,515, filed November 8, 1990, 07/919,297, filed July 24, 1992, 07/922,649, filed July 30, 1992, 08/031,801, filed March 15, 1993, 08/112,848, filed August 27, 1993, 08/234,145, filed April 28, 1994, 08/376,279, filed January 20, 1995, 08/430, 938, filed April 27, 1995, 08/464,584, filed June 5, 1995, 08/464,582, filed June 5, 1995, 08/463,191, filed June 5, 1995, 08/462,837, filed June 5, 1995, 08/486,853, filed June 5, 1995, 08/486,857, filed June 5, 1995, 08/486,859, filed June 5, 1995, 08/462,513, filed June 5, 1995, 08/724,752, filed October 2, 1996, 08/759,620, filed December 3, 1996, U.S. Publication 2003/0093820, filed November 30, 2001 and U.S. Patent Nos. 6,162,963, 6,150,584, 6,114,598, 6,075,181, and 5,939,598 and Japanese Patent Nos. 3 068 180 B2, 3 068 506 B2, and 3 068 507 B2. *See, also* European Patent No., EP 0 463 151 B1, grant

published June 12, 1996, International Patent Application No., WO 94/02602, published February 3, 1994, International Patent Application No., WO 96/34096, published October 31, 1996, WO 98/24893, published June 11, 1998, WO 00/76310, published December 21, 2000. The disclosures of each of the above-cited patents, applications, and references are hereby incorporated by reference in their entirety.

[000186]In an alternative approach, others, including GenPharm International, Inc., have utilized a "minilocus" approach. In the minilocus approach, an exogenous Ig locus is mimicked through the inclusion of pieces (individual genes) from the Ig locus. Thus, one or more V_H genes, one or more D_H genes, one or more J_H genes, a mu constant region, and usually a second constant region (preferably a gamma constant region) are formed into a construct for insertion into an animal. This approach is described in U.S. Patent No. 5,545,807 to Surani *et al.* and U.S. Patent Nos. 5,545,806, 5,625,825, 5,625,126, 5,633,425, 5,661,016, 5,770,429, 5,789,650, 5,814,318, 5,877,397, 5,874,299, and 6,255,458 each to Lonberg and Kay, U.S. Patent No. 5,591,669 and 6,023.010 to Krimpenfort and Berns, U.S. Patent Nos. 5,612,205, 5,721,367, and 5,789,215 to Berns *et al.*, and U.S. Patent No. 5,643,763 to Choi and Dunn, and GenPharm International U.S. Patent Application Serial Nos. 07/574,748, filed August 29, 1990, 07/575,962, filed August 31, 1990, 07/810,279, filed December 17, 1991, 07/853,408, filed March 18, 1992, 07/904,068, filed June 23, 1992, 07/990,860, filed December 16, 1992, 08/053,131, filed April 26, 1993, 08/096,762, filed July 22, 1993, 08/155,301; filed November 18, 1993, 08/161,739, filed December 3, 1993, 08/165,699, filed December 10, 1993, 08/209,741, filed March 9, 1994, the disclosures of which are hereby incorporated by reference. *See, also* European Patent No. 0 546 073 B1, International Patent Application Nos. WO 92/03918, WO 92/22645, WO 92/22647, WO 92/22670, WO 93/12227, WO 94/00569, WO 94/25585, WO 96/14436, WO 97/13852, and WO 98/24884 and U.S. Patent No. 5,981,175, the disclosures of which are hereby incorporated by reference in their entirety.

[000187]Kirin has also demonstrated the generation of human antibodies from mice in which, through microcell fusion, large pieces of chromosomes, or entire chromosomes, have been introduced. *See,* European Patent Application Nos. 773 288 and 843 961, the disclosures of which are hereby incorporated by reference. Additionally, KM™ mice, which are the result of cross-breeding of Kirin's Tc mice with Medarex's minilocus (Humab) mice have been generated. These mice possess the human IgH transchromosome of the Kirin mice and the kappa chain transgene of the Genpharm mice (Ishida *et al.*, 2002, *Cloning Stem Cells* 4:91-102).

[000188]Human antibodies can also be derived by *in vitro* methods. Suitable examples include but are not limited to phage display (CAT, Morphosys, Dyax, Biosite/Medarex, Xoma, Symphogen, Alexion (formerly Proliferon), Affimed) ribosome display (CAT), yeast display, and the like.

E. Preparation of Antibodies

[000189]Antibodies, as described herein, were prepared through the utilization of the XenoMouse® technology, as described herein. Such mice are capable of producing human immunoglobulin molecules and antibodies and are substantially deficient in the production of murine immunoglobulin molecules and antibodies. Technologies utilized for achieving production of human antibodies are disclosed in the patents, applications, and references disclosed herein. In some embodiments, transgenic production of mice and human antibodies is performed as disclosed in U.S. Patent Application Serial No. 08/759,620, filed December 3, 1996 and International Patent Application Nos. WO 98/24893, published June 11, 1998 and WO 00/76310, published December 21, 2000, the disclosures of which are hereby incorporated by reference. *See, also* Mendez *et al.*, 1997, *Nature Genetics* 15:146-156, the disclosure of which is hereby incorporated by reference.

[000190]Through the use of such technology, fully human monoclonal antibodies to a variety of antigens have been produced. Essentially, XenoMouse® lines of mice are immunized with an antigen of interest (*e.g.*,HB-EGF), lymphatic cells (such as B-cells) are recovered from the hyper-immunized mice, and the recovered lymphocytes are fused with a myeloid-type cell line to prepare immortal hybridoma cell lines. These hybridoma cell lines are screened and selected to identify hybridoma cell lines that produced antibodies specific to the antigen of interest. The supernatants might also be screened for immunoreactivity against fragments of HB-EGF to further map the different antibodies for binding to domains of functional interest on HB-EGF. The antibodies may also be screened for binding to other ligand of EGFR or its family members, other related human chemokines and against the rat, the mouse, and non-human primate, such as cynomolgus monkey, orthologues of HB-EGF, the last to determine species cross-reactivity. Provided herein are methods for the production of multiple hybridoma cell lines that produce antibodies specific to HB-EGF. Further, provided herein are characterization of the antibodies produced by such cell lines, including nucleotide and amino acid sequence analyses of the heavy and light chains of such antibodies.

[000191]Alternatively, instead of being fused to myeloma cells to generate hybridomas, B cells can be directly assayed. For example, B cells can be isolated from hyperimmune XenoMouse® mice and allowed to proliferate and differentiate into antibody-secreting plasma cells. Antibodies from the cell supernatants are then screened by ELISA for reactivity against the HB-EGF immunogen. The supernatants might also be screened for immunoreactivity against fragments of HB-EGF to further map the different antibodies for binding to domains of functional interest on HB-EGF. The antibodies may also be screened for binding to other ligands of EGF receptor, or its family members, other related human chemokines and against the rat, the mouse, and non-

human primate, such as cynomolgus monkey, orthologues of HB-EGF, the last to determine species cross-reactivity. B cells from wells containing antibodies of interest may be immortalized by various methods including fusion to make hybridomas either from individual or from pooled wells, or by infection with EBV or transfection by known immortalizing genes and then plating in suitable medium. Alternatively, single plasma cells secreting antibodies with the desired specificities are then isolated using an HB-EGF-specific hemolytic plaque assay (Babcook *et al.*, 1996, *Proc. Natl. Acad. Sci. USA* 93:7843-48). Cells targeted for lysis are preferably sheep red blood cells (SRBCs) coated with the HB-EGF antigen.

[000192]As discussed, *supra*, there are a number of isotypes of antibodies including without limitation the following: human IgG1, IgG2, IgG3 and IgG4. It will be appreciated that antibodies that are generated need not initially possess such an isotype but, rather the antibody as generated can possess any isotype and that the antibody can be isotype-switched by using the molecularly cloned V region genes or cloned constant region genes or cDNAs in appropriate expression vectors using conventional molecular biological techniques that are well known in the art and then expressing the antibodies in host cells using techniques known in the art

[000193]In general, antibodies produced by the fused hybridomas were either human IgG2 heavy chains or human IgG4 heavy chains with fully human kappa chains. Antibodies can also be of other human isotypes, including IgG1 or IgG3. The antibodies possessed high affinities, typically possessing a K_D of from about 10^{-6} through about 10^{-12} M or below, when measured by solid phase and solution phase techniques. Antibodies possessing a K_D of at least 10^{-9} M are preferred to inhibit the activity of HB-EGF. Antibodies possessing a K_D of at least 10^{-10} M are also preferred to inhibit the activity of HB-EGF. Antibodies possessing a K_D of at least 10^{-11} M are also preferred to inhibit the activity of HB-EGF.

[000194]As will be appreciated, anti-HB-EGF antibodies can be expressed in cell lines other than hybridoma cell lines. Sequences encoding particular antibodies can be used to transfect a suitable mammalian host cell. During construction of appropriate vectors for transfection and subsequent expression of antibody, the antibody may be class-switched from one isotype to another, *e.g.*, IgG4 antibodies may be class-switched to IgG2, by techniques known in the art. Transfection can be by any known method for introducing polynucleotides into a host cell, including, for example packaging the polynucleotide in a virus (or into a viral vector) and transducing a host cell with the virus (or vector) or by transfection procedures known in the art, as exemplified by U.S. Patent Nos. 4,399,216, 4,912,040, 4,740,461, and 4,959,455 (which patents are hereby incorporated herein by reference). The transformation procedure used depends upon the host to be transformed. Methods for introducing heterologous polynucleotides into mammalian cells are well known in the art and include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion,

electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

[000195]Mammalian cell lines available as hosts for expression are well known in the art and include many immortalized cell lines available from the American Type Culture Collection (ATCC), including but not limited to Chinese hamster ovary (CHO) cells, HeLa cells, baby hamster kidney (BHK) cells, monkey kidney cells (COS), human hepatocellular carcinoma cells (*e.g.*, Hep G2), human epithelial kidney 293 cells, and a number of other cell lines. Cell lines of particular preference are selected through determining which cell lines have high expression levels and produce high amounts of anti-HB-EGF antibodies.

[000196]Alternatively, these antibodies may be prepared from animals genetically engineered to make fully human antibodies or from an antibody display library made in bacteriophage, yeast, ribosome or *E. coli*. *See, e.g.,*Clackson *et al.*,1991, *Nature* 352:624-628, Marks *et al.*,1991, *J. Mol. Biol.* 222: 581-597, Feldhaus and Siegel, 2004, *J. Immunol. Methods.* 290:69-80, Groves and Osbourn, 2005, *Expert Opin Biol Ther.* 5:125-135 and Jostock and Dubel, 2005, *Comb Chem High Throughput Screen.* 8:127-133.

[000197]Another aspect relates to an isolated nucleic acid molecule encoding an HB-EGF antigen binding protein such as an antibody. Within the context herein, the term "isolated nucleic acid molecule", as used herein, means a polynucleotide of genomic, cDNA, or synthetic origin or some combination thereof, which by virtue of its origin, the "isolated nucleic acid molecule" (1) is not associated with all or a portion of a polynucleotide in which the "isolated polynucleotide" is found in nature, (2) is operably linked to a polynucleotide which it is not linked to in nature, or (3) does not occur in nature as part of a larger sequence. Further, the term "nucleic acid molecule", as referred to herein, means a polymeric form of nucleotides of at least 10 bases in length, either ribonucleotides or deoxynucleotides or a modified form of either type of nucleotide, such as nucleotides with modified or substituted sugar groups and the like. The term also includes single and double stranded forms of DNA. Exemplatory nucleic acids encoding antigen binding proteins or portions thereof are described in more detail, *infra*.

[000198]In a one embodiment, a nucleic acid molecule is operably linked to a control sequence. The term "control sequence", as used herein, refers to polynucleotide sequences that are necessary to effect the expression and processing of coding sequences to which they are ligated. The nature of such control sequences differs depending upon the host organism. In prokaryotes, such control sequences generally include promoters, ribosomal binding sites, and transcription termination sequences. In eukaryotes, generally, such control sequences include promoters and transcription termination sequences. The term "control sequence" is intended to include, at a minimum, all components whose presence is essential for expression and processing, and can also include additional components whose presence is advantageous, for

example, leader sequences and fusion partner sequences. Furthermore, the term "operably linked", as used herein, refers to positions of components so described which are in a relationship permitting them to function in their intended manner. Moreover, as provided herein, an expression control sequence operably linked to a coding sequence is ligated in such a way that expression of the coding sequence is achieved under conditions compatible with the expression control sequence.

[000199]A further aspect is a vector comprising a nucleic acid molecule that encodes an HB-EGF antigen binding protein provided herein. The nucleic acid molecule can be operably linked to a control sequence. Furthermore, the vector may additionally contain a replication origin or a selection marker gene. Examples of vectors that may be used are *e.g.*,plasmids, cosmids, phages, viruses, etc.

F. Antigen Binding Proteins Based On Basic Antibody Structure

[000200]As discussed, *supra*, the basic antibody structural unit is known to comprise a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kDa) and one "heavy" chain (about 50-70 kDa). The amino-terminal portion of each chain includes a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The carboxy-terminal portion of each chain defines a constant region responsible for dimerization effector function, circulating half-life and other functions. Human light chains are classified as kappa and lambda light chains. Heavy chains are classified as mu, delta, gamma, alpha, or epsilon, and define the antibody's isotype as IgM, IgD, IgG, IgA, and IgE, respectively. Within light and heavy chains, the variable and constant regions are joined by a "J" region of about 12 or more amino acids, with the heavy chain also including a "D" region of about 10 more amino acids. *See*, generally, Fundamental Immunology Ch. 7 (Paul, W., ed., 2nd ed. Raven Press, N.Y. (1989)) (incorporated by reference in its entirety for all purposes). The variable regions of each light/heavy chain pair form the antigen binding site of the antibody.

[000201]Thus, an intact IgG antibody has two binding sites. Except in bifunctional or bispecific antibodies, the two binding sites are the same.

[000202]The variable regions of the chains all exhibit the same general structure of relatively conserved framework regions (FR) joined by three hyper variable regions, also called complementarity determining regions or CDRs. The CDRs from the two variable regions of each pair are aligned by the framework regions, enabling binding to a specific epitope on the antigen. From N-terminal to C-terminal, the variable regions of both light and heavy chains comprise the domains FR1, CDR1, FR2, CDR2, FR3, CDR3 and FR4. The assignment of amino acids to each domain is in accordance with the definitions of Kabat Sequences of Proteins of

Immunological Interest (National Institutes of Health, Bethesda, Md. (1987 and 1991)), or Chothia & Lesk, 1897, *J. Mol. Biol.* 196:901-917; Chothia *et al.*, 1989, *Nature* 342:878-883.

[000203]Thus, the antibodies provided herein may include at least one variable region polypeptide chain of the formula: FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4, wherein FR1 is a first human framework region, CDR1 is a first complementarity determining region, FR2 is a second human framework region, CDR2 is a second complementarity determining region, FR3 is a third human framework region, CDR3 is a third complementarity determining region, and FR4 is a fourth human framework region. The CDR3 is generally the most diverse region of the antibody variable region.

[000204]In some embodiments, the FR1 region includes but is not limited to any one of amino acid sequences SEQ ID NOs:373-393 and/or 453-469; the CDR1 region includes but is not limited to any one of amino acid sequences SEQ ID NOs:189-217 and/or 275-299; the FR2 region includes but is not limited to any one of amino acid sequences SEQ ID NOs:394-414 and/or 470-481; the CDR2 region includes but is not limited to any one of amino acid sequences SEQ ID NOs:218-233 and/or 300-331; the FR3 region includes but is not limited to any one of amino acid sequences SEQ ID NOs:415-440 and/or 482-511; the CDR3 region includes but is not limited to any one of amino acid sequences SEQ ID NOs:234-274 and/or 332-372; and the FR4 region includes but is not limited to any one of amino acid sequences SEQ ID NOs:441-452 and/or 512-517. Thus, in some embodiments, the human antibodies provided herein have one or more of the amino acid sequences provided herein.

[000205]It is to be understood, that the amino acid sequence of the antibodies provided herein is not limited to the twenty conventional amino acids (*See, Immunology - A Synthesis* (2nd Edition, E.S. Golub and D.R. Gren, Eds., Sinauer Associates, Sunderland, Mass. (1991)), which is incorporated herein by reference). For example, the amino acids may include stereoisomers (*e.g.*,D-amino acids) of the twenty conventional amino acids, unnatural amino acids such as α-,α-disubstituted amino acids, N-alkyl amino acids, lactic acid, and other unconventional amino acids. Examples of unconventional amino acids, which may also be suitable components for the antibody provided, include: 4-hydroxyproline, γ-carboxyglutamate, ε-N,N,N-trimethyllysine, ε-N-acetyllysine, O-phosphoserine, N-acetylserine, N-formylmethionine, 3-methylhistidine, 5-hydroxylysine, σ-N-methylarginine, and other similar amino acids and imino acids, *e.g.*,4-hydroxyproline.

[000206]Furthermore, minor variations in the amino acid sequences shown in SEQ ID NOs:1-517 and 1035-1071 are contemplated as being encompassed, providing that the variations in the amino acid sequence maintain at least 75%, more preferably at least 80%, 90%, 95%, and most preferably 99% of the sequences shown in SEQ ID NOs:1-517 and 1035-1071. Preferred variations in the amino acid sequences shown in SEQ ID Nos:1-517 and 1035-1071, *i.e.*,

deletions, insertions and/or replacements of at least one amino acid, occur near boundaries of functional domains. Structural and functional domains can be identified by comparison of the nucleotide and/or amino acid sequence data to public or proprietary sequence databases. Computerized comparison methods can be used to identify sequence motifs or predicted protein conformation domains that occur in other antibodies of known structure and/or function. Methods to identify protein sequences that fold into a known three-dimensional structure are known. *See, e.g.,* Bowie *et al.*,1991, *Science* 253:164; *Proteins, Structures and Molecular Principles* (Creighton, Ed., W. H. Freeman and Company, New York (1984)); *Introduction to Protein Structure* (C. Branden and J. Tooze, eds., Garland Publishing, New York, N.Y. (1991)); and Thornton *et al.*, 1991, *Nature* 354:105, which are all incorporated herein by reference. Thus, those of skill in the art can recognize sequence motifs and structural conformations that may be used to define structural and functional domains.

[000207]Especially preferred variations in the amino acid sequences shown in SEQ ID NOs:1-517 and 1035-1071 are those that lead to a reduced susceptibility to proteolysis or oxidation, alter glycosylation patterns or alter binding affinities or confer or modify other physicochemical or functional properties of the antibody. In particular, conservative amino acid replacements are contemplated. Conservative replacements are those that take place within a family of amino acids that are related in their side chains. Preferred amino acid families are the following: acidic family = aspartate, glutamate; basic family = lysine, arginine, histidine; non-polar family = alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan; and uncharged polar family = glycine, asparagine, glutamine, cysteine, serine, threonine, tyrosine. More preferred families are: aliphatic-hydroxy family = serine and threonine; amide-containing family = asparagine and glutamine; aliphatic family = alanine, valine, leucine and isoleucine; and aromatic family = phenylalanine, tryptophan, and tyrosine. For example, it is reasonable to expect that an isolated replacement of a leucine with an isoleucine or valine, an aspartate with a glutamate, a threonine with a serine, or a similar replacement of an amino acid with a structurally related amino acid will not have a major effect on the binding or properties of the resulting antibody, especially if the replacement does not involve an amino acid within a framework site. However, all other possible amino acid replacements are also encompassed. Whether an amino acid change results in a functional antibody, *i.e.,* in a antibody that binds to HB-EGF and reduces, neutralizes or substantially inhibits the function of HB-EGF, can readily be determined by assaying the specific activity of the resulting antibody in ELISA or FACS for binding to HB-EGF or *in vitro* or *in vivo* functional assay.

[000208]A reduction, neutralization or substantially inhibition of HB-EGF mediated signal transduction may be caused by influencing, *e.g.,* decreasing or inhibiting, the binding of HB-EGF to its receptor, *e.g.,* to the EGFR or HER4.

[000209]The term "antibody" or "anti-HB-EGF antibody", as used herein, means a monoclonal antibody, a polyclonal antibody, a recombinant antibody, a humanized antibody (Jones *et al.*, 1986, *Nature* 321:522-525; Riechmann *et al.*, 1988, *Nature* 332:323-329; and Presta, 1992, *Curr. Op. Struct. Biol.* 2: 593-596), a chimeric antibody (Morrison *et al.*, 1984, *Proc. Natl. Acad. Sci. U.S.A.* 81: 6851-6855), a multispecific antibody (*e.g.*,a bispecific antibody) formed from at least two antibodies, or an antibody fragment thereof. The term "antibody fragment" comprises any portion of the afore-mentioned antibodies, preferably at least one of their antigen binding or variable regions. Examples of antibody fragments include Fab fragments, Fab' fragments, $F(ab')_2$ fragments, Fv fragments, diabodies (Hollinger *et al.*, 1993, *Proc. Natl. Acad. Sci. U.S.A.* 90: 6444-6448), single chain antibody molecules (Plückthun in: The Pharmacology of Monoclonal Antibodies 113, Rosenburg and Moore, EDS, Springer Verlag, N.Y. (1994), 269-315) and other fragments as long as they exhibit the desired capability of binding to HB-EGF.

[000210]In addition, the term "antibody" or "anti-HB-EGF antibody", as used herein, may include antibody-like molecules that contain engineered sub-domains of antibodies or naturally occurring antibody variants. These antibody-like molecules may be single-domain antibodies such as VH-only or VL-only domains derived either from natural sources such as camelids (Muyldermans *et al.*, 2001, *Reviews in Molecular Biotechnology* 74, 277-302) or through *in vitro* display of libraries from humans, camelids or other species (Holt *et al.*, 2003,*Trends Biotechnol.* 21:484-90).

[000211]A "Fv fragment" is the minimum antibody fragment that contains a complete antigen-recognition and -binding site. This region consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. It is in this configuration that the three CDR´s of each variable domain interact to define an antigen-binding site on the surface of the V_H-V_L dimer. Collectively, the six CDR´s confer antigen binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDR´s specific for an antigen) has the ability to recognize and bind the antigen, although usually at a lower affinity than the entire binding site. The "Fab fragment" also contains the constant domain of the light chain and the first constant domain (C_H1) of the heavy chain. The "Fab fragment" differs from the "Fab' fragment" by the addition of a few residues at the carboxy terminus of the heavy chain C_H1 domain including one or more cysteines from the antibody hinge region. The "$F(ab')_2$ fragment" originally is produced as a pair of "Fab' fragments" which have hinge cysteines between them. Methods of preparing such antibody fragments, such as papain or pepsin digestion, are known to those skilled in the art.

[000212]An antibody provided herein may fix complement (CDC) or activate antibody-dependent cellular cytotoxicity (ADCC), especially an IgG1 antibody, IgG1 variant class-switched from IgG2 or IgG4 or another isotype of human or mammalian origin, by molecular biology or generated de

novo from human IgG1 producing mice. Other methods may also be used. An antibody provided herein may sometimes be coupled to a labelling group or an effector group, *e.g.*,a toxin, chemotherapeutic agent, reporter molecule or imaging agent.

G. Further types of HB-EGF Binding Proteins

[000213]In another aspect, the HB-EGF antigen binding protein as provided herein is a scaffold protein having an antibody like binding activity, *i.e.*, binds to HB-EGF.

[000214]Within the context of the present invention, the term "scaffold protein", as used herein, means a polypeptidic framework with a high tolerance of its fold for modifications such as multiple insertions, deletions or substitutions. This intrinsic conformational stability enables the directed randomization and drastic changes within a defined region of the protein. Thus, it acquires certain novel properties, whereas its overall structural integrity and original physicochemical behaviour remains conserved. This *de novo* adopted property mostly, but not exclusively, comprises the binding specificity for a pre-defined target molecule.

[000215]Currently, a broad variety of scaffold proteins are in use that imitate the binding principle of a conventional antibody to different degrees (Hey et al., 2005, *Trends in Biotechnol.* 23:514-22). Examples of scaffold proteins that can be used in accordance with the present invention can be subdivided into different groups. Antibody related scaffolds, which are defined as derivatives of antibodies that are either naturally smaller in size and simpler in structure, or have been engineered in this way. This group includes for example so called Nanobodies (reviewed in Hey et al., Trends in Biotechnol. 2005; 23 (10); 514-522), domain antibodies (Holt et al., 2003, *Trends in Biotechnol.* 21:484-489) or shark antigen reactive proteins (Holt et al.,Trends in Biotechnol. 2003; 21; 484-489). A second group of scaffold proteins are rigid protein folds which tolerate the insertion or randomization of single loop peptides like the Kunitz-type domain (Dennis *et al.*, 1995; *J. Biol. Cell.* 270:25411-25417), huma transferrin (Ali *et al.*, 1999; *J. Biol. Cell.* 274:24066-24074) or cystein-knot structural motives (Christmann *et al.*, 1999, *Protein Eng.* 12:797-806). Proteins that share the principle of multiple hypervariable loops on a rigid conserved framework in analogy to antibodies are represented by human CTLA-4 (Hufton *et al.*, 2000 *FEBS Lett.* 475:225-231), human fibronectin type III domains (Koide *et al.*, 1998; *J. Mol. Biol.* 284:1141-1151), C-type lectin like domains or lipocalins (Skerra, 2001, *J. Biotechnol.* 74:257-275). Scaffolds with the binding specificity accomplished through aminoacid residues which are positioned partially or completely within the rigid secondary structure of the protein are for example ankyrin repeat proteins (Binz, 2003, *J. Mol. Biol.* 332:489-503), the Z domain of proteinA (Nord *et al.*, 1995, *Protein Eng.* 8:601-608) or γ-crystalline (Fiedler and Rudolph, 2001, International Patent Application WO 01/04144). Scaffold proteins and peptides and applications

thereof are reviewed in Hey *et al.*, 2005, *Trends in Biotechnol.* 23:514-522; Binz *et al.*, 2005, *Nature Biotechnol.* 23:1257-1268) and Holliger *et al.*, 2005, *Nature Biotechnol.* 23:11261136.

[000216]Engineering of a scaffold protein can be regarded as grafting or integrating an affinity function onto or into the structural framework of a polypeptidic framework with a high tolerance of its fold for modifications. Affinity function means a protein binding affinity according to the present invention. A scaffold can be structurally separable from the amino acid sequences conferring binding specificity. In general, proteins appearing suitable for the development of such artificial affinity reagents may be obtained by rational, or most commonly, combinatorial protein engineering techniques such as panning against an antigen, *e.g* , HB-EGF, either purified protein or protein displayed on the cell surface, for binding agents in an artificial scaffold library displayed in vitro, using skills which are known in the art (Skerra, 2000, *J. Mol. Recog.* Jul-Aug;13(4):167-87; Binz and Plückthun, 2005, Aug;16(4):459-69). In addition, a scaffold protein having an antibody like binding activity can be derived from an acceptor polypeptide, e.g one of the foregoing proteins, containing the scaffold domain, which can be grafted with binding domains of a donor polypeptide to confer the binding specificity of the donor polypeptide onto the scaffold domain containing the acceptor polypeptide. Said inserted binding domains may be, for example, one or more of the complementarity determining region (CDR) of an antibody, in particular an HB-EGF antibody. Preferably the CDR is a CDR3. Insertion can be accomplished by various methods known to those skilled in the art including, for example, polypeptide synthesis, nucleic acid synthesis of an encoding amino acid as well by various forms of recombinant methods well known to those skilled in the art.

H. HB-EGF Antigen Binding Protein Conjugates

[000217]In another embodiment, an HB-EGF antigen binding protein, *e.g.*,an antibody provided herein is coupled to a labelling group. Such a labelled antigen binding protein is particularly suitable for diagnostic applications. As used herein, the term "labelling group" refers to a detectable marker, *e.g.*,a radiolabelled amino acid or biotinyl moiety that can be detected by marked avidin (*e.g.*,streptavidin bound to a fluorescent marker or enzymatic activity that can be detected by optical or colorimetric methods). Various methods for labelling polypeptides and glycoproteins, such as antibodies, are known in the art and may be used. Examples of suitable labelling groups include, but are not limited to, the following: radioisotopes or radionuclides (*e.g.*,^{3}H, ^{14}C, ^{15}N, ^{35}S, ^{90}Y, ^{99}Tc, ^{111}In, ^{125}I, ^{131}I), fluorescent groups (*e.g.*,FITC, rhodamine, lanthanide phosphors), enzymatic groups (*e.g.*, horseradish peroxidase, β-galactosidase, luciferase, alkaline phosphatase), chemiluminescent groups, biotinyl groups, or predetermined polypeptide epitopes recognized by a secondary reporter (*e.g.*,leucine zipper pair sequences, binding sites for secondary antibodies, metal binding domains, epitope tags). In certain

respects, it may be desirable that the labelling groups are attached by spacer arms of various lengths to reduce potential steric hindrance.

[000218]Alternatively, an HB-EGF antigen binding protein provided herein, such as an antibody, may be coupled to an effector group. Such an effector-modified antigen binding protein is especially suitable for therapeutic applications. As used herein, the term "effector group" refers to a cytotoxic group such as a radioisotope or radionuclide, a toxin, a therapeutic group or other effector group known in the art. Examples for suitable effector groups are radioisotopes or radionuclides (*e.g.*, ^{3}H, ^{14}C, ^{15}N, ^{35}S, ^{90}Y, ^{99}Tc, ^{111}In, ^{125}I, ^{131}I), calicheamicin, dolastatin analogs such as auristatins, and chemotherapeutic agents such as geldanamycin and maytansine derivates, including DM1. In certain respects, it may be desirable that the effector groups are attached by spacer arms of various lengths to reduce potential steric hindrance.

[000219]Also as described herein, many of the highly useful HB-EGF antigen binding protein, *e.g.*,antibody preparations provided herein recognize epitopes within the EGF-like domain of HB-EGF, which includes residues 106-149 of the protein, for example, with the following sequence:

[000220]PCLRKYKDFCIHGECKYVKELRAPSCICHPGY HGERCHGLSLP (SEQ ID NO:1076).

In some embodiments, the epidermal pgrowth factor epitope recognized by the antigen binding proteins provided herein includes amino acid sequence IHGE. Accordingly, antibody preparations are provided that bind to and recognize an IHGE-containing epitope and/or an EGF-like domain of HB-EGF, for example, SEQ ID NO:1076.

[000221]Anti-HB-EGF antigen binding proteins are useful in the detection of HB-EGF in patient samples and accordingly are useful as diagnostics for disease states as described herein. In addition, based on their ability to significantly inhibit HB-EGF and/or EGF receptor activity (as demonstrated in the Examples below), HB-EGF antigen binding proteins have therapeutic effects in treating symptoms and conditions resulting from HB-EGF expression and/or HB-EGF activity. In specific embodiments, the antigen binding proteins and methods herein relate to the treatment of symptoms resulting from HB-EGF-associated diseases, HER4-associated diseases or EGF receptor-associated disease states, for example, cancerous conditions. Further embodiments involve using the antigen binding proteins and methods described herein to treat undesired angiogenesis, neoplastic diseases, such as, melanoma, non-small cell lung cancer, glioma, hepatocellular (liver) carcinoma, thyroid tumor, gastric (stomach) cancer, prostrate cancer, breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma, endometrial cancer, kidney cancer, colon cancer, and pancreatic cancer.

[000222]

I. Nucleic Acids Encoding HB-EGF Antigen Binding Proteins

[000223]Nucleic acids that encode for the antigen binding proteins described herein, or portions thereof, are also provided, including nucleic acids encoding one or both chains of an antibody, or

a fragment, derivative, mutein, or variant thereof, polynucleotides encoding heavy chain variable regions or only CDRs, polynucleotides sufficient for use as hybridization probes, PCR primers or sequencing primers for identifying, analyzing, mutating or amplifying a polynucleotide encoding a polypeptide, anti-sense nucleic acids for inhibiting expression of a polynucleotide, and complementary sequences of the foregoing. The nucleic acids can be any length. They can be, for example, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 125, 150, 175, 200, 250, 300, 350, 400, 450, 500, 750, 1,000, 1,500, 3,000, 5,000 or more nucleotides in length, and/or can comprise one or more additional sequences, for example, regulatory sequences and/or be part of a larger nucleic acid, for example, a vector. The nucleic acids can be single-stranded or double-stranded and can comprise RNA and/or DNA nucleotides, and artificial variants thereof (*e.g.*, peptide nucleic acids). FIGURES 15A - 15V depict the nucleotide sequences for the various light chains of the antigen binding proteins. FIGURES 16A – 16AC deptice the nucleotide sequences for the various heavy chains of the antigen binding proteins. FIGURES 13A - 13M depict the nucleotide sequences of various light chain variable regions of the antigen binding proteins. FIGURES 14A – 14L depict the nucleotide sequences of various heavy chain variable regions of the antigen binding proteins. FIGURES 18A - 18F depict the nucleotide sequences for various CDR regions of the light chain variable regions of the antigen binding proteins. FIGURES 19A-19G depict the nucleotide sequences for various CDR regions of the heavy chain variable regions of the antigen binding proteins. FIGURES 20A – 20K depict the nucleotide sequences for various FR regions of the light chain variable regions of the antigen binding proteins. FIGURES 21A – 21K depict the nucleotide sequences for various FR regions of the heavy chain, variable regions of the antigen binding proteins. FIGURE 17A depicts the nucleotide sequence of the light chain constant region of the antigen binding proteins. Finally, FIGURE 17B depicts the nucleotide sequence of the heavy chain constant region of the antigen binding proteins.

[000224]Nucleic acids encoding certain antigen binding proteins, or portions thereof (*e.g.*, full length antibody, heavy or light chain variable domain or CDRH1, CDRH2, CDRH3, CDRL1, CDRL2, or CDRL3) may be isolated from B-cells of mice that have been immunized with HB-EGF or an immunogenic fragment thereof. The nucleic acid may be isolated by conventional procedures such as polymerase chain reaction (PCR). Phage display is another example of a known technique whereby derivatives of antibodies and other antigen binding proteins may be prepared. In one approach, polypeptides that are components of an antigen binding protein of interest are expressed in any suitable recombinant expression system, and the expressed polypeptides are allowed to assemble to form antigen binding protein molecules.

[000225]An aspect further provides nucleic acids that hybridize to other nucleic acids (*e.g.*, nucleic acids comprising a nucleotide sequence depicted in FIGURES 13 through 21) under

particular hybridization conditions. Methods for hybridizing nucleic acids are well-known in the art. *See, e.g.*, Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. As defined herein, a moderately stringent hybridization condition uses a prewashing solution containing 5x sodium chloride/sodium citrate (SSC), 0.5% SDS, 1.0 mM EDTA (pH 8.0), hybridization buffer of about 50% formamide, 6x SSC, and a hybridization temperature of 55°C (or other similar hybridization solutions, such as one containing about 50% formamide, with a hybridization temperature of 42°C), and washing conditions of 60°C, in 0.5x SSC, 0.1% SDS. A stringent hybridization condition hybridizes in 6x SSC at 45°C, followed by one or more washes in 0.1 x SSC, 0.2% SDS at 68°C. Furthermore, one of skill in the art can manipulate the hybridization and/or washing conditions to increase or decrease the stringency of hybridization such that nucleic acids comprising nucleotide sequences that are at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or 99% identical to each other typically remain hybridized to each other.

[000226]The basic parameters affecting the choice of hybridization conditions and guidance for devising suitable conditions are set forth by, for example, Sambrook, Fritsch, and Maniatis (2001, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., *supra* and Current Protocols in Molecular Biology, 1995, Ausubel *et al.*, eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4), and can be readily determined by those having ordinary skill in the art based on, *e.g.*, the length and/or base composition of the nucleic acid.

[000227]Changes can be introduced by mutation into a nucleic acid, thereby leading to changes in the amino acid sequence of a polypeptide (*e.g.*, an antibody or antibody derivative) that it encodes. Mutations can be introduced using any technique known in the art. In one embodiment, one or more particular amino acid residues are changed using, for example, a site-directed mutagenesis protocol. In another embodiment, one or more randomly selected residues is changed using, for example, a random mutagenesis protocol. However it is made, a mutant polypeptide can be expressed and screened for a desired property.

[000228]Mutations can be introduced into a nucleic acid without significantly altering the biological activity of a polypeptide that it encodes. For example, one can make nucleotide substitutions leading to amino acid substitutions at non-essential amino acid residues. Alternatively, one or more mutations can be introduced into a nucleic acid that selectively changes the biological activity of a polypeptide that it encodes. For example, the mutation can quantitatively or qualitatively change the biological activity. Examples of quantitative changes include increasing, reducing or eliminating the activity. Examples of qualitative changes include changing the antigen specificity of an antibody.

[000229]Another aspect provides nucleic acid molecules that are suitable for use as primers or hybridization probes for the detection of nucleic acid sequences. A nucleic acid molecule can

comprise only a portion of a nucleic acid sequence encoding a full-length polypeptide, for example, a fragment that can be used as a probe or primer or a fragment encoding an active portion (*e.g.*, a HB-EGF binding portion) of a polypeptide.

[000230]Probes based on the sequence of a nucleic acid can be used to detect the nucleic acid or similar nucleic acids, for example, transcripts encoding a polypeptide. The probe can comprise a label group, *e.g.*, a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used to identify a cell that expresses the polypeptide.

[000231]Another aspect provides vectors comprising a nucleic acid encoding a polypeptide or a portion thereof (*e.g.*, a fragment containing one or more CDRs or one or more variable region domains). Examples of vectors include, but are not limited to, plasmids, viral vectors, non-episomal mammalian vectors and expression vectors, for example, recombinant expression vectors. The recombinant expression vectors can comprise a nucleic acid in a form suitable for expression of the nucleic acid in a host cell. The recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operably linked to the nucleic acid sequence to be expressed. Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cells (*e.g.*, SV40 early gene enhancer. Rous sarcoma virus promoter and cytomegalovirus promoter), those that direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences, *see*, Voss *et al.*, 1986 *Trends Biochem. Sci.* 11:287, Maniatis *et al.*, 1987, *Science* 236:1237, incorporated by reference herein in their entireties), and those that direct inducible expression of a nucleotide sequence in response to particular treatment or condition (*e.g.*, the metallothionin promoter in mammalian cells and the tet-responsive and/or streptomycin responsive promoter in both prokaryotic and eukaryotic systems (*see*, *id.*). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein.

[000232]Another aspect provides host cells into which a recombinant expression vector has been introduced. A host cell can be any prokaryotic cell (for example, *E. coli*) or eukaryotic cell (for example, yeast, insect, or mammalian cells (*e.g.*, CHO cells)). Vector DNA can be introduced into prokaryotic or eukaryotic cells *via* conventional transformation or transfection techniques. For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, for resistance to antibiotics) is generally introduced into the

host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die), among other methods.

J. Use of HB-EGF Antigen Binding Proteins for Diagnostic and Therapeutic Purposes

1. Indications

[000233]The HB-EGF antigen binding proteins as described herein can be used to detect or treat a number of diseases and disorders, including those involving excessive cellular proliferation, undesirable cellular migration and/or aberrant angiogenesis. For example, these HB-EGF antigen binding proteins can inhibit HB-EGF-induced EGFR and/or HER4 tyrosine phosphorylation in cancerous cells (FIGURES 22-29). Such inhibition can interrupt the cascade of the signaling events that drives cell proliferation and migration, and angiogenesis. Further, the HB-EGF antigen binding proteins can interfere with the transactivation of the EGFR. In addition, these antigen binding proteins inhibit basal HUVEC cell proliferation (FIGURE 32B), endothelial cell tube formation (FIGURE 33) and HB-EGF-induced vessel formation in a matrigel plug assay *in vivo* (FIGURE 36). These results indicate that the HB-EGF antigen binding proteins as described herein inhibit angiogenesis *in vitro* and *in vivo*. Moreover, these antigen binding proteins also inhibit anchorage independent cell growth (FIGURE 34 and FIGURE 35) and xenograft tumor growth in mice (FIGURE 37 and FIGURE 38). Significantly, the HB-EGF antigen binding proteins also inhibit migration of MCF-7 and MDA-MB231 cancer cells (*see*, FIGURES 27 and 27). Thus, the HB-EGF antigen binding proteins as described herein attack several steps in the development of tumors and other cancerous conditions, including signaling events that control cell proliferation, angiogenesis and cell migration associated with the spread and development of metastatic cancer. Such multi-faceted intervention is highly beneficial for controlling and inhibiting the process by which cancer develops. Furthermore, cancers at any stage of progression (*e.g.*, primary, metastatic and recurrent cancers) can be treated.

[000234]In addition to the HB-EGF antigen binding proteins' use in detecting and treating cancers in various stages of progression, these antigen binding proteins may also be useful for detecting a number of different types of cancer. For example, HB-EGF is expressed at very low levels in normal breast and pancreatic tissues. However, HB-EGF is expressed at high levels in about 55% pancreatic cancer cells and about 70% of breast cancer cells. Furthermore, as described in the Examples, HB-EGF expression was detected in various cancer cell lines,

indicating that the HB-EGF antigen binding proteins described herein can be used for detection of a variety of cancer types.

[000235]For example, cancers that can be detected or treated by the claimed antigen binding proteins include solid mammalian tumors as well as hematological malignancies. Solid mammalian tumors include cancers in children such as, for example, germ cell tumors, soft tissue sarcomas, primary brain tumors, neuroblastoma, nephroblastoma and carcinoma, in particular squamous carcinoma and epithelial carcinoma. Solid mammalian tumors may also include adult cancers such as, for example, tumors of unknown origin, primary brain cancer in adults, tumors of the pituitary gland, lip, oral cavity, Nasopharynx, larynx, maxillary sinus, Ethmoid sinus, salivary glands, thyroid gland (including para thyroid glands and carcinoid), esophagus, stomach, pancreas, small intestine, colon, rectum, anal canal, liver, gallbladder, extra hepatic bile ducts, ampulla of vater, carcinoid, endocrine tumors of gastro-entero-hepatic system, pheochromocytoma and paraganglioma, adrenal glands, lung, pleura, mediastinum, thymus, tumors of bone and soft tissue, skin tumors of lip, eyelid, external ear, other unspecified parts of the face, scalp and neck, trunk, upper limpb and shoulder, lower limb and hip, vulva, penis, scrotum, breast tumors, gynecological tumors of vulva, vagina, cervix uteri, corpus uteri, ovary, fallopian tube, gestational and trophoblastic tumors, penis, prostate, testis, kidney, renal pelvis and ureter, urinary bladder, urethra, ophthalmic tumors of eyelid, conjunctiva, uvea, retina, orbit and lacrimal gland. Hematological malignancies include childhood, for example, leukemia and lymphomas, acute and chronic leukemia (AML, ANLL, ALL, CML, MDS), Hodgkin's disease, B-Cell, T-Cell, large cell, follicular, indolent/low grade, aggressive/high grade lymphomas of lymphocytic and cutaneous origin, plasma cell neoplasm and cancers associated with AIDS.

[000236]In addition, the HB-EGF antigen binding proteins described herein may also be used to detect or treat cancerous conditions or neoplasia disorders, which include, for example, adenoma, tubulovillous adenoma, villous adenoma, angiofibroma, atypical proliferating mucinous neoplasias, Brenner tumor, carcinoid, cavernous hemangioma, cellular leiomyoma, chorangioma, congenital mesoblastic nephroma, mucinous cystadenoma, serous cystadenoma, dermoid, desmoid, fibroadenoma, fibroma, fibrothecoma, follicular adenoma, ganglioneuroma, giant cell tumor, granular cell tumor, granulosa cell tumor, hemangioma, intraductal papilloma, islet cell tumor, leiomyoma, lipoma, luteoma, meningioma, mole, myelolipoma, myxoma, neurofibroma, nevus, osteochondroma, pheochromocytoma, polyposis, schwannoma, serous cystadenoma, struma ovarii, synovial chrondromatosis, benign thymoma.

[000237]Further examples of the types of cancers that can be detected or treated with the HB-EGF proteins as described herein may be found, for example, from the American Cancer Society (www.cancer.org), or from Wilson *et al.* (1991) Harrison's Principles of Internal Medicine, 12th Edition, McGraw-Hill, Inc.

[000238]Therefore, the HB-EGF antigen binding proteins as described herein can be used to treat and/or prevent cancer, cancerous conditions, tumor growth, metastasis of cancer cells, angiogenic processes and/or neoplastic disorders. Thus, these antigen binding proteins provide a method of treating or preventing cancer in a subject that involves administering to the subject an effective amount of a composition comprising one of the human and/or monoclonal HB-EGF antigen binding protein preparations as described herein, or a combination thereof.

[000239]A high proportion of solid tumor diseases are often characterized by tumor angiogenesis, the excessive growth of (abnormal) vessels in the tumor tissue mediated by growth factors (*i.e.*, VEGF) and other factors (*i.e.*, HB-EGF). Targeting HB-EGF through a HB-EGF-specific antigen binding protein could prevent the formation of new vessels and therefore limit the expansion of existing tumors and the development of new tumors (*i.e.*, metastases).

[000240]Besides its role as a mitogenic and pro-invasive ligand several studies have substantiated the picture of HB-EGF as an important regulator of angiogenic processes in cancer. As illustrated in the Examples, a function of HB-EGF in the regulation of angiogenesis *in vivo* was shown. Thus, the antigen binding proteins as described herein can be used for treating diseases associated with or caused by angiogenesis, *e.g.*, cancerous or non-cancerous diseases.

[000241]For example HB-EGF antigen binding proteins as described herein may interfere with the communication between smooth muscle cells (SMCs) and endothelial cells, a fundamental process in the development and functionality of blood vessels in angiogenesis, *e.g.*, tumor angiogenesis.

[000242]Furthermore, these antigen binding proteins may at least partially inhibit the HB-EGF induced expression and release of VEGF from SMCs which acts subsequently as a powerful endothelial mitogen. Similarly, VEGF increases HB-EGF production in endothelial cells which therefore constitutes a pro-angiogenic feedback loop consisting of these two important ligands that can be disrupted by administering the HB-EGF antigen binding proteins as described herein. Recently, and in addition to VEGF, further critical pro-angiogenic constituents such as angiopoetin 1 and 2 (Ang-1 & 2) and their receptor TIE-2 as well as the potent smooth muscle cell GPCR stimulus angiotensin II (ATII) were identified. Interestingly, HB-EGF is a critical mediator of ATII-induced EGFR transactivation and downstream upregulation of VEGF and Ang-2 in endothelial cells. *In vivo*, ATII induces angiogenesis in an HB-EGF-dependent manner and enhanced the angiogenic activity of VEGF. These findings support that in parallel to VEGF, HB-EGF is able to activate additional angiogenic pathways *via* Ang2. Therefore, aberrant angiogenesis or cancer in a mammal may be treated with the administration of an effective amount of the HB-EGF antigen binding protein described herein.

[000243]Besides its role as an important regulator of angiogenic processes in cancer, various non-cancer indications with activated angiogenic pathways and the requirement of collateral blood flow are putative disease areas for HB-EGF antigen binding protein therapy.

[000244]Chronic inflammatory diseases (*e.g.*,nephritis, COPD, inflammatory bowel disease) including immune system mediated "inflammatory reactions" (*e.g.*,graft versus host disease, transplant rejection, restenosis), metabolic diseases (*e.g.*,diabetes), or chronic hypoxic conditions are often characterized by hyper- and/or neo-vascularization (*e.g.*,chronic ulcers). The described HB-EGF antigen binding proteins may at least partially inhibit the essential process for angiogenesis - the recruitment of vascular smooth muscle cells by endothelial cells induced by HB-EGF either produced by inflammatory cells or upregulated by hypoxia - and represent therefore an attractive route for interventional therapy of excessive/pathological vascularization.

[000245]In obese subjects, increased levels of HB-EGF derived from the accumulated fat which contribute to the higher incidence of vascular disease in obesity, can be neutralized by the HB-EGF antigen binding proteins described herein. A therapeutic intervention with an HB-EGF antigen binding protein may act therefore directly as an anti-adipocytokine in interrupting the adipovascular axis.

[000246]In fibroblasts, HB-EGF significantly downregulates elastin mRNA *via* activation of epidermal growth factor receptor. This effect provides an avenue of intervention in the development of lung fibrosis.

[000247]Moreover HB-EGF is a mitogen of keratinocytes involved in the pathogenesis of inflammatory diseases. In addition, expression of HB-EGF and co-localization with the EGFR may play an important role in the early pathogenesis of psoriasis which opens a potential therapeutic window in the treatment of cutaneous inflammatory diseases and specifically in the early treatment of psoriasis with the claimed antigen binding proteins.

[000248]Targeting HB-EGF with the described antigen binding proteins may also result in a treatment option for patients with proliferative vitreoretinopathy (PVR), since the development of PVR is accompanied by a significant upregulation of HB-EGF in PVR retinas. In addition HB-EGF expression in fibroproliferative tissue and its stimulatory effect on glial cell proliferation, chemotaxis, and VEGF secretion suggest that HB-EGF may be a factor mediating glial cell responses during PVR. These principles can also be applied to further angiogenesis-dependent eye diseases such as age-related and non age-related macular degeneration, diabetic retinopathy, rubeotic glaucoma, interstitial keratitis, retinopathy of prematurity and corneal graft failure.

[000249]GPCRs such as adrenoceptors and angiotensin receptors have been linked to the pathogenesis of hypertension due to their vasoconstrictive and growth promoting abilities. Since

HB-EGF is a critical mediator of these pathways, neutralizing antigen binding proteins are suitable for targeted intervention in hypertensive disorders such as cardiac hypertrophy and congestive heart failure, kidney failure or stroke.

[000250]HB-EGF, a potent mitogen and chemoattractant for smooth muscle cells (SMCs), was detected in atherosclerotic plaques of coronary arteries with intimal thickening and produced by SMCs and macrophages. Remnant lipoproteins which are known causative agents of atherosclerosis were furthermore shown to induce SMC proliferation *via* HB-EGF mediated EGFR transactivation. Therefore, the HB-EGF antigen binding proteins as described herein represent selective and efficient agents targeting atherosclerosis by blocking critical smooth muscle cell functions. In addition restenosis after percutaneous coronary intervention which is characterized by proliferation of smooth muscle cells might also be prevented by specific neutralization of HB-EGF function.

[000251]Thus, the HB-EGF antigen binding proteins as described herein can be used to treat a variety of diseases, including non-malignant proliferative diseases such as aberrant angiogenesis, leiomyoma (uterine fibrosis), benign smooth muscle cell tumors, glomerulosclerosis (hyperproliferation of mesangial cells), smooth muscle cell hyperplasia, atherosclerosis (hyperproliferation of vascular smooth muscle cells), rubeosis; neovascular glaucoma, diabetic retinopathy, diabetic blindness, macular degeneration, rheumatoid arthritis, cardiac hypertrophy, psoriasis, and the like.

[000252]In a further aspect, these HB-EGF antigen binding proteins can be used to treat disorders associated with or accompanied by a disturbed, *e.g.*,pathologically enhanced growth factor receptor activation.

[000253]In another aspect, this enhanced growth factor receptor activation may be associated with or caused by a pathological increase in the activity of a G protein and/or a G protein coupled receptor. It should be noted that disorders that are associated with or accompanied by a disturbed, *e.g.*,pathologically enhanced growth factor receptor activation and which are may be associated with or caused by a pathological increase in the activity of a G protein and/or a G protein coupled receptor, can be delimited from other disorders characterized by an enhanced activity of growth factor receptor activation in that a transactivation of the growth factor receptor *via* G protein coupled receptor takes place.

2. Diagnostic Methods

[000254]The HB-EGF antigen binding molecules as described herein may be used in a method for detecting cancer cells in a test sample that includes contacting the test sample with the antigen binding molecule and detecting whether the antibody binds to a cell expressing proHB-EGF or HB-EGF molecules in the sample. The degree to which binding occurs can be assessed

by use of a control sample. The test and control samples can, for example, be blood, serum, ascites, pleural effusion, cerebro-spinal fluid, tissue, cell, urine, lymph, saliva, milk or other samples. Such a control sample can be a non-cancerous sample of the fluid or tissue or cell type. In some embodiments, the control sample is a non-cancerous sample obtained from the same subject as the test sample. "Subject" or "patient" refers to a mammal, preferably a human, in need of treatment for or detection of a condition, disorder or disease.

[000255]The binding of antibody to components of the test sample can be detected by detecting a reporting molecule, imaging agent or label that is bound or can be selectively bound to a antigen binding protein as described herein. These HB-EGF antigen binding proteins can have one or more reporter molecules, labels or imaging agents. A reporter molecule is defined as any moiety that may be detected using an assay. Non-limiting examples of reporter molecules that have been conjugated to antibodies include enzymes, radiolabels, haptens, fluorescent labels, phosphorescent molecules, chemiluminescent molecules, chromophores, luminescent molecules, photoaffinity molecules, colored particles or ligands, such as biotin. The reporting molecule can provide a detectable signal. For example, the detectable signal can be a fluorescent, phosphorescent, chemiluminescent, electrochemiluminescent, electrochemical, color change or enzymatic signal. Anti-HB-EGF antibodies provided herein can be used as capturing antibodies for ELISA-based detection of the growth factor or immunohistochemical analysis of tissue samples as shown in FIGURE 39.

[000256]In some embodiments, the reporting molecule is covalently bound to a antigen binding protein as described herein. In other embodiments, the reporting molecule can be selectively bound to the HB-EGF antigen binding protein as described herein. Such selective binding of a reporting molecule to the described antigen binding protein can be accomplished by a secondary antibody with the label covalently bound thereto, where the secondary antibody selectively binds to an HB-EGB antigen binding protein as described herein.

3. Methods Of Treatment: Pharmaceutical Formulations, Routes Of Administration

[000257]Treatment of, or treating, cancer is intended to include the alleviation of or diminishment of at least one symptom typically associated with the disease. The treatment also includes alleviation or diminishment of more than one of the associated symptoms. The treatment may cure the cancer, *e.g.*, it may substantially eliminate the cancer cells and/or arrest the growth of the cancerous tumor. Alternatively, treatment may slow the progression of the cancer.

[000258]Anti-cancer activity can be evaluated against varieties of cancers or cancer cells using methods available to one of skill in the art. Anti-cancer activity, for example, can be determined by identifying the LD_{100} or ED_{50} of a preparation of the antigen binding proteins described herein

that prevents the growth of a cancer. In one embodiment, anti-cancer activity is the amount of antibody that kills 50% or 100% of the cancer cells when measured using standard dose response methods.

[000259]The HB-EGF antigen binding proteins as described herein can be administered alone, or in combination with antibodies, chemotherapeutic drugs or radiation therapy. Pharmaceutical compositions according to the invention may be administered as monotherapy or in combination with another pharmaceutical composition, preferably comprising another anti-neoplastic agent, in particular Cisplantin or Avastin. For example, the described HB-EGF antigen binding proteins can be co-administered with anti-tumor antibodies, (*e.g.*,chimeric, humanized or human anti-tumor antibodies), with antibodies that specifically bind to VEGF to further inhibit tumor angiogenesis, or with antibodies that specifically bind to a receptor tyrosine kinase such as HER2, HER4 or EGFR and therefore further inhibit tumor cell proliferation. In FIGURE 38, the synergistic effect of an anti-EGFR antibody and antiHB-EGF antibodies could be shown for both therapeutic antiHB-EGF antibodies tested. Further, the HB-EGF antigen binding proteins described herein may be co-administered with other anti-tumor agents. Specific examples of anti-tumor agents which can be co-administered with the antibodies provided herein include, for example, gefitinib, lapatinib, sunitinib, pemetrexed, bevacisumab, cetuximab, imatinib, trastuzumab, alemtuzumab, rituximab, erlotinib, bortezomib and the like. Any other anti-cancer agent or drug that can inhibit cancer or tumor cell proliferation can also be used in the compositions as described and claimed herein. For example, the claimed compositions can include chemotherapeutic agents such as capecitabine, daunorubicin, daunomycin, dactinomycin, doxorubicin, epirubicin, idarubicin, esorubicin, bleomycin, mafosfamide, ifosfamide, cytosine arabinoside, bis-chloroethylnitrosurea, busulfan, mitomycin C, actinomycin D, mithramycin, prednisone, hydroxyprogesterone, testosterone, tamoxifen, dacarbazine, procarbazine, hexamethylmelamine, pentamethylmelamine, mitoxantrone, amsacrine, chlorambucil, methylcyclohexylnitrosurea, nitrogen mustards, melphalan, cyclophosphamide, 6-mercaptopurine, 6-thioguanine, cytarabine (CA), 5-azacytidine, hydroxyurea, deoxycoformycin, 4-hydroxyperoxycyclophosphor-amide, 5-fluorouracil (5-FU), 5-fluorodeoxyuridine (5-FUdR), methotrexate (MTX), colchicine, taxol, vincristine, vinblastine, etoposide, trimetrexate, teniposide, cisplatin, avastin and diethylstilbestrol (DES). *See*, generally, The Merck Manual of Diagnosis and Therapy, 15th Ed. 1987, pp. 1206-1228, Berkow *et al.*, eds., Rahway, N.J. When used with the described HB-EGF antigen binding proteins, such chemotherapeutic agents may be used individually (*e.g.*, 5-FU and an antibody), sequentially (*e.g.*, 5-FU and an antibody for a period of time followed by MTX and an antibody), or in combination with one or more other such chemotherapeutic agents (*e.g.*, 5-FU, MTX and an antibody, or 5-FU, radiotherapy and an antibody).

[000260]Also provided is a method of evaluating a therapeutically effective dosage for treating a cancer with an antibody having an amino acid sequence disclosed herein, that includes determining the LD_{100} or ED_{50} of the HB-EGF antigen binding protein preparation *in vivo* or *in vitro*. Such a method permits calculation of the approximate amount of antigen binding protein needed per volume to inhibit cancer cell growth or metastasis by about 10% to 100%, or about 20% to 100%, or about 25% to 100%, or about 30% to 100%, or about 40% to 100%, or about 50% to 100%. In some embodiments, less than 100% inhibition of cancer cell growth or metastasis is observed. For example, cancer cell growth and/or metastasis is inhibited by about 90%, 80%, 70%, 60%, or 50%. Percentage inhibition can be determined, for example, by administration of the antigen binding protein preparation to SCID or nu/nu mice available in the art wherein tumor cells have been introduced and/or by standard methods using cultured cancer cells (*see*, FIGURE 38B). Several methods are described in the Examples.

[000261]Also included are sterile pharmaceutical formulations of the HB-EGF antigen binding proteins as described herein that are useful as treatments for diseases including, for example, cancer and/or aberrant angiogenesis. Such formulations would inhibit the binding of HB-EGF to its receptor, *e.g.*,EGFR or to HER4, thereby effectively treating pathological conditions where, for example, serum, cellular or tissue HB-EGF is abnormally elevated or where its receptors, *e.g.*,EGFR or HER4, are abnormally active. As illustrated herein the HB-EGF antigen binding proteins possess adequate affinity to potently neutralize HB-EGF and to modulate the signaling events associated with the HB-EGF receptors.

[000262]The HB-EGF antigen binding proteins as described herein are preferably humanized antigen binding proteins. Administration of these humanized antigen binding proteins reduce the probability of a negative side effect. Moreover, these antigen binding proteins are stable *in vivo*, for example, because they are recognized as normal human products, thereby minimizing the risk of immune system responses. Moreover, these antigen binding proteins are not prone to proteolytic destruction, improving their circulating half-lives. Hence, the HB-EGF preparations as described herein have an excellent half-life *in vivo* so that administration in humans is comparatively infrequent. Such a prolonged duration of action may allow for less frequent and more convenient dosing schedules by alternate parenteral routes such as subcutaneous or intramuscular injection.

[000263]Sterile formulations can be created, for example, by filtration through sterile filtration membranes, prior to or following lyophilization and reconstitution of the antibody. The antigen binding proteins as described herein are ordinarily stored in lyophilized form or in solution. Therapeutic antibody compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having an adapter that allows retrieval of the formulation, such as a stopper pierceable by a hypodermic injection needle.

[000264]The route of administration of the HB-EGF antigen binding proteins are in accord with known methods, *e.g.*, injection or infusion by intravenous, subcutaneous, intradermal, intraperitoneal, intracerebral, intramuscular, intraocular, intraarterial, intrathecal, intravesical, intra-cavernous, inhalation, intralesional routes, or by sustained release systems as noted below. In some embodiments, the antigen binding proteins as described herein are administered continuously by infusion or by bolus injection.

[000265]The HB-EGF antigen binding proteins, as described herein, can be prepared in a mixture with a pharmaceutically acceptable carrier. This therapeutic composition can be administered intravenously or through the nose or lung, preferably as a liquid or powder aerosol (lyophilized). The composition may also be administered parenterally or subcutaneously as desired. When administered systemically, the therapeutic composition should be sterile, pyrogen-free and in a parenterally acceptable solution with consideration for what are physiologically acceptable pH values, isotonicity, and stability. These conditions are known to those skilled in the art. Briefly, dosage formulations of the compounds described herein are prepared for storage or administration by mixing the compound having the desired degree of purity with physiologically acceptable carriers, excipients, or stabilizers. Such materials are non-toxic to the recipients at the dosages and concentrations employed, and include buffers such as TRIS HCl, phosphate, citrate, acetate and other organic acid salts; antioxidants such as ascorbic acid; low molecular weight (less than about ten residues) peptides such as polyarginine, proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidinone; amino acids such as glycine, glutamic acid, aspartic acid, or arginine; monosaccharides, disaccharides, and other carbohydrates including cellulose or its derivatives, glucose, mannose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; counterions such as sodium and/or nonionic surfactants such as TWEEN, PLURONICS or polyethyleneglycol.

[000266]Sterile compositions for injection can be formulated according to conventional pharmaceutical practice as described in *Remington: The Science and Practice of Pharmacy* (20th ed, Lippincott Williams & Wilkens Publishers (2003)). For example, dissolution or suspension of the active compound in a vehicle such as water or naturally occurring vegetable oil like sesame, peanut, or cottonseed oil or a synthetic fatty vehicle like ethyl oleate or the like may be desired. Buffers, preservatives, antioxidants and the like can be incorporated according to accepted pharmaceutical practice.

[000267]Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the polypeptide, which matrices are in the form of shaped articles, films or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (*e.g.*, poly(2-hydroxyethyl-methacrylate) as described by Langer *et al.*;

1981, *J. Biomed Mater. Res.* 15:167-277 and Langer, 1982, *Chem. Tech.* 12:98-105, or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma ethyl-L-glutamate (Sidman *et al.*, 1983, *Biopolymers* 22:547-556), non-degradable ethylene-vinyl acetate (Langer *et al.*, *supra*), degradable lactic acid-glycolic acid copolymers such as the LUPRON Depot™ (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid (EP 133,988).

[000268]While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated proteins remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37°C, resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for protein stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S-S bond formation through disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

[000269]Sustained-released compositions also include preparations of crystals of the antigen binding protein suspended in suitable formulations capable of maintaining crystals in suspension. These preparations when injected subcutaneously or intraperitoneally can produce a sustained release effect. Other compositions also include liposomally entrapped antibodies. Liposomes containing such antibodies are prepared by methods known per se: U.S. Pat. No. DE 3,218,121; Epstein *et al.*, 1985, *Proc. Natl. Acad. Sci. USA* 82:3688-3692; Hwang *et al.*, 1980, *Proc. Natl. Acad. Sci. USA* 77:4030-4034; EP 52,322; EP 36,676; EP 88,046; EP 143,949; 142,641; Japanese patent application 83-118008; U.S. Pat. Nos. 4,485,045 and 4,544,545; and EP 102,324.

[000270]The dosage of the antigen binding protein formulation for a given patient will be determined by the attending physician taking into consideration various factors known to modify the action of drugs including severity and type of disease, body weight, sex, diet, time and route of administration, other medications and other relevant clinical factors. Therapeutically effective dosages may be determined by either *in vitro* or *in vivo* methods.

[000271]An effective amount of the antigen binding proteins, described herein, to be employed therapeutically will depend, for example, upon the therapeutic objectives, the route of administration, and the condition of the patient. Accordingly, it is preferred for the therapist to titer the dosage and modify the route of administration as required to obtain the optimal therapeutic effect. A typical daily dosage might range from about 0.001 mg/kg to up to 100

mg/kg or more, depending on the factors mentioned above. Typically, the clinician will administer the therapeutic antigen binding protein until a dosage is reached that achieves the desired effect. The progress of this therapy is easily monitored by conventional assays or as described herein.

[000272]It will be appreciated that administration of therapeutic entities in accordance with the compositions and methods herein will be administered with suitable carriers, excipients, and other agents that are incorporated into formulations to provide improved transfer, delivery, tolerance, and the like. These formulations include, for example, powders, pastes, ointments, jellies, waxes, oils, lipids, lipid (cationic or anionic) containing vesicles (such as Lipofectin™), DNA conjugates, anhydrous absorption pastes, oil-in-water and water-in-oil emulsions, emulsions carbowax (polyethylene glycols of various molecular weights), semi-solid gels, and semi-solid mixtures containing carbowax. Any of the foregoing mixtures may be appropriate in treatments and therapies involving the HB-EGF antigen binding protein as described herein, provided that the active ingredient in the formulation is not inactivated by the formulation and the formulation is physiologically compatible and tolerable with the route of administration. *See,* also Baldrick P. "Pharmaceutical excipient development: the need for preclinical guidance," 2000, *Regul. Toxicol. Pharmacol.* 32:210-218; Wang, "Lyophilization and development of solid protein pharmaceuticals," 2000, *Int. J. Pharm.* 203:1-60; Charman WN "Lipids, lipophilic drugs, and oral drug delivery-some emerging concepts," *J. Pharm. Sci* .89:967-978; Powell *et al.,* 1998, "Compendium of excipients for parenteral formulations," *PDA J. Pharm. Sci. Technol.* 52:238-311 and the citations therein for additional information related to formulations, excipients and carriers well known to pharmaceutical chemists.

[000273]The following examples, including the experiments conducted and results achieved are provided for illustrative purposes only and are not to be construed as limiting upon the teachings herein.

EXAMPLES

K. Example 1: Generation Of Immunogen

[000274]HB-EGF including EGF-like domain (aa 1-149) was amplified from a pcDNA3-VSV-HB-EGF expression construct (Prenzel *et al.*, 1999, *supra*) and cloned into an expression vector that provides an in-frame 6His tag at the carboxyl-terminus (pcDNA 3.1 myc-his, InVitrogen). This HB-EGF immunogen with C-terminal myc(HIS)6 tag was expressed in HEK293 cells and purified by a two step purification on Ni-NTA sepharose (Amersham Pharmacia) and heparin sepharose (Sigma).

[000275]The HB-EGF portion of the immunogen had the following sequence (SEQ ID NO:1077).

1 MKLLPSVVLK LFLAAVLSAL VTGESLERLR RGLAAGTSNP

41 DPPTVSTDQL LPLGGGRDRK VRDLQEADLD LLRVTLSSKP
81 QALATPNKEE HGKRKKKGKG LGKKRDPCLR KYKDFCIHGE
121 CKYVKELRAP SCICHPGYHG ERCHGLSLP

B. Example 2: Immunization Of Xenomouse Mice And Titers Observed

[000276]Monoclonal antibodies against HB-EGF were developed by sequentially immunizing XenoMouse® mice (XenoMouse strains: XMG2 (human IgG2-producing) and XM3C-1 (human IgG4-producing), Abgenix, Inc. Fremont, CA).

1. Immunization

[000277]XenoMouse animals were immunized *via* the footpad for all injections. The total volume of each injection was 50 µl per mouse, 25 µl per footpad.

[000278]For both cohort 1 (10 XMG2 mice) and Cohort 2 (10 XM3C-1), the initial immunization was with 10 µg of HB-EGF protein admixed 1:1 (v/v) with TITERMAX GOLD® (Sigma, Oakville, ON) per mouse. The subsequent four boosts were made with 10 µg of HB-EGF protein admixed 1:1 (v/v) with 100 µg alum gel (Sigma, Oakville, ON) in pyrogen-free D-PBS. The fifth boost consisted of 10 µg of HB-EGF protein admixed 1:1 (v/v) with TITERMAX GOLD®. The sixth and seventh injection consisted of 10 µg of HB-EGF protein admixed 1:1 v/v with 100 µg alum gel. A final boost was made with 10 µg of HB-EGF protein in pyrogen-free DPBS, without adjuvant. The XenoMouse mice were immunized on days 0, 4, 8, 14, 18, 21, 25, and 28 for this protocol and fusions were performed on day 32. The two bleeds were made through Retro-Orbital Bleed procedure on day 16 after the fourth boost, on day 23 after the sixth boost.

2. Selection Of Animals For Harvest By Titer

[000279]Anti-HB-EGF antibody titers in the serum from immunized XenoMouse mice were determined by ELISA. Briefly, the HB-EGF protein (2 µg/ml) was coated onto Costar Labcoat Universal Binding Polystyrene 96-well plates (Corning, Acton, MA) overnight at 4°C in Antigen Coating Buffer (0.1 M Carbonate Buffer, pH 9.6 $NaHCO_3$ (MW 84) 8.4 g/L). The next day, the plates were washed one time with washing buffer (0.05% Tween 20 in 1x PBS) using a Biotek plate washer. The plates were then blocked with 200 µl/well blocking buffer (0.5% BSA, 0.1% Tween 20, 0.01% Thimerosal in 1x PBS) and incubated at room temperature for 1 hour. After the one-hour blocking, the plates were washed one time with washing buffer using a Biotek plate washer. Sera from either the HB-EGF protein immunized XenoMouse mice or naïve XenoMouse animals were titrated in 0.5% BSA/PBS buffer at 1:3 dilutions in duplicate from a 1:100 initial dilution. The last well was left blank. These plates were incubated at room temperature for 2 hours, and the plates were then washed three times with washing buffer using

a Biotek plate washer. A goat anti-human IgG Fc-specific horseradish peroxidase (CALTAG, Cat NO, H10507) conjugated antibody was added at a final concentration of 1:2000 in blocking buffer and incubated for 1 hour at room temperature. The plates were washed three times with washing buffer using a Biotek plate washer. After washing, the plates were developed with the addition of TMB chromogenic substrate (BioFx BSTP-0100-01) for 10-20 minutes or until negative control wells start to show color. Then the ELISA was stopped by the addition of Stop Solution (650 nM Stop reagent for TMB (BioFx BSTP-0100-01), reconstituted with 100 ml H_2O per bottle). The specific titer of each XenoMouse animal was determined from the optical density at 650 nm and is shown in TABLE 1 below. The titer value is the reciprocal of the greatest dilution of sera with an OD reading two-fold that of background. Therefore, the higher the number, the greater was the humoral immune response to HB-EGF.

[000280]

[000281]TABLE 1

[000282]

Group 1, fp, XMG2,10 mice,		
	After 4 inj.	After 6 inj.
Mouse ID	Reactivity to HB-EGF	
P4721	3,800	59,000
P4722	6,500	68,000
P4723	2,500	43,000
P4724	2,400	22,000
P4725	2,400	71,000
P4726	450	58,000
P4727	1,600	20,000
P4728	2,700	61,000
P4729	800	61,000
P47210	5,700	78,000
NC	<100	<100
PC	<100	<100

Group 2, fp, XM3C-1,10 mice,		
	After 4 inj.	After 6 inj.
Mouse ID	Reactivity to HB-EGF	
P2664	35	2,300
P2666	20	750
P2669	30	850
P26610	75	1,900
P2892	60	550
P2894	60	1,400
P2895	95	2,600
P2896	45	2,500
P3672	50	2,000
P3678	60	1,800
NC	<100	<100
PC	35	20

C. Example 3: Hybridoma Generation And Primary Screen For Binders

[000283]Immunized mice were sacrificed and the lymph nodes were harvested and pooled from each cohort. The lymphoid cells were dissociated by grinding in DMEM to release the cells from the tissues, and the cells were suspended in DMEM. The cells were counted, and 0.9 ml DMEM per 100 million lymphocytes was added to the cell pellet to resuspend the cells gently but completely. Using 100 µl of CD90+ magnetic beads per 100 million cells, the cells were labeled by incubating the cells with the magnetic beads at 4°C for 15 minutes. The magnetically-labeled cell suspension containing up to 10^8 positive cells (or up to $2x10^9$ total cells) was loaded onto a LS+ column and the column washed with DMEM. The total effluent was collected as the CD90-negative fraction (most of these cells were expected to be B cells).

[000284]The fusion was performed by mixing washed enriched B cells from above and nonsecretory myeloma P3X63Ag8.653 cells purchased from ATCC, cat.# CRL 1580 (Kearney *et al*, 1979, *J. Immunol.* 123:1548-1550) at a ratio of 1:1. The cell mixture was gently centrifuged at 800 g. After complete removal of the supernatant, the cellular pellet was treated with 2-4 ml of Pronase solution (CalBiochem, cat. # 53702; 0.5 mg/ml in PBS) for no more than 2 minutes. Then, 3-5 ml of FBS was added to stop the enzyme activity and the suspension was adjusted to

40 ml total volume using electro cell fusion solution, ECFS (0.3 M Sucrose, Sigma, Cat# S7903, 0.1 mM Magnesium Acetate, Sigma, Cat# M2545, 0.1 mM Calcium Acetate, Sigma, Cat# C4705). The supernatant was removed after centrifugation and the cells were resuspended in 40 ml ECFS. This wash step was repeated and the cells again were resuspended in ECFS to a concentration of $2x10^6$ cells/ml.

[000285]Electro-cell fusion was performed using a fusion generator, model ECM2001, Genetronic, Inc., San Diego, CA. The fusion chamber size used was 2.0 ml, using the following instrument settings: Alignment condition: voltage: 50 V, time: 50 seconds; membrane breaking at: voltage: 3000 V, time: 30 µsec; post-fusion holding time: 3 seconds.

[000286]After electro-cell fusion, the cell suspensions were carefully removed from the fusion chamber under sterile conditions and transferred into a sterile tube containing the same volume of Hybridoma Culture Medium (DMEM (JRH Biosciences), 15% FBS (Hyclone), supplemented with L-glutamine, pen/strep, OPI (oxaloacetate, pyruvate, bovine insulin) (all from Sigma) and IL-6 (Boehringer Mannheim)). The cells were incubated for 15-30 minutes at 37°C, and then centrifuged at 400 g for five minutes. The cells were gently resuspended in a small volume of Hybridoma Selection Medium (Hybridoma Culture Medium supplemented with 0.5x HA (Sigma, cat. # A9666)), and the volume was adjusted appropriately with more Hybridoma Selection Medium, based on a final plating of $5x10^6$ B cells total per 96-well plate and 200 µL per well. The cells were mixed gently and pipetted into 96-well plates and allowed to grow. On day 7 or 10, one-half the medium was removed, and the cells were re-fed with Hybridoma Selection Medium.

[000287]After 14 days of culture, hybridoma supernatants from the cohort #1 and cohort #2 were screened for HB-EGF-specific monoclonal antibodies by ELISA. In the Primary screen, the ELISA plates (Fisher, Cat. No. 12-565-136) were coated with 50 µL/well of HB-EGF protein (2 µg/ml) in Coating Buffer (0.1 M Carbonate Buffer, pH 9.6, $NaHCO_3$ 8.4 g/L), then incubated at 4°C overnight. After incubation, the plates were washed with Washing Buffer (0.05% Tween 20 in PBS) one time. 200 µL/well Blocking Buffer (0.5% BSA, 0.1% Tween 20, 0.01% Thimerosal in 1x PBS) were added and the plates were incubated at room temperature for 1 hour. After incubation, the plates were washed with Washing Buffer one time. Aliquots (50 µL/well) of hybridoma supernatants and positive and negative controls were added, and the plates were incubated at room temperature for 2 h. The positive control used throughout was serum from the relevant HB-EGF protein-immunized XenoMouse mouse and the negative control was serum from a KLH-immunized relevant strain of XenoMouse mouse. After incubation, the plates were washed three times with Washing Buffer. 100 µL/well of detection antibody goat anti-huIgGFc-HRP (Caltag Inc., Cat. No. H10507, using concentration was 1:2000 dilution) was added and the plates were incubated at room temperature for 1 hour. After incubation, the plates were

washed three times with Washing Buffer and 100 µl/well of TMB (BioFX Lab. Cat. No. TMSK-0100-01) was added. Plates were then allowed to develop for about 10 minutes (until negative control wells barely started to show color). 50 µl/well stop solution (TMB Stop Solution (BioFX Lab. Cat. No. STPR-0100-01) was then added and the plates were read on an ELISA plate reader at a wavelength of 450 nm.

[000288]The old culture supernatants from the positive hybridoma cells growth wells based on primary screen were removed and the HB-EGF positive hybridoma cells were suspended with fresh hybridoma culture medium and were transferred to 24-well plates. After 2 days in culture, these supernatants were ready for a secondary confirmation screen. In the secondary confirmation screen, the positives in the first screening were screened by ELISA (described as above) with two sets of detective antibodies: goat anti-hulgGFc-HRP (Caltag Inc., Cat. No. H10507, using concentration was 1:2000 dilution) for human gamma chain detection and goat anti-hIg kappa-HRP (Southern Biotechnology, Cat. No. 2060-05) for human kappa light chain detection in order to demonstrate that the antibody preparation was HB-EGF-specific and fully human in its composition. The two sets of ELISA procedures were identical to the descriptions above except the two different detection antibodies were used separately.

[000289]In parallel with the secondary confirmation screen, the counter ELISA screen was performed to exclude those antibodies that respond to myc(his)6 tag. The ELISA procedures were identical to the descriptions above except the coated with irrelevant myc(his)6 tag protein (ML-myc(his)6 protein) instead of coating with HB-EGF myc(his)6 protein.

[000290]After the secondary confirmation and the counter ELISA screen, 49 fully human IgG/kappa HB-EGF specific monoclonal antibodies were identified from cohorts 1 and 2.

D. Example 4: Scale-Up And Testing Of Antibodies In Functional Assays

[000291]This Example describes the identification of hybridoma cell lines that produce anti-HB-EGF antibodies with affinity for HB-EGF.

1. FACS Detection Of Hybridoma-Produced Anti-HB-EGF Antibodies Bound To HB-EGF Expressing Cell-Lines

[000292]HB-EGF expression on cell-lines was determined by FACS analysis. To perform this analysis $2x10^5$ selected HB-EGF-expressing cells were harvested with 10 mM EDTA in PBS, resuspended in FACS-buffer (PBS, 3% FCS, 0.4% azide) and seeded on a 96-well round bottom plate. After centrifugation for 3 minutes at 1000 rpm to remove supernatant, the cells were resuspended in hybridoma-derived anti-HB-EGF antibody dilution (100 µl/well) and incubated at 4°C for 45 min. The cells were washed twice with FACS buffer and resuspended with secondary antibody (100 µl/well) donkey-anti-human-PE (Jackson) diluted 1:100 in FACS buffer. The cell

suspensions were incubated at 4 °C in the dark for 30 min, washed twice with FACS buffer and analyzed (FACS, Beckman Coulter).

[000293]The results of these assays are provided in TABLES 2 and 3 below, which provide the fluorescence mean values for each FACS assay. As illustrated in TABLES 3 and 4, substantially no HB-EGF expression was detected in CHO control cells that do not express HB-EGF. However, when HB-EGF is recombinantly overexpressed in CHO cells, several monoclonal antibody preparations exhibit significant binding to those HB-EGF-expressing cells. Binding to MDA-MB231, SCC-9 and COS-7 cells was somewhat variable but an antibody preparation that bound to one HB-EGF-expressing cell type typically bound to another. As shown in TABLE 2, several antibody preparations, including, for example, the U2-24, U2-5, U2-19, U2-21, U2-15 and U2-42 antibody preparations exhibited strong binding to HB-EGF-expressing CHO cells. Similarly, antibody preparations U2-39, U2-26, U2-44, U2-45 and U2-48 also exhibited good binding to HB-EGF-expressing CHO cells.

[000294]

[000295]

TABLE 2
FACS Analysis Of Anti-HB-EGF Antibody Supernatants (Cohort 1)

	CHO control cells vs. HB-EGF-expressing CHO cells		Cell Lines Endogenously Expressing HB-EGF		
Antibody	CHO-K1	CHO-HB-EGF	MDA-MB231	SCC-9	COS-7
KLH	0.2	0.3	0.4	0.2	0.4
U2-18	0.3	154	3.1	1.2	1.6
U2-68	0.2	238	1.7	0.6	1.1
U2-24	0.2	360	2	0.6	6.7
U2-14	0.3	132	2.8	0.8	1.1
U2-1	0.2	64	1.8	0.7	3.1
U2-32	0.2	76	1.7	1.2	1.8
U2-40	0.2	137	2.1	1.3	1.1
U2-5	0.3	371	6.9	1.7	2.2
U2-8	0.3	148	3.7	1.4	1.4
U2-13	0.2	136	0.4(2.6)	0.5	0.8
U2-17	0.2	170	1.6	0.6	1.4
U2-19	0.4	347	5.5	1.8	6.1
U2-38	0.3	30	3.9	0.9	1.4
U2-21	0.2	344	3.9	3.4	2.1
U2-15	0.2	370	3	0.6	0.9
U2-16	0.2	197	1.5	0.4	0.9
U2-30	0.3	273	3.5	1	3.4
U2-44	0.3	5.6	0.8	0.2	5.2
U2-42	1.2	277	3.3	0.5	6.7
U2-36	0.9	112	1.6	0.3	4.9
U2-22	0.3	221	1.1	0.2	4.9
U2-56	0.2	38	0.5	0.2	1.8
Neg	0.2	0.2	0.3		
Pos (goat aHB)	0.2	80	3		

[000296]

[000297]

TABLE 3
FACS Analysis Of Anti-HB-EGF Antibody Supernatants (Cohort 2)

	CHO control cells vs. HB-EGF-expressing CHO cells		Cell Lines Endogenously Expressing HB-EGF		
Antibody	CHO-K1	CHO-HB-EGF	MDA-MB231	SCC-9	COS-7
U2-63	0.2	36(0.4)	0.5	0.2	0.6
U2-54	0.3	49	0.6	0.2	2.4
U2-65	0.2	1.9	0.4	0.2	0.3
U2-10	0.2	2.3	0.5	0.2	1.2
U2-53	0.2	144	0.5	0.2	0.6
U2-66	0.2	149	0.5	0.2	0.5
U2-61	0.4	28	0.4	0.2	1.4
U2-67	0.2	82	0.5	0.2	0.6
U2-28	0.3	198	1	0.2	3.2
U2-2	0.2	127	0.5	0.2	0.5
U2-62	0.2	47	0.5	0.2	0.6
U2-39	0.2	205	2.6	0.6	8.3
U2-3	0.2	168	0.9	0.2	2.5
U2-43	0.4	185	0.8	0.2	1.7
U2-34	0.7	125	1.2	0.3	6.4
U2-26	0.2	242	1.5	0.3	4.7
U2-41	0.3	186	1.2	0.2	3.3
U2-44	0.4	248	1.2	0.2	2.2
U2-45	0.6	248	1.4	0.2	6.4
U2-57	0.2	201	0.7	0.2	0.5
U2-12	0.6	1.2	1.2	0.5	1.6
U2-46	0.4	129	1	0.2	2.5
U2-48	0.4	273	1.3	0.3	2.1
U2-6	0.5	108	3.9	1.5	5.9
U2-58	0.2	277	0.9	0.2	0.4
U2-51	0.5	176	1.1	0.2	3.6
U2-60	0.2	3.6	0.4	0.2	0.3
Neg	0.2	0.2	0.3		
Pos (goat aHB)	0.2	80	3		

2. Inhibition of HB-EGF-Induced EGFR tyrosine phosphorylation

[000298]The following protocol was used to identify which anti-HB-EGF antibody preparations inhibit HB-EGF-induced epidermal growth factor receptor tyrosine phosphorylation. Such experiments further characterize the antibodies and help identify which hybridoma cell lines produce antibody that inhibit HB-EGF activity and then should be cloned and expanded.

[000299]40000 SCC9 human squamous cancer cells were seeded on a 96-well plate in 100 µl medium. Cells were starved in 60 µl serum free medium for 24 hr. A black Maxisorp 96-well plate was coated with 100 µl anti-EGFR antibody (2 µg/ml) overnight at 4°C. The coating solution was replaced by 300 µl blocking solution (PBS + 0.5% BSA) without washing and left to incubate 2 hours at room temperature. 10 µg/ml of IgG2-control (Sigma) or anti-HB-EGF hybridoma-derived antibodies were added to 20 ng/ml HB-EGF (R&D Systems) and preincubated for 30 minutes at 37 °C (volume: 40 µl). Cells were treated with medium alone or with the antibody/ligand solution for 3 minutes at 37°C. The medium was removed and cells were lysed on ice with 100 µl Triton-X-100-based lysis buffer containing 1 mM PMSF, 10 µg/ml Aprotinin, 10 mM NaF and 2 mM Na-Orthovanadate. The blocked Maxisorp plate was washed 6 times with PBS + 0.05% Tween-20. 80 µl of the cell lysate was transferred directly to the washed Maxisorp plate and incubated overnight at 4 °C with gentle agitation. The plate was washed 6 times with PBS + 0.05% Tween-20, then 100 µl 4G10-biotin (UBI) diluted 1:4000 in dilution buffer (PBS+0.5% BSA+0,05% Tween-20+5 mM EDTA) was added to each well and incubated for 2 hours at room temperature. The plate was washed 6 times with PBS + 0.05% Tween20 and 100 µl AP-conjugated streptavidin (UBI) diluted 1:20000 in dilution buffer (PBS+0.5% BSA+0,05% Tween20+5 mM EDTA) was added to each well for 30 minutes at room temperature. The plate was washed 6 times with PBS + 0.05% Tween-20 and 100 µl AttoPhos substrate was added to each well. The plate was incubated for up to 3 hours at room temperature in the dark and the developing fluorescence was monitored at 30, 90 and 180 min (Excitation: 430 nm, emission: 580 nm).

[000300]The percent inhibition of HB-EGF-induced EGFR tyrosine phosphorylation was calculated by reduction in the amount of phosphorylation observed with IgG2-control (Sigma) by each hybridoma-derived anti-HB-EGF antibody preparation.

[000301]Results for the different anti-HB-EGF antibody preparations are provided in FIGURES 23A and 23B. As illustrated, monoclonal antibody preparations U2-18, U2-24, U2-19, U2-42, U2-39, U2-34, U2-45 and U2-6 strongly inhibit EGFR tyrosine phosphorylation.

3. Anti-HB-EGF Antibody Preparations Inhibit LPA-Induced EGFR Phosphorylation

[000302]EGFR-dependent signaling pathways can be activated upon stimulation of G-protein-coupled receptors (GPCR). Ligand activation of heterotrimeric G proteins by interaction with a GPCR results in an intracellular signal that induces the extracellular activity of a transmembrane metalloproteinase. Ligands that can activate the GPCR pathway include LPA (lysophosphatidic acid), thrombin, carbachol, bombesin, and endothelin. Such activation leads to extracellular processing of a transmembrane growth factor precursor and release of the mature factor which, directly or through the proteoglycan matrix, interacts with the ectodomain of EGFR and activates it through phosphorylation. *See*, Prenzel *et al.*,1999, *Nature* 402:884-888.

[000303]The anti-HB-EGF antibody preparations provided herein were tested to ascertain whether they could inhibit EGFR tyrosine phosphorylation induced by the GPCR ligand LPA in COS-7 cells, using the following procedure.

[000304]250.000 COS-7 cells were seeded on a 6-well plate, in 2 ml medium and cultured over night. Cells were starved in 1 ml serum free medium for 24 hours. Following preincubation with antibodies (37°C, 1h), cells were stimulated with 10 µM LPA (37°C, 3 min) and lysed on ice with 400 µl Triton-X-100-based lysis buffer containing 1 mM PMSF, 10 µg/ml Aprotinin, 10 mM NaF and 2 mM Na-Orthovanadate. Following immunoprecipitation of the EGFR (340 µl lysate, 340 µl HNTG, 30 µl Prot. A Sepharose, 1.5µl αEGFR (108.1, Prenzel *et al.*, 1999, *supra*)) for 4 hours in the coldroom precipitates were washed 3 times with 500 µl HNTG buffer and run on a 7.5% SDS PAGE. Following transfer on a nitrocellulose membrane (Schleicher & Schuell) the blot was probed with an antibody recognizing phosphotyrosine residues (primary ab 4G10 (1:2000, Upstate biotechnology); secondary anti-mouse Ab 1:10000, Jackson laboratories). Reblot with sheep anti EGFR (Upstate technology) after stripping showed that equal amounts of the receptor were precipitated in each lane.

[000305]FIGURE 24 provides a western blot illustrating which anti-HB-EGF antibody preparations inhibit LPA-induced EGFR tyrosine phosphorylation. As shown in FIGURE 24, the U2-19 and U2-42 anti-HB-EGF antibody preparations strongly inhibited LPA-induced EGFR phosphorylation. The U2-24 anti-HB-EGF antibody preparation inhibited LPA-induced EGFR phosphorylation to a somewhat lesser extent.

E. Example 5: Hybridoma Cloning To Generate Monoclonal Antibodies

[000306]Based on the test results observed from experiments described in the preceding Examples, of the 49 original isolates, 43 hybridoma cell lines were selected for cloning by limiting dilution and further characterization of their monoclonal antibody. The lines selected for cloning bound to HB-EGF-expressing cell lines as exhibited by FACS analysis and inhibited HB-EGF-stimulation of EGF receptor tyrosine phosphorylation. For some hybridomas, insufficient

antibody was generated to run all the primary screening assays. This subset of hybridomas was advanced to hybridoma cloning as well.

F. Example 6: Further Characterization Of Antibody-Related Inhibition Of GPCR Induced Tyrosine Phosphorylation Of EGFR

[000307]This Example provides further data showing that several anti-HB-EGF antibody preparations provided herein exhibit dose-dependent inhibition of GPCR-induced EGF receptor tyrosine phosphorylation.

[000308]Inhibition by candidate antibody preparations U2-42, U2-39 and U2-45 was examined using different concentrations of these antibody preparations and the following procedure.

[000309]150,000 cells (MDA-MB231, PPC1) were seeded on a 12-well plate in 1 ml medium. Cells were starved in 500 µl serum free medium for 24 hr. A black Maxisorp 96-well plate was coated with 100 µl anti-EGFR antibody (2 µg/ml) overnight at 4°C. The coating solution was replaced by 300 µl blocking solution (PBS + 0.5% BSA) without washing and left to incubate 2 hours at room temperature.Cells were pre-incubated with 10 µg/ml anti-HB-EGF Abs for 30 minutes at 37°C and then treated with the GPCR ligands LPA (10 µM, PPC1 cells) or Thrombin (1U/ml, MDA-MB231 cells) for 3 minutes at 37 °C. The medium was removed and cells were lysed on ice with 200µl Triton-X-100-based lysis buffer containing 1 mM PMSF, 10 µg/ml Aprotinin, 10 mM NaF and 2 mM Na-Orthovanadate. The blocked Maxisorp plate was washed 6x with PBS + 0.05% Tween-20. Cell lysate was transferred directly to a washed Maxisorp plate and incubated overnight at 4 °C with gentle agitation.

[000310]The plate was washed 6 times with PBS + 0.05% Tween-20, then 100 µl 4G10-biotin (UBI) diluted 1:4000 in dilution buffer (PBS+0.5%BSA+0.05% Tween-20+5mM EDTA) was added to each well and incubated for 2 hours at room temperature. The plate was washed 6 times with PBS + 0.05% Tween-20 and 100µl AP-conjugated streptavidin (UBI) diluted 1:20000 in dilution buffer (PBS+0.5% BSA+0,05% Tween-20+5mM EDTA) was added to each well for 30 minutes at room temperature. The plate was washed 6 times with PBS + 0.05% Tween-20 and 100 µl Attophos substrate was added to each well. The plate was incubated for 3 hours at room temperature in the dark and the developing fluorescence was monitored at 30, 90 and 180 min (Excitation: 430 nm, emission: 580 nm).

[000311]As shown in FIGURE 26, inhibition of LPA-induced EGFR tyrosine phosphorylation was dose dependent – greater inhibition of EGFR tyrosine phosphorylation was observed as the amount of anti-HB-EGF antibody was increased.

[000312]FIGURE 25 illustrates that candidate antibody preparations U2-42, U2-39 and U2-45 also effectively inhibit thrombin-induced EGFR phosphorylation in MDA-MB231 cells. A dosage dependent inhibition is observed, with increased inhibition as more anti-HB-EGF antibody is added. FIGURE 26 illustrates that inhibition of LPA-induced EGFR tyrosine phosphorylation in

PPC-1 cells by anti-HB-EGF antibody preparations provided herein is dose dependent. As shown, greater inhibition of EGFR tyrosine phosphorylation was detected as the amount of anti-HB-EGF antibody was increased.

G. Example 7: Inhibition Of GPCR-Induced MDA-MB231 Cell Migration By Human Anti-HB-EGF Antibodies

[000313]Transmigration experiments were performed in order to investigate whether the antibodies provided herein block cell migration induced by the GPCR ligand Sphingosine-1-phosphate.

[000314]Serum-starved human breast cancer MDA-MB231 cells were preincubated with the indicated antibody to the cell suspension for 45 min at 37°C. Thereafter, 500 ml cell suspension (50,000 cells) was placed in the top chamber of collagen I-coated transwells (BD Falcon, 8 µm pores). 750 ml medium (MEM, amino acids, Na-Pyruvate, Pen.-Strept., 0.1% BSA) alone or containing the GPCR ligand Sphingosine-1-phosphate (R&D Systems) was used in the bottom chamber. After migration for 8 hours at 37°C cells were fixed, stained with DAPI and cell nuclei were counted for statistical evaluation.

[000315]The results for these MDA-MB231 cell migration assays using candidate anti-HB-EGF antibody preparations U2-42, U2-39 and U2-45 are provided in FIGURE 27. As shown, anti-HB-EGF antibody preparation U2-42 inhibited MDA-MB231 cell migration by about 70%; anti-HB-EGF antibody preparation U2-45 inhibited MDA-MB231 cell migration by about 100%; and anti-HB-EGF antibody preparation U2-39 inhibited MDA-MB231 cell migration by about 100%. Hence, the ability of these anti-HB-EGF antibodies to inhibit MDA-MB231 cell migration is substantial.

[000316]

H. Example 8: Inhibition Of HB-EGF-Induced Migration Of MCF-7 Cells By Human Anti-HB-EGF Antibodies

[000317]Transmigration experiments were performed in order to investigate whether the antibodies provided herein block cell migration that would otherwise be directly induced by HB-EGF. The results of these tests highlight which antibody preparations may be use for development as anti-metastatic cancer agents.

[000318]A 500 ml cell suspension of serum-starved human breast cancer MCF7 cells (50,000 cells) was placed in the top chamber of collagen I-coated transwells (BD Falcon, 8 µm pores). Aliquots of 750 ml medium (MEM, amino acids, Na-pyruvate, Pen.-Strept., 0,1% BSA) alone or containing 20 ng/ml HB-EGF (R&D Systems) in the presence or absence of 10 µg/ml HB-EGF antibodies were placed in the bottom chamber. After incubation and migration for 8 hours at 37°C, cells were fixed, stained with DAPI and cell nuclei were counted for statistical evaluation.

[000319]The results for these migration assays using candidate anti-HB-EGF antibody preparations U2-42, U2-39 and U2-45 are provided in FIGURE 28. As shown, anti-HB-EGF antibody preparation U2-42 inhibited MCF-7 cell migration by about 55%; anti-HB-EGF antibody preparation U2-45 inhibited MCF-7 cell migration by about 93%; and anti-HB-EGF antibody preparation U2-39 inhibited MCF-7 cell migration by about 98%. Hence, the ability of these anti-HB-EGF antibodies to inhibit MCF-7 cell migration is substantial.

I. Example 9: Characteristics Of Top 10 Anti-HB-EGF Antibodies

[000320]A summary of results is provided in TABLE 4, *infra*, for top 10 hybridoma-derived antibody preparations in GPCR-induced triple membrane-passing signal (TMPS) experiments. The TMPS experiments involved LPA-stimulation in SCC9 cells, thrombin stimulation in MDA-MB231 cells, LPA stimulation of SkOV-8 cells and Sphingosine-1-phosphate migration of MDA-MB231 cells. The data provided represent the percent inhibition of the TMPS transactivation signal that was observed when antibody preparations were used in the assays compared to the same assay when no antibody was present. The top three antibodies of each experiment are highlighted in bold letters.

[000321]

TABLE 4
Percent Inhibition of TMPS Transactivation Signal

	TMPS					Migration
Ab	**SCC9.3**	**MDA-MB231**	**MDA-MB231**	**SkoV-8**	**SkoV-8**	**MDA-MB231**
U2-39	**56.9**	**126.6**	**131.1**	**130.7**	65.5	**115**
U2-45	**58.5**	**136.8**	**95.7**	99.4	**75.1**	**104**
U2-42	**62.8**	123.2	**125.6**	**110.7**	**73.1**	69.9
U2-34	50.6	109.5	93.6	95.1	73	**99.6**
U2-46	36.6	88.1	77.5	80.5	**76.1**	n.d.
U2-19	n.d.	n.d.	n.d.	n.d.	n.d.	85
U2-26	n.d.	**143**	91.8	**106.1**	31.4	55.9
U2-51	n.d.	n.d.	n.d.	n.d.	n.d.	85.3
U2-15	n.d.	121.7	92.6	87	17.6	45.5
U2-22	n.d.	74.2	94.3	64.4	18.2	n.d.

J. Example 10: Inhibition Of HB-EGF-Induced HER4 Tyrosine Phosphorylationby Human Anti-HB-EGF Antibodies

[000322]This Example shows that anti-HB-EGF antibody preparations inhibit HB-EGF induced tyrosine phosphorylation of HER4. The following procedures were employed to assess the effects of anti-HB-EGF antibodies on HER4 tyrosine phosphorylation.

[000323]125,000 cells T47D human breast cancer cells were seeded on a 24-well plate in 500 µl medium. Cells were starved in 200 µl serum free medium for 24 hr. An R&D Systems Human Phospho-ErbB4 ELISA-Kit was used for detection of HER4 tyrosine phosphorylation. A clear Maxisorp 96-well plate was coated with 100 µl mouse anti-human-ErbB4 antibody (Capture Antibody 1 µg/ml) overnight at room temperature. The coated Maxisorp plate was washed 6 times with PBS+0.05%Tween-20, the washing solution was replaced by 300 µl blocking solution (PBS + 0.5% BSA) and incubated 2 hours at room temperature. 50 µl serum-free medium with 5x-concentration of anti-HB-EGF Abs (10 µg/ml) was incubated with 5x-concentration HB-EGF (20 ng/ml) for 30min at 37 °C, then added to each well (in duplicate). The medium was removed and cells were lysed on ice with 200 µl Triton-X-100-based lysis buffer containing 1 mM PMSF, 10 µg/ml Aprotinin, 10 mM NaF and 2 mM Na-Orthovanadate. The blocked Maxisorp plate was washed 3 times with PBS + 0.05% Tween-20. Cell lysate was transferred directly to a washed Maxisorp plate and incubated overnight at 4 °C with gentle agitation. The plate was washed 6 times with PBS+0.05% Tween-20, then 100 µl anti-Phospho-tyrosine-HRP (Detection Antibody 600ng/ml) diluted in dilution buffer (PBS+0.5%BSA+0,05% Tween-20+5 mM EDTA) was added to each well and incubated for 2 hours at room temperature. The plate was washed 6 times with PBS + 0.05% Tween20 and 100 µl Tetramethylbenzidine (TMB, Calbiochem) was added to each well for 20 minutes at room temperature. The reaction was stopped by addition of 50 µl 1 M H_2SO_4 and the absorbance was read at 450 nm (Thermo Lab Systems plate reader).

[000324]The results are shown in FIGURE 29. As illustrated, increasing concentrations of U2-42.1 or U2-39.1 anti-HB-EGF antibody preparations led to increased inhibition of HB-EGF-induced HER4 phosphorylation.

K. Example 11: Monoclonal Antibody Cross-Reactivity

[000325]This Example provides further data showing cross reactivity of anti-HB-EGF antibody preparations for the cyno HB-EGF, mouse HB-EGF and the related EGF-like growth factor Amphiregulin. Following cloning of the monkey and mouse form of HB-EGF, each expression construct was transfected in HEK293 cells and anti-HB-EGF antibodies were tested on their ability to bind these proteins in a FACS experiment. Amphiregulin cross reactivity was tested by ELISA format assay.

1. Cloning Cyno HB-EGF

[000326]In the present study, cyno HB-EGF plasmids were prepared. The cyno HB-EGF cDNA was cloned by polymerase chain reaction (PCR) from cyno kidney cDNA with primers based on the sequence of cyno HB-EGF.

[000327]The primers used for the amplification of cyno HB-EGF were as follows:

[000328]Forward primer: 5'-GGG TTA ACG CCA CCA TGA AGC TGC TGC CGT CG-3' (SEQ ID NO:1078)

[000329]Reverse primer: 5'-CCG CTC GAG GTG GGA ATT AGT CAT GCC C -3' (SEQ ID NO:1079)

[000330]The PCR product was digested with Hpa1 and Xho1 and ligated into pCDNA3.1 digested with Hind3. After purification, cyno HB-EGF plasmids were transformed into DH5α bacterial cells and multiplied under ampicilin selection. The plasmid was then highly expressed in ampicilin selection media using a single transformed colony. After purifying using a commercially available DNA-purification kit, cyno HB-EGF plasmids were transiently transfected in HEK293T cells.

2. Cloning Mouse HB-EGF

[000331]In the present study, mouse HB-EGF plasmids were prepared. The mouse HB-EGF cDNA was cloned by polymerase chain reaction (PCR) from mouse lung cDNA with primers based on the sequence of mouse HB-EGF.

[000332]The primers used for the amplification of mouse HB-EGF were as follows:

[000333]Forward primer: 5'-GGA ATT CGC CAC CAT GAA GCT GCT GCC GTC G-3' (SEQ ID NO:1080)

[000334]Reverse primer: 5'-CCG CTC GAG GTG GGA GCT AGC AGC CAC GCC-3' (SEQ ID NO:1081)

[000335]The PCR product and pCDNA3.1 vector DNA were digested with EcoR1 and Xho1 and ligated. After purification, mouse HB-EGF plasmids were transformed into DH5α bacterial cells and multiplied under ampicillin selection. The plasmid was then highly expressed in ampicillin selection media using a single transformed colony. After purifying using a commercially available DNA-purification kit, mouse HB-EGF plasmids were transiently transfected in HEK293T cells.

3. Transfection And Expression Of Cyno And Mouse HB-EGF

[000336]To screen for cross-reactivity of antibodies provided herein HEK293T cells were transiently transfected with either cyno or mouse HB-EGF plasmids using a Ca-phosphate method and subsequently analysed by FACS analysis.

[000337]Therefore, 30 hours before transfection, 3x106 HEK293T-cells were seeded in 16ml on a 15cm- cell culture plate and incubated at 7% CO_2 and 37°C. 32 µg DNA of either cyno or mouse HB-EGF DNA or empty vector in 720 µl ddH_2O were mixed with 2.5 M $CaCl_2$ and 2 x BBS (pH6.96) and incubated at room temperature for 10 minutes. After incubation, the solution was added drop wise onto the cells and incubated at 3% CO_2 and 37°C for 8 hours. After soaking the media, the cells were incubated with fresh growing media at 7% CO_2 and 37°C for 24 hours.

4. FACS Analysis Was Performed To Screen For Cross-Reactivity Of The Antibodies

[000338]Therefore, $2x10^5$ transfected cells were harvested with 10 mM EDTA in PBS, resuspended in FACS-buffer (PBS, 3% FCS, 0.4% azide) and seeded on a 96-well round bottom plate. After centrifugation for 3 min at 1000 rpm to remove supernatant, the cells were resuspended in anti-HB-EGF antibody dilution (100 µl/well) and incubated at 4°C for 45 min. The cells were washed twice with FACS buffer and resuspended with secondary antibody (100 µl/well) donkey-anti-human-PE (Jackson) diluted 1:100 in FACS buffer. The cell suspensions were incubated at 4 °C in the dark for 30 min, washed twice with FACS buffer and analyzed (FACS, Beckman Coulter).

[000339]FIGURE 30A shows that three mAb preparations cross-react with pro-HB-EGF from Cynomolgus monkeys.

[000340]FIGURE 30B shows that the U2-45 mAb preparation cross-reacts with mouse HB-EGF as detected by FACS analysis. Further testing showed that antibodies U2-46 and U2-51 were also detecting mouse HB-EGF. However, the antibody U2-45.1 was only very weakly (5-10%) neutralizing mouse HB-EGF induced tyrosine phosphorylation of the EGFR.

5. Protocol For Amphiregulin Cross Reactivity ELISA Assay

[000341]Different concentrations of Amphiregulin (R & D systems, conc. 1 ng/ml, 10ng/ml, 100ng/ml in PBS) were coated overnight at 4°C in a 96-well plate (Nunc, Maxisorp). Following plate wash (6-times) with washing buffer (PBS + 0,05% Tween 20; 150 µl per well), the plate was incubated with blocking buffer (PBS + 0,5% BSA, 100 µl / well) for 4 hours at room temperature. The plate was washed 6-times with washing buffer. As primary antibody 5 µg/ml purified human anti-HB-EGF antibodies in Ab dilution buffer (PBS containing 0.5% BSA, 0.05% Tween 20, 5 mM EDTA) were used and incubated for 90 minutes at room temperature. The plate was washed 6-times with washing buffer and a secondary anti human-POD (Dianova) antibody was added (1:10 000 in PBS, 0.5% BSA, 0.05% Tween 20, 5 mM EDTA) and incubated for 60 minutes at room temperature.

[000342]The plate was washed 6-times with washing buffer and the TMB substrate (Merck Biosciences) was added for 15 minutes at room temperature. After stopping the development of the blue color by adding 100 µl of 250 mM HCl the absorbance was measured at 450nm with a plate reader (Thermo labsystems).

[000343]FIGURE 30C shows that antibody U2-45 and weakly antibody U2-46 bind to Amphiregulin as determined by an ELISA format assay. The U2-45 mAb binds Amphiregulin but the U2-45.1 K_D for Amphiregulin was only 8 nM (versus 0.043 nM for HB-EGF). The U2-45.1 mAb was also non-neutralizing for AR.

L. Example 12: Kinetic Exclusion Assay Analysis Of K_d Values For Anti-HB-EGF Mabs U2-42.2, U2-39.1, U2-45.3, U2-26.2, And U2-34.1

[000344]The K_Ds of mAbs U2-42.2, U2-39.1, U2-45.3, and U2-26.2, and U2-34.1 binding to human HB-EGF, were determined using KinExA technology. For this purpose, a KinExA 3000 instrument was utilized. For all mAb titrations, 50 mg of azlactone beads were coupled with HB-EGF (~29 µg) in 50 mM sodium carbonate buffer, pH 9.0 overnight at 4 °C. After conjugation of HB-EGF to the beads, the beads were centrifuged and washed once with blocking buffer (1 M Tris buffer, pH 8.3, 10 mg/ml BSA) and centrifuged again, and then incubated in blocking buffer for one to two hours at ~23 °C in order to block any remaining reactive azlactone groups present on the surface of the beads. After blocking, the beads were transferred to a standard KinExA bead vial and placed on the instrument.

[000345]MAb U2-42.2: A dual curve analysis was performed to determine the K_D. Twelve solutions containing a nominal mAb binding site concentration of 37 pM were titrated with increasing concentrations of HB-EGF for the K_D-controlled titration, and 1110 pM binding site was titrated in the mAb-controlled titration curve. Each solution had a total volume of 10 ml (K_D-controlled) or 2 ml (mAb-controlled) and was allowed to equilibrate for 30-36 hours (K_D-controlled) or 6 hours (mAb-controlled) at ~23 °C. All solutions for the titration were prepared using volumetric glassware and the HB-EGF concentrations varied from 10.5 nM to 205 fM. The instrument method used for the analysis of these solutions consisted of a bead packing step in which the beads were packed into a glass capillary, and the equilibrated solutions were flowed through the bead column at 0.25 ml/min for 10 min (2.5 ml, K_D-controlled) or 1 min (0.25 ml, mAb-controlled) in triplicate. Subsequently, a fluorescently labeled cy-5 goat anti-human (Fc specific) polyclonal antibody at 3.4 nM (K_D-controlled) or 1.1 nM (mAb-controlled) was flowed through the bead pack for 2 min at 0.5 ml/min to label the free mAb binding site captured on the beads. The fluorescence emission from the bead pack was measured at 670 nm with excitation at 620 nm.

[000346]The resulting fluorescence measurements were converted into %-free mAb binding site versus total antigen concentration as standardly done with the accompanying KinExA software package (version 1.0.3). The dual titration curves were fit with the KinExA software to a 1:1 equilibrium isotherm with drift correction factors included.

[000347]The value of the K_D that fit the data optimally was 53 pM with low and high 95% confidence limits at 34 pM and 81 pM, respectively.

[000348]MAb U2-39.1: A K_D-controlled titration curve was performed to determine the K_D. Twelve solutions containing a nominal mAb binding site concentration of 55 pM were titrated with increasing concentrations of HB-EGF. Each solution had a total volume of 10 ml and was allowed to equilibrate for 30-36 hours at ~23 °C. All solutions for the titration were prepared using volumetric glassware and the HB-EGF concentrations varied from 10.5 nM to 205 fM. The instrument method used for the analysis of these solutions consisted of a bead packing step in which the beads were packed into a glass capillary, and the equilibrated solutions were flowed through the bead column at 0.25 ml/min for 10 min (2.5 ml) in triplicate. Subsequently, a fluorescently labeled cy-5 goat anti-human (Fc specific) polyclonal antibody at 3.4 nM was flowed through the bead pack for 2 min at 0.5 ml/min to label the free mAb binding site captured on the beads. The fluorescence emission from the bead pack was measured at 670 nm with excitation at 620 nm. The resulting fluorescence measurements were converted into %free mAb binding site versus total antigen concentration using the accompanying KinExA software package (version 1.0.3). Owing to ligand nonspecific binding to the bead pack, the titration curve was fit with the KinExA software to a 1:1 equilibrium isotherm with a term for ligand nonspecific binding included.

[000349]The value of the K_D that fit the data optimally was 7.8 pM with low and high 95% confidence limits at 5.6 pM and 11 pM, respectively.

[000350]MAb U2-45.3: A dual curve analysis was performed to determine the K_D. Twelve solutions containing a nominal mAb binding site concentration of 40 pM were titrated with increasing concentrations of HB-EGF for the K_D-controlled titration, and 1060 pM binding was titrated in the mAb-controlled titration curve. Each solution had a total volume of 10 ml (K_D-controlled) or 2 ml (mAb-controlled) and was allowed to equilibrate for 30-36 hours (K_D-controlled) or 6 hours (mAb-controlled) at ~23 °C. All solutions for the titration were prepared using volumetric glassware and the HB-EGF concentrations varied from 5.25 nM to 102 fM. The instrument method used for the analysis of these solutions consisted of a bead packing step in which the beads were packed into a glass capillary, and the equilibrated solutions were flowed through the bead column at 0.25 ml/min for 10 min (2.5 ml, K_D-controlled) or 1 min (0.25 ml, mAb-controlled) in triplicate. Subsequently, a fluorescently labeled cy-5 goat anti-human (Fc specific) polyclonal antibody at 3.4 nM (K_D-controlled) or 1.1 nM (mAb-controlled) was flowed

through the bead pack for 2 min at 0.5 ml/min to label the free mAb binding site captured on the beads. The fluorescence emission from the bead pack was measured at 670 nm with excitation at 620 nm. The resulting fluorescence measurements were converted into %free mAb binding site versus total antigen concentration as standardly done with the accompanying KinExA software package (version 1.0.3). The dual titration curves were fit with the KinExA software to a 1:1 equilibrium isotherm with drift correction factors included.

[000351]The value of the K_D that fit the data optimally was 43 pM with low and high 95% confidence limits at 27 pM and 65 pM, respectively.

[000352]MAb U2-26.2: A dual curve analysis was performed to determine the K_D. Twelve solutions containing a nominal mAb binding site concentration of 41 pM were titrated with increasing concentrations of HB-EGF for the K_D-controlled titration, and 1060 pM binding site was titrated in the mAb-controlled titration curve. Each solution had a total volume of 10 ml (K_D-controlled) or 2 ml (mAb-controlled) and was allowed to equilibrate for 30-36 hours (K_D-controlled) or 6 hours (mAb-controlled) at ~23 °C. All solutions for the titration were prepared using volumetric glassware and the HB-EGF concentrations varied from 2.63 nM-51.4 fM (K_D-controlled) and 5.26 nM-103 fM (mAb-controlled). The instrument method used for the analysis of these solutions consisted of a bead packing step in which the beads were packed into a glass capillary, and the equilibrated solutions were flowed through the bead column at 0.25 ml/min for 10 min (2.5 ml, K_D-controlled) or 1 min (0.25 ml, mAb-controlled) in triplicate. Subsequently, a fluorescently labeled cy-5 goat anti-human (Fc specific) polyclonal antibody at 3.4 nM (K_D-controlled) or 1.1 nM (mAb-controlled) was flowed through the bead pack for 2 min at 0.5 ml/min to label the free mAb binding site captured on the beads. The fluorescence emission from the bead pack was measured at 670 nm with excitation at 620 nm. The resulting fluorescence measurements were converted into %free mAb binding site versus total antigen concentration as standardly done with the accompanying KinExA software package (version 1.0.3). The dual titration curves were fit with the KinExA software to a 1:1 equilibrium isotherm with drift correction factors included.

[000353]The value of the K_D that fit the data optimally was 61 pM with low and high 95% confidence limits at 37 pM and 100 pM, respectively.

[000354]MAb U2-34.1: A K_D-controlled titration curve was performed to determine the K_D. Twelve solutions containing a nominal mAb binding site concentration of 40 pM were titrated with increasing concentrations of HB-EGF. Each solution had a total volume of 10 ml and was allowed to equilibrate for 30-36 hours at ~23 °C. All solutions for the titration were prepared using volumetric glassware and the HB-EGF concentrations varied from 5.26 nM-103 fM. The instrument method used for the analysis of these solutions consisted of a bead packing step in which the beads were packed into a glass capillary, and the equilibrated solutions were flowed

through the bead column at 0.25 ml/min for 10 minutes (2.5 ml) in triplicate. Subsequently, a fluorescently labeled cy-5 goat anti-human (Fc specific) polyclonal antibody at 5.1 nM was flowed through the bead pack for 2 minutes at 0.5 ml/min to label the free mAb binding site captured on the beads. The fluorescence emission from the bead pack was measured at 670 nm with excitation at 620 nm. The resulting fluorescence measurements were converted into %free mAb binding site versus total antigen concentration as standardly done with the accompanying KinExA software package (version 1.0.3). Owing to ligand nonspecific binding to the bead pack, the titration curve was fit with the KinExA software to a 1:1 equilibrium isotherm with a term for ligand nonspecific binding included.

[000355]The value of the K_D that fit the data optimally was 59 pM with low and high 95% confidence limits at 32 pM and 87 pM, respectively.

M. Example 13: Determination Of Antibody Affinity Scatchard Analysis

[000356]Affinity measurements of antibodies provided herein were performed by indirect FACS Scatchard analysis. To perform this analysis $2x10^5$ cells of interest were harvested with 10 mM EDTA in PBS, resuspended in FACS-buffer (PBS, 3% FCS, 0.4% azide) and seeded on a 96-well round bottom plate. After centrifugation for 3 min at 1000 rpm to remove supernatant, the cells were resuspended in anti-HB-EGF antibody dilution (100 µl/well) starting with 20 µg/ml, diluted in 1:2 dilution steps. Cell suspensions were incubated at 4 °C for 45 min, washed twice with FACS buffer and resuspended with secondary antibody (100 µl/well) donkey-anti-human-PE (Jackson) diluted 1:100 in FACS buffer. The cell suspensions were incubated at 4 °C in the dark for 30 min, washed twice with FACS buffer and analyzed (FACS, Beckman Coulter).

[000357]According to the FACS Scatchard analysis, the fluorescence mean was calculated for each measurement. Background fluorescence of cells without HB-EGF antibodies was subtracted from each fluorescence mean. Scatchard plot with x-value = fluorescence mean and y-value = fluorescence mean/concentration of mAb (nM) was generated. The K_D was taken as the absolute value of 1/m of linear equation.

TABLE 5
FACS Scatchard Determined Affinities Of Antibodies U2-42 And U2-39 On Three Different Human Cancer Cell Lines

Cell line / Antibody	DLD-1	NCI-ADR	MDA-MB231
U2-42	4,88	5,98	0,41
U2-39	9,05	7,63	6,21

N. Example 14: Kinetic Exclusion Assay Analysis Of K_d Values For Anti-HB-EGF Mab U2-45.3 Binding To Amphiregulin

[000358]A K_D-controlled titration curve was performed to determine the K_D. Twelve solutions containing a nominal mAb binding site concentration of 4.4 nM were titrated with increasing concentrations of Amphiregulin. Each solution had a total volume of 10 ml and was allowed to equilibrate for 30-36 hours at ~23 °C. All solutions for the titration were prepared using volumetric glassware and the Amphiregulin concentrations varied from 1.23 µM to 24 pM. The instrument method used for the analysis of these solutions consisted of a bead packing step in which the beads were packed into a glass capillary, and the equilibrated solutions were flowed through the bead column at 0.25 ml/min for 1 minute (0.25 ml) in triplicate. Subsequently, a fluorescently labeled cy-5 goat anti-human (Fc specific) polyclonal antibody at 684 pM was flowed through the bead pack for 2 minutes at 0.5 ml/min to label the free mAb binding site captured on the beads. The fluorescence emission from the bead pack was measured at 670 nm with excitation at 620 nm. The resulting fluorescence measurements were converted into %free mAb binding site versus total antigen concentration as standardly done with the accompanying KinExA software package (version 1.0.3). Owing to ligand nonspecific binding to the bead pack, only one replicate out of the three collected at each concentration (the highest three 2-fold Amphiregulin concentrations were excluded from the analysis) could be analyzed and fit with the KinExA software to a 1:1 equilibrium isotherm.

[000359]The value of the K_D that fit the data optimally was 5.0 nM with low and high 95% confidence limits at 3.1 nM and 7.7 nM, respectively.

O. Example 15: Selection Criterion For Top Antibody Preparations

[000360]The following criteria were used to identify the top antibody preparations: potency in inhibiting TMPS, potency in directly inhibiting HB-EGF as measured by observing the degree to which the antibodies inhibited tyrosine phosphorylation of EGF receptor and HER4, the affinity of the antibodies for HB-EGF, the cross-reactivity of the antibodies for other molecules and the characteristics of the epitopes.

P. Example 16: Anti-Hb-Egf Antibodies Inhibit HB-EGF Stimulation Of Huvec Cellular Proliferation And Tube Formation

[000361]This Example illustrates that while HB-EGF stimulates human vascular endothelial cell (HUVEC) proliferation, anti-HB-EGF antibodies provided herein inhibit basal HUVEC cell proliferation. Also, as shown by this Example, anti-HB-EGF antibodies inhibit HUVEC tube formation, which is an *in vitro* model for neo-angiogenesis. Antibody preparations that inhibit

HUVEC proliferation and/or angiogenesis are useful not only for treating cancer but also for treating non-cancerous conditions involving undesired angiogenesis (*e.g.*,diabetic retinopathy).

1. **Procedures: Determination of HB-EGF Expression on HUVEC Cells by Flow Cytometry**

[000362]HB-EGF expression on human endothelial cells was determined by FACS analysis. Therefore, $2x10^5$ cells of interest were harvested with 10 mM EDTA in PBS, resuspended in FACS-buffer (PBS, 3% FCS, 0.4% azide) and plated on a 96-well round bottom plate. After centrifugation for 3 min at 1000 rpm, supernatant was removed, the cells were resuspended in anti-HB-EGF antibody dilution (100 µl/well, 10 µg/ml anti-HB-EGF antibody) and incubated at 4°C for 45 min. The cells were washed twice with FACS buffer and resuspended with secondary antibody (100 µl/well) anti-human-PE (Jackson) diluted 1:100 in FACS buffer. The cell suspensions were incubated at 4 °C in the dark for 30 min, washed twice with FACS buffer and analyzed (FACS, Beckman Coulter).

[000363]To test for the effects of anti-HB-EGF antibodies on HUVEC proliferation, approximately 5000 HUVEC cells were seeded into each of 48 wells containing media with EGM-2, hydrocortisone, ascorbic acid, gentamycin-amphothericin and 2% FCS containing bFGF, VEGF, EGF and IGF-1 (Cambrex). After incubating the cells overnight at 37 C, the cells were washed twice with PBS containing 0.5% FCS. The cells were then starved 8h in EGM-2, 0.5% FCS without supplementation of growth factors. HB-EGF or anti-HB-EGF antibody preparations were added in 500 µl starvation media.

[000364]Cells were then cultured for an additional 60 hours, trypsinized and counted.

[000365]To test for the effects of anti-HB-EGF antibodies on HUVEC tube formation, 200 µl growth factor reduced matrigel (BD biosciences) was plated on 48 wells. 250 µl HUVEC medium was added per 48 well (EBM-2 + hydrocortisone + ascorbic acid gentamycin-amphothericin + 0,25% FCS from Cambrex). Following preincubation for 20 min, 20,000 HUVEC cells in 50 µl medium + 0.25% FCS containing HB-EGF (10 ng/ml) or U2-42, U2-39 or U2-45 anti-HB-EGF antibodies (10 µg/ml) were added. Tube formation was monitored by obtaining photomicrographs of representative areas of the culture wells. For a quantitative analysis closed areas of HUVEC tubes were counted.

2. **Results**

[000366]As shown by the FACS analysis in FIGURE 30, HB-EGF is expressed on HUVECs. The results of the cellular proliferation tests are provided in FIGURES 32A-B. As shown in FIGURE 32A, HB-EGF stimulates HUVEC cellular proliferation by about 38%. However, upon addition of anti-HB-EGF antibody preparations U2-42, U2-39 or U2-45, such stimulation of

cellular proliferation is inhibited by about 8% to 14% (FIGURE 31B). In this assay, the U2-39 anti-HB-EGF antibody preparation provided the highest level of inhibition.

[000367]The results of the tube formation tests are provided in FIGURES 33A-M. Control assays, without anti-HB-EGF antibodies shown in FIGURES 34A-C, show that HUVEC cells join to form circular structures or "tubes." However, upon addition of anti-HB-EGF antibody preparations U2-42, U2-39 or U2-45, such tube formation is inhibited. A summary of the number of tubes observed is provided in FIGURE 33M. As shown in FIGURE 33M, the U2-42 anti-HB-EGF antibody preparation provided the highest acceleration of tube regression, followed by the U2-39 anti-HB-EGF antibody preparation.

Q. Example 17: Anti-HB-EGF Antibodies Inhibit HB-EGF-Stimulated And Basal Colony Formation

[000368]Soft agar assays were conducted in order to investigate the ability of the antibodies provided herein to inhibit anchorage independent cell growth. The soft agar colony formation assay is a standard *in vitro* assay to test for transformed cells, as only such transformed cells can grow in soft agar.

[000369]To perform this assay, OVCAR-8, BM-1640 and NCI-H226 cells were incubated with 10 ng/ml HB-EGF and with anti-HB-EGF antibodies or IgG2 (SIGMA) as negative control, at 20 µg/ml in IMDM medium (Gibco) and resuspended in 0.2% Difco noble agar. The cell suspension was plated on a 0.4% agar-underlayer in quadruplicate in a 96-well plate and overlaid with IMDM medium. Colonies were allowed to form for approximately 14 days and were then stained with 40µl MTT (Sigma, 1 mg/ml in PBS) for 4 hours. Stimulation of HB-EGF and inhibitory effects of anti-HB-EGF antibodies were quantified by HTSBonit (LemnaTec) colony formation software.

[000370]In another assay, 750 or 1000 cells (depending on SkOV-3 clone 71 or 74, FIGURE 34D and E) were preincubated with anti-HB-EGF antibodies or IgG2 (SIGMA) as negative control, at 20 µg/ml in IMDM medium (Gibco) for 30 min at 37 °C and resuspended in 0.4% Difco noble agar (or 0.2% for clone 74). The cell suspension was plated on a 0.75% agar-underlayer (0.4% for clone 74) in quadruplicate in a 96-well plate and overlaid with IMDM medium. In a similar assay, 2000 BxPC-3 cells (FIGURE 34F) were preincubated with 20 µg/ml anti-HB-EGF antibodies or 20 µg/ml IgG2 (SIGMA) as negative control, in IMDM medium (Gibco) containing 20% FCS for 30 min at 37 °C. Cells were resuspended in 0.4% Difco noble agar and the cell suspension was plated on a 0.75% agar-underlayer in quadruplicate in a 96-well plate. The wells were overlaid with IMDM medium. Both layers contained 20% FCS.

[000371]Colonies were allowed to form for approximately 14 days and were then stained with 40µl MTT (Sigma, 1 mg/ml in PBS) for 4 hours. Results are shown in FIGURES 34A-F, which illustrate that HB-EGF stimulated colony formation (FIGURE 34A-C) and basal colony formation

(FIGURES 34D-F) is significantly reduced by the anti-HB-EGF antibodies. As shown, for example, in FIGURE 34A, HB-EGF stimulated OVCAR-8 cells to form a significantly larger mean colony size than control OVCER-8 cells cultured without HB-EGF. However, when OVCAR-8 cells were cultured with anti-HB-EGF U2-39 antibodies in the presence of HB-EGF, mean colony size was reduced to a size similar to that observed for control cells without HB-EGF treatment (FIGURE 34A). Similar results were observed for BM1604 cells (derived from prostate cancer tissue) (*see,* FIGURE 34B). Anti-HB-EGF U2-45 and U2-42 antibodies also inhibited BM1604 colony formation.

[000372]Anti-HB-EGF antibodies also inhibit HB-EGF-stimulated colony formation of NCI-H226 lung carcinoma cells (FIGURE 34C). As shown in FIGURE 36C, when NCI-H226 cells were cultured with anti-HB-EGF U2-39 antibodies in the presence of HB-EGF, mean colony size was reduced to a size similar to that observed for control cells without HB-EGF treatment.

[000373]The numbers of colonies, as well as the colony size, are reduced by the treatment with the present anti-HB-EGF antibodies (FIGURES 34D-F). Thus, FIGURE 34D illustrates that anti-HB-EGF antibodies reduce the number of basal colonies formed by SkOV-3 HB-EGF clone 71 cells (derived from SkOV-3 ovarian cancer cells stably transfected with a proHB-EGF expression construct). As shown, control SkOV-3 cells overexpressing HB-EGF formed large numbers of colonies. However, when SkOV-3 HB-EGF cl. 71 cells were cultured with either anti-HB-EGF U2-42 or U2-39 antibodies in the presence of HB-EGF, the number of colonies was dramatically reduced. Similarly, anti-HB-EGF antibodies inhibit colony formation of SkOV-3 (clone 74) cells, derived from ovarian cancer tissue, and BxPC3 cells, derived from pancreatic adenocarcinoma tissue (FIGURES 34E-F).

[000374]These data indicate that colony formation and tumors by a large variety of cancer cell types can be inhibited by the present anti-HB-EGF antibodies, including the U2-42, U2-39 and U2-45 antibody preparations provided herein.

R. Example 18: Anti HB-EGF Antibodies Inhibit Tumor Growth *In Vivo*

[000375]FIGURES 37 illustrates the mean volume of pancreatic BxPC3 tumors formed in xenograft experiments with SCID mice. As shown, established tumor growth was significantly inhibited in the presence of antibody preparations U2-42 and/or U2-39 when compared to the vehicle control. In FIGURE 38A it is shown that anti-HB-EGF antibodies U2-42, U2-39 and U2-45 inhibit the established growth of EFO-27 HB-EGF clone 58 cells *in vivo*. The effect of tumor growth inhibition could be shown to be dose-dependent, with 25 mg/kg as a highly effective treatment while lower doses such as 1 or 5 mg/kg were less efficient (FIGURE 38B).

S. Example 19: Anti-HB-EGF Antibodies In Combination Therapy With The Antiegfr Antibody Erbitux

[000376]FIGURE 35 shows that single agent inhibition of EFO-27 HB-EGF cl. 58 cells with anti-HB-EGF antibodies is moderate to strong. However, in a dose-controlled combination of anti-HB-EGF and anti-EGFR antibodies the inhibition of colony formation is extremely effective. Moreover, *in vivo* xenograft growth is strongly inhibited by the anti-HB-EGF and anti-EGFR antibody combination leading to a complete regression of ovarian cancer tumor growth (FIGURE 38C).

T. Example 20: HB-EGF Expression On A Variety Of Cancer Cell Types

[000377]HB-EGF expression on human cancer cell-lines was determined by FACS analysis. To perform this analysis $2x10^5$ cells were harvested with 10 mM EDTA in PBS, resuspended in FACS-buffer (PBS, 3% FCS, 0.4% azide) and transferred to a 96-well round bottom plate. After centrifugation for 3 min at 1000 rpm to remove supernatant, the cells were resuspended in anti-HB-EGF antibody dilution (100 µl/well) and incubated at 4°C for 45 min. The cells were washed twice with FACS buffer and resuspended with secondary antibody (100 µl/well) donkey-anti-human-PE (Jackson) diluted 1:100 in FACS buffer. The cell suspensions were incubated at 4 °C in the dark for 30 minutes, washed twice with FACS buffer and analyzed (FACS, Beckman Coulter).

[000378]The results of these assays are shown in TABLE 6, below.

[000379]

TABLE 6
HB-EGF Expression in Cancer Cells

Cell line	Tissue	Expression Level
MDA-MB231	Breast	++
NCI-ADR	Breast	+++
ZR75-1	Breast	-/+
MKN-1	Gastric	+
MKN-28	Gastric	+++
PPC1	Prostate	++
PC3	Prostate	++
HT144	Melanoma	-/+
MelGerlach	Melanoma	+++
IGROV-1	Ovarian	+
ES2	Ovarian	++
SkOV-3	Ovarian	+
SkOV-8	Ovarian	+
TOV21G	Ovarian	++
OVCAR-8	Ovarian	+++
Calu-6	Lung	+
NCI-H460	Lung	++
MS-751	Cervix	++
SIHA	Cervix	+
HelaS3	Cervix	+
U266	Myeloma	-
SCABER	Bladder	++
HCT-116	Colon	++
HCT-15	Colon	+
SW620	Colon	++

U. Example 21: Anti-HB-EGF Antibodies For The Detection Of HB-EGF In Tissue And Body Fluids By Immunohistochemistry And Elisa

[000380]Anti-HB-EGF antibodies U2-42 and U2-39 were tested for their ability to stain HB-EGF expressed in human fixed samples. As shown in FIGURE 39A both antibodies show a prominent membrane and cytoplasmic staining of human kidney tubular cells while the control does not show any staining. In addition to the immunohistochemical detection of HB-EGF in

patient tissue samples HB-EGF is released as a growth factor into various body fluids. Based on human anti-HB-EGF antibodies as coating reagents an ELISA was established which detects HB-EGF in liquid samples down to levels below 40 pg/ml (FIGURE 39B).

V. Example 22: Canonical Classes Of Antibodies

[000381]The genes encoding top antibodies were sequenced as described in the last Example. This sequence data was used to assign the antibodies to canonical classes.

[000382]Chothia *et al.* have described antibody structure in terms of "canonical classes" for the hypervariable regions of each immunoglobulin chain (Chothia, *et al.*, 1987, *J. Mol. Biol.*, 196(4) :901-17). The atomic structures of the Fab and VL fragments of a variety of immunoglobulins were analyzed to determine the relationship between their amino acid sequences and the three-dimensional structures of their antigen binding sites. Chothia *et al.* found that there were relatively few residues that, through their packing, hydrogen bonding or the ability to assume unusual phi, psi or omega conformations, were primarily responsible for the main-chain conformations of the hypervariable regions. These residues were found to occur at sites within the hypervariable regions and in the conserved α-sheet framework. By examining sequences of immunoglobulins having unknown structure, Chothia, *et al.* show that many immunoglobulins have hypervariable regions that are similar in size to one of the known structures and additionally contained identical residues at the sites responsible for the observed conformation.

[000383]Their discovery indicated that these hypervariable regions have conformations close to those in the known structures. For five of the hypervariable regions, the repertoire of conformations appeared to be limited to a relatively small number of discrete structural classes. These commonly occurring main-chain conformations of the hypervariable regions were termed "canonical structures." Further work by Chothia, *et al.*, 1989; *Nature* 342:877-83) and others (Martin *et al.*, 1996; J. *Mol. Biol.* 263:800-15) confirmed that there is a small repertoire of main-chain conformations for at least five of the six hypervariable regions of antibodies.

[000384]The complementarity determining regions (CDRs) of each antibody preparation were analyzed to determine their canonical class. As is known, canonical classes have only been assigned for CDR1 and CDR2 of the antibody heavy chain, along with CDR1, CDR2 and CDR3 of the antibody light chain. The TABLES below summarize the results of the analysis. The Canonical Class data is in the form of HCDR1-HCDR2-LCDR1-LCDR2-LCDR3 (H1-H2-L1-L2-L3), wherein "HCDR" refers to the heavy chain CDR and "LCDR" refers to the light chain CDR. Thus, for example, a canonical class of 1-3-2-1-1 refers to an antibody that has a HCDR1 that falls into canonical class 1, a HCDR2 that falls into canonical class 3, a LCDR1 that falls into canonical class 2, a LCDR2 that falls into canonical class 1, and a LCDR3 that falls into canonical class 1.

[000385]Assignments were made to a particular canonical class where the amino acids in the antibody match with the amino acids defined for each canonical class. The amino acids defined for each canonical class can be found, for example, in the articles by Chothia, *et al.* referred to above. TABLE 7 and TABLE 8 report the canonical class assignments for each of the HB-EGF antibodies. Where there was no matching canonical class, the canonical class assignment is marked with a letter s and a number, such as "s18", meaning the CDR is of size 18.

[000386]

TABLE 7

Antibody (sorted)	H1-H2-L1-L2-L3	H3length
U2-18.1	3-1-2-1-1	17
U2-13.1	1-3-4-1-1	14
U2-19.1	3-1-3-1-1	13
U2-38.1	3-1-2-1-1	23
U2-21.1	3-1-3-1-s9	8
U2-15.1	1-3-4-1-1	14
U2-16.1	1-2-8-1-1	11
U2-30.1	1-2-3-1-1	13
U2-42.1	1-3-2-1-s9	8
U2-36.1	3-s18-2-1-s10	13
U2-22.1	1-3-3-1-1	11
U2-56.1	3-1-2-1-1	8
U2-24.1	3-s16-3-1-s9	12
U2-24.2.1	3-s16-3-1-s9	12
U2-14.1	1-3-4-1-1	14
U2-1.1	1-3-4-1-1	5
U2-32.1	1-1-3-1-1	15
U2-40.1	1-3-2-1-3	8
U2-5.1	1-3-4-1-1	6
U2-8.1	3-1-4-1-1	17
U2-39.1	1-3-2-1-1	6
U2-3.1	3-1-4-1-1	16
U2-43.1	1-1-2-1-1	12
U2-34.1	1-3-2-1-1	16
U2-26.1	3-1-3-1-s9	9

U2-41.1	1-3-2-1-1	12
U2-45.1	1-3-2-1-1	19
U2-54.1	3-1-2-1-1	15
U2-57.1	3-1-2-1-1	8
U2-12.1	1-3-2-1-s9	9
U2-46.1	1-3-2-1-1	16
U2-48.2	1-1-2-1-1	12
U2-6.1.1	1-3-4-1-1	11
U2-6.1.2	1-3-2-1-1	16
U2-58.1	3-s16-2-1-1	8
U2-51.1	1-3-2-1-1	16
U2-65.2	3-1-2-1-1	8
U2-53.1	1-1-2-1-1	12
U2-61.1	1-3-2-1-1	9
U2-28.1	3-1-3-1-s9	12

TABLE 8

Antibody	H1-H2-L1-L2-L3 (sorted)	H3 Length
U2-43.1	1-1-2-1-1	12
U2-48.2	1-1-2-1-1	12
U2-53.1	1-1-2-1-1	12
U2-32.1	1-1-3-1-1	15
U2-30.1	1-2-3-1-1	13
U2-16.1	1-2-8-1-1	11
U2-39.1	1-3-2-1-1	6
U2-61.1	1-3-2-1-1	9
U2-41.1	1-3-2-1-1	12
U2-34.1	1-3-2-1-1	16
U2-46.1	1-3-2-1-1	16
U2-6.1.2	1-3-2-1-1	16
U2-51.1	1-3-2-1-1	16
U2-45.1	1-3-2-1-1	19
U2-40.1	1-3-2-1-3	8
U2-42.1	1-3-2-1-s9	8
U2-12.1	1-3-2-1-s9	9
U2-22.1	1-3-3-1-1	11
U2-1.1	1-3-4-1-1	5
U2-5.1	1-3-4-1-1	6
U2-6.1.1	1-3-4-1-1	11
U2-13.1	1-3-4-1-1	14
U2-15.1	1-3-4-1-1	14
U2-14.1	1-3-4-1-1	14
U2-56.1	3-1-2-1-1	8
U2-57.1	3-1-2-1-1	8
U2-65.2	3-1-2-1-1	8
U2-54.1	3-1-2-1-1	15
U2-18.1	3-1-2-1-1	17
U2-19.1	3-1-3-1-1	13
U2-21.1	3-1-3-1-s9	8

U2-26.1	3-1-3-1-s9	9
U2-28.1	3-1-3-1-s9	12
U2-3.1	3-1-4-1-1	16
U2-8.1	3-1-4-1-1	17
U2-58.1	3-s16-2-1-1	8
U2-24.1	3-s16-3-1-s9	12
U2-24.2.1	3-s16-3-1-s9	12
U2-36.1	3-s18-2-1-s10	13
U2-38.1	3-1-2-1-1	23

[000387]TABLE 9 is an analysis of the number of antibodies per class. The number of antibodies having the particular canonical class designated in the left column is shown in the right column.

[000388]The most commonly seen structure is 1-3-2-1-1. Eight out of a total of 40 mAbs had this combination.

[000389]

TABLE 9
Number of Anti-HB-EGF Antibodies in Each Canonical Class Combination

H1-H2-L1-L2-L3	Count
1-1-2-1-1	3
1-1-3-1-1	1
1-2-3-1-1	1
1-2-8-1-1	1
1-3-2-1-1	8
1-3-2-1-3	1
1-3-2-1-s9	2
1-3-3-1-1	1
1-3-4-1-1	6
3-1-2-1-1	5
3-1-3-1-1	1
3-1-3-1-s9	3
3-1-4-1-1	2
3-s16-2-1-1	1
3-s16-3-1-s9	2
3-s18-2-1-s10	1
3-1-2-1-1	1

W. Example 23: Epitope Mapping Of Anti HB-EGF Antibodies

[000390]This Example describes the mapping of epitopes recognized by antibody preparations.

[000391]Antibodies tested: Five XenoMouse derived human monoclonal antibody preparations capable of neutralizing the activity of HB-EGF were analyzed: U2-39; U2-42; U2-45; U2-26 and U2-19. Four of these monoclonal antibody preparations were shown to be specific for human HB-EGF while antibody preparation U2-45 exhibited some cross-reactivity with mouse HB-EGF and human Amphiregulin. All of these neutralizing antibody preparations map to MCAB Bins 7 & 8 (*see*, below).

1. Epitope Mapping

[000392]The human HB-EGF cDNA was isolated from HeLa mRNA by PCR amplification and the mature HB-EGF sequence was cloned into a pSecTAg vector as a myc-His fusion protein,

using the Ig kappa signal peptide sequence. The mature HB-EGF polypeptide was expressed in 293T cells, with secretion into the media.

[000393]The diphtheria toxin binding site of HB-EGF was mutated as well as the EGF receptor binding site by site-directed mutagenesis.

[000394]The short form of HB-EGF (Loukianov *et al*; *Gene* 195:81-86), missing the third disulphide bond of the EGF-like domain, was also cloned.

[000395]The EGF-like domain of HB-EGF having SEQ ID NO:1082 (DPCLRKYKD FCIHGECKYVKELRAPSCICHPGYHGERCHGLSLP) was cloned into pSecTag and expressed and secreted as a Myc-His fusion protein.

2. Results

[000396]All of the U2-39; U2-42; U2-45; U2-26 and U2-19 antibody preparations recognize a discontinuous epitope. None of the antibodies recognize the Short form of the HB-EGF.

[000397]The binding site for all five antibody preparations is within the EGF-like domain, which included residues 44-86 of the mature protein having the following sequence: DPCLRKYKDFCIHGECKYVKELRAPSCICHPGYHGER CHGLSLP (SEQ ID NO:1082). The third disulfide bond in the EGF-like domain is required for binding of all of the U2-39; U2-42; U2-45; U2-26 and U2-19 antibody preparations.

3. Structure-Function Analysis of Antibody Binding Site by Site Directed Mutagenesis

[000398]Twelve independent mutations were created in HB-EGF by replacing one to four residues within the EGF-like domain of human pro-HB-EGF with the corresponding amino acid residue normally found in the mouse pro-HB-EGF.

[000399]Given that many of the present antibody preparations were species selective, site-directed mutagenesis for the purpose of identifying HB-EGF epitopes was done at known difference between the human HB-EGF protein and related proteins from different species. In particular, the amino acid differences between human and mouse HB-EGF are as follows: K122R; V124L; K125Q; I133K; and H135L.

[000400]A complete list of HB-EGF mutant polypeptide sequences for epitope mapping is provided in TABLE 10. Mutant HB-EGF nucleic acids encoding the desired mutant protein were transiently expressed in 293T cells, and monoclonal antibody binding was measured by ELISA.

[000401]Thus, HB-EGF mutant polypeptides were made with these mutations and such mutant polypeptides were tested to ascertain if the present antibody preparations still bound to the HB-EGF mutant polypeptide. If not, then the mutated amino acid was likely important for antibody binding, and hence formed an important part of an epitope.

[000402]TABLE 11 summarizes the binding results obtained, where "Yes" indicates that binding took place despite the indicated mutation, "No" indicates that binding was substantially eliminated by the indicated mutation, and "Reduced" indicates that reduced binding occurred when the mutation was present.

[000403]

[000404]TABLE 10

Wild type	LGKKRDPCLRKYKDFCIHGE- CKYVKELRAPSCICHPGYHGERCHGLSLP	SEQ ID NO:
F115Y	----------Y----------	1083
L127F	----------F----------	1084
E141H	----------H----------	1085
K122R; V124L; K125Q	----------R-LQ----------	1086
F115Y; K122R; V124L; K125Q	----------Y-----R-LQ----------	1087
K122R; V124L; K125Q; E141H	----------R-LQ----------H----------	1088
I133K; H135L	----------K-L----------	1089
F115Y; I133K; H135L	----------Y----------K-L----------	1090
L127F; I133K; H135L	----------F-----K-L----------	1091
L148T	----------T-	1092
E141H; L148T	----------H-----T-	1093
117-120 IHGE changed to LHDGV	----------LHDGV----------	1094

TABLE 11
Binding Results

	Construct/ Mab	U2-42.3	U2-39.1	U2-19.3	U2-26.1	U2-45
1	Human proHB-EGF (WT)	Yes	Yes	Yes	Yes	Yes
2	F115Y	**No**	**No**	Yes	Yes	**Reduced**
3	L127F	Yes	**No**	Yes	Yes	Yes
4	E141H	**No**	Yes	Yes	Yes	Yes
5	K122R, V124L, K125Q	Yes	Yes	Yes	Yes	Yes
6	F115Y,K122R, V124L, K125Q	**No**	**No**	Yes	Yes	**Reduced**
7	K122R, V124L, K125Q, E141H	**No**	Yes	Yes	Yes	Yes
8	I133K, H135L	Yes	Yes	**No**	**No**	Yes
9	F115Y, I133K, H135L	**No**	**No**	**No**	**No**	**Reduced**
10	L127F,I133K, H135L,	Yes	**No**	**No**	**No**	Yes
11	S147T	Yes	Yes	Yes	Yes	Yes
12	E141H, S147T	**No**	Yes	Yes	Yes	Yes
13	IHGE (117-120) to LHDGV	Yes	Yes	**No**	**No**	**No**
	Critical residues	F115 & E141	F115 & L127	I133 or H135	I133 or H135	F115?

[000405]These binding studies indicate that the U2-42 and U2-39 antibody preparations recognize the diphtheria toxin binding domain and the F115, L127 and E141 residues are important for diphtheria toxin binding.

[000406]Furthermore, when the F115Y or E141H mutations are present in HB-EGF, binding is substantially eliminated for the U2-42 antibody preparations. Thus, Phe-115 and Glu-141 are important for U2-42 antibody binding. The U2-45 antibody preparation also appears to require Phe-115 because binding by this antibody preparation is reduced when Phe-115 is mutated.

[000407]The U2-39 antibody preparation requires Phe-115 and Leu-127 for binding HB-EGF because mutation of either of those residues substantially eliminates antibody binding.

[000408]The U2-19, U2-26 and U2-45 antibody preparations bind the conserved region between residues 117-120 (IHGE). As shown in TABLE 11, antibody preparations U2-19 and U2-26 also recognize an epitope at Ile-133 and/or His-135, because at least one of these residues is critical for their binding.

[000409]Based on their binding properties, of the antibodies were placed in the relationship "bins" listed in TABLE 12.

[000410]Binning is a method to group antibodies based on their competition for binding to the antigen (*see*, Jia *et al.*, 2004, *J. Immunol. Methods* 288:91-98).

[000411]The assignment of bins depended on how different the observed binding patterns for all the antibodies tested are. Therefore, bins do not always correlate with epitopes determined by other means and can be used to only roughly define epitopes.

[000412]

TABLE 12
Antibody Relationship Bins

Bin#1	Bin#2	Bin#3	Bin#4	Bin#5	Bin#6	Bin#7	Bin#8
U2-24.2	U2-1.3	U2-15.3	U2-13.3	U2-16.3	U2-18.3	U2-19.2	U2-3.2
U2-32.3		U2-30.2	U2-14.3		U2-38.1	U2-21.3	
U2-5.3			U2-2.1		1.19.2	U2-34.1	
U2-17.1			U2-57.1		U2-36.3	U2-26.2	
U2-56.3			U2-58.3		U2-40.3	U2-41.3	
			U2-61.1		U2-8.3	U2-45.3	
					U2-22.3	U2-46.3	
						U2-	
					U2-39.1	48.2.1	
					U2-54.2	U2-6.1	
						U2-51.2	
						U2-53.3	
						U2-28.2	

[000413]In general the epitope mapping of U2-45 antibody preparation indicates that the Bin 7 antibody preparations cross-react with mouse HB-EGF and human Amphiregulin.

[000414]Mutations of F115 to Ala or Tyr affect the binding affinity of U2-45 antibodies. However, U2-45 antibody binding was not affected by mutations of I133 and H135, which did affect some other Bin 7 antibody preparations. When the IHGE human HB-EGF sequence was changed to LHDGV, which is present in mouse HB-EGF and human Aphiregulin, all Bin7 antibody preparations failed to bind. Therefore, the IHGE residues (117-120) likely form the epitope for bin 7 antibody preparations.

[000415]Further site-directed mutagenesis studies involving binding of HB-EGF mutants to EGFR, indicate that residues including Asp-106 and Pro-107 are both necessary for optimal binding of HB-EGF to the EGF receptor. Moreover, Leu-148, which is necessary for HB-EGF

binding to the EGF receptor, did not appear to be involved in the binding of any of the anti-HB-EGF antibody preparations.

[000416]

HH. Example 24: Sequences Of Key Elements Of Anti HB-EGF Antibodies

[000417]This Example provides the sequences of antibody preparations in Figures 1 – 21.

[000418]Example 25A: Scratch assay - Inhibition of HB-EGF-induced migration of CLS354 epithelial squamous carcinoma cells (mouth)

Scratch experiments were performed in order to investigate whether the antibodies of the invention block cell migration that would otherwise be directly induced by HB-EGF.

[000419]1 x 10^6 CLS354 cells were seeded in medium (RPMI medium with 10% FCS) in 1 ml on a 12-well plate and serum starved (medium with 0.5% FCS) over night. After cells have reached a confluent layer, a scratch was performed in the middle of the well using a sterile plasic tip. Cells were washed with PBS and scratched CLS354 cells were treated alone or containing 20 ng/ml HB-EGF in the presence or absence of 10 µg/ml U2-39, Erbitux or human IgG. The experiment was stopped after 12 hour incubation at 37°C. Medium was withdrawn, cells were washed with PBS and fixed with 100% ice-cold methanol at -20°C, stained with crysal-violet, washed and dried over night. Photographes were taken for documentation.

[000420]Figure 40A shows that HB-EGF treatment stimulates the closure of the scratch and that the antibody of invention, U2-39, inhibits HB-EGF-mediated migration of CLS354 epithelial squamous carcinoma cells into the scratch.

[000421]Example 25B: Transmigration assay - Inhibition of HB-EGF-induced migration of Detroit 562 epithelial carcinoma cells (pharynx)

[000422]Transmigration experiments were performed in order to investigate whether the antibodies of the invention block cell migration that would otherwise be directly induced by HB-EGF.

[000423]A 500 ml cell suspension of serum-starved human epithelial carcinoma cells (50,000 cells) was placed in the top chamber of fibronectin-coated transwells (BD Falcon, 8 µm pores). Aliquots of 750 ml medium (Minimum essential medium (Eagle) in Earle's BSS with non-essential amino acids, sodium pyruvate (1 mM) and lactalbumin hydrolysate (0.1%), 90%; fetal bovine serum 10%, Pen.-Strept., 0,1% BSA) alone or containing 20 ng/ml HB-EGF (R&D Systems) in the presence or absence of 10 µg/ml human IgG, U2-39 or Erbitux antibodies were placed in the bottom chamber after 30 min pre-incubation at 37°C. After incubation and migration for 6hours at 37°C, cells were fixed, stained with DAPI and transwells were photographed for evaluation.

[000424]The result demonstrates that-HB-EGF antibody U2-39 effectively inhibits HB-EGF-induced Detroit 562 epithelial carcinoma cell migration comparable to the inhibition of HB-EGF-mediated cell migration by Erbitux treatment.

[000425]Example 26: Spheroid-based cellular angiogenesis assay – Inhibition of VEGF-stimulated endothelial cell sprouting

[000426]Spheroid-based cellular angiogenesis assays were performed in order to investigate whether the antibodies of the invention are able to inhibit VEGF-induced endothelial cell (EC) sprouting in a collagen matrix. Primary human umbilical vein endothelial cells (HUVEC) were seeded out at 500 cells in a hanging drop on plastic dishes to allow overnight spheroid aggregation. 50 EC spheroids were seeded in 0.9 ml of collagen solution (2 mg/ml) and pipetted into individual wells of a 24 well plate to allow polymerization The antibody of invention U2-39 was directly mixed in the collagen solution before polymerization (different concentrations) and the growth factor VEGF-A (25ng/ml) was added after 30 min by pipetting 100µl of a 10-fold concentrated working dilution on top of the polymerized gel. Plates were incubated at 37°C for 24 hours and fixed by adding 4% paraformaldehyde. Sprouting intensity of EC spheroids was quantitated by an image analysis system determining the cumulative sprout length per spheroid using an inverted microscope and the digital imaging software Analysis 3.2.

[000427]Figure 41A depicts the mean of the cumulative sprout length of 10 randomly selected spheroids per data point. Figure 41B shows the relative inhibition of the cumulative sprout length of 10 randomly selected spheroids per data point by U2-39. The fitting of IC50 curves and calculation of IC50 values was performed with GraphPad Prism 4.03.

[000428]The results of Example 26 demonstrate that the antibody of the invention U2-39 inhibits VEGF-A-stimulated human umbilical vein endothelial cell sprouting in a dose-dependent manner in the spheroid-based assay using a collagen matrix. HUVEC sprouting was inhibited with an IC50 value of 5.2×10^{-8} Molar.

[000429]Example 27: Immunohistochemistry (IHC) analysis of human tumor xenograft samples – Inhibition of CD31 staining of tumor *in vivo*.

[000430]In order to investigate the efficacy of the antibody of invention, U2-39, on inhibition of angiogenesis *in vivo*, human tumor xenografts treated with U2-39 or Erbitux were analyzed by immunohistochemistry analysis.

[000431]The human ovarian adenocarcinoma cell line EFO27 was genetically engineered to overexpress HB-EGF and the clone EFO27-Cl58 was chosen for xenograft studies in SCID mice. 3 x 10^6 EFO27-Cl58 cells in 100µl PBS/Matrigel (1:1) were injected subcutaneously into the left flank of 7 week old female C.B-17 SCID mice. Tumor-bearing mice with mean tumor volumes of 250 mm^3 were randomized into groups containing 10 animals. Animals were treated intraperitoneally with weekly doses of 25 mg/kg U2-39 or 25 mg/kg Erbitux or control vehicle, PBS, for 3 weeks. After 28 days mice were sacrificed, primary tumor tissues were collected and one half of the tumor was snap-frozen in liquid nitrogen and stored at -80°C.

[000432]5 to 8 µm sections of the tumor prepared on glass chamber slides were fixed in 100% acetone for 10 min at 4°C and dried completely. To block unspecific binding sites slides with fixed tumor sections were treated with Avidin D block (15 minutes), Biotin block (15 minutes) and a 1.25% BSA solution (1 hour). Between each treatment step slides were washed twice with PBS. For immunohistochemical examination of the tumor vasculature the expression of the classical endothelial cell marker CD31, also known as PECAM-1 (Platelet Endothelial Cell Adhesion Molecule-1) was analyzed by treatment of the slides with 2µg/ml anti-CD31 antibody (diluted in 1.25% BSA solution and incubated for 2h at room temperature in a humidified chamber). Detection was performed by applying a biotinylated goat ant-rat IgG antibody (30 min at room temperature) and Alexa 546 Streptavidin (15 min in the dark). PBS washing steps were performed between each treatment step. Sections were mounted with VECTASHIELD mounting medium with DAPI in the dark, photographed (fluorescence microscope) for documentation and stored at 4°C.

[000433]Figure 42 demonstrates that human tumor xenografts treated with U2-39 show a reduced endothelial cell marker staining (CD31 staining) compared to Erbitux-treated or control treated tumor xenografts. This result demonstrates the anti-angiogenic efficacy of the antibody of invention in vivo.

[000434]Example 28: In vivo ovarian tumor xenograft model – combination treatment of U2-39 with Cisplatin and Avastin

[000435]In order to evaluate the anti-tumor efficacy of the antibody of invention administered as a monotherapy or in combination with Cisplatin or Avastin, an ovarian cancer xenograft study was conducted.

[000436]The human ovarian adenocarcinoma cell line EFO27 was genetically engineered to overexpress HB-EGF. The clone EFO27-Cl58 was chosen for xenograft studies in SCID mice. 3 x 10^6 EFO27-Cl58 cells in 100µl PBS/Matrigel (1:1) were injected subcutaneously into the left flank of 7 week old female C.B-17 SCID mice. Tumor-bearing mice with mean tumor volumes between 75 and 175 mm^3 were randomized into groups containing 10 animals. Animals were treated intraperitoneally with weekly doses of 25 mg/kg U2-39, 25 mg/kg Avastin or 5 mg/kg Cisplatin or control vehicle, PBS. Combination of U2-39 with Avastin was given at 12.5 mg/kg each and combination of U2-39 with Cisplatin was given at 25 mg/kg antibody with 5 mg/kg Cisplatin. Primary tumor sizes were determined 3 times a week. Following calliper measurement, tumor size was calculated according to the formula W2xL/2 with L=length and W= the perpendicular width of the tumor. Kaplan-Meier log-rank method was used to define time to progression to 500 mm^3 (defined as "event" for statistical reasons).

[000437]Figure 43A demonstrates that combination of U2-39 with Cisplatin led to a stronger tumor reduction during the administration period than treatment with Cisplatin alone. In addition, a combination of U2-39 and Cisplatin delayed the time to progression of the median tumor size to 500 mm^3 compared to U2-39 monotherapy.

[000438]The result in Figure 43B shows that combination of U2-39 with Avastin significantly delayed the time to progression to 500 mm^3 tumor volumes compared to the treatment with Avastin as monotherapy although only half of the single agent dose was administered.

[000439]All patents and publications referenced or mentioned herein are indicative of the levels of skill of those skilled in the art to which the invention pertains, and each such referenced patent or publication is hereby incorporated by reference to the same extent as if it had been incorporated by reference in its entirety individually or set forth herein in its entirety. Applicants reserve the right to physically incorporate into this specification any and all materials and information from any such cited patents or publications.

[000440]The specific methods and compositions described herein are representative of preferred embodiments and are exemplary and not intended as limitations on the scope of the invention. Other objects, aspects, and embodiments will occur to those skilled in the art upon consideration of this specification, and are encompassed within the spirit of the invention as defined by the scope of the claims. It will be readily apparent to one skilled in the art that varying substitutions and modifications may be made to the invention disclosed herein without departing from the scope and spirit of the invention. The invention illustratively described herein suitably may be practiced in the absence of any element or elements, or limitation or limitations, which is not specifically disclosed herein as essential. The methods and processes illustratively described herein suitably may be practiced in differing orders of steps, and they are not

necessarily restricted to the orders of steps indicated herein or in the claims. As used herein and in the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, a reference to "an antibody" includes a plurality (for example, a solution of antibodies or a series of antibody preparations) of such antibodies, and so forth. Under no circumstances may the patent be interpreted to be limited to the specific examples or embodiments or methods specifically disclosed herein. Under no circumstances may the patent be interpreted to be limited by any statement made by any Examiner or any other official or employee of the Patent and Trademark Office unless such statement is specifically and without qualification or reservation expressly adopted in a responsive writing by Applicants.

[000441]The terms and expressions that have been employed are used as terms of description and not of limitation, and there is no intent in the use of such terms and expressions to exclude any equivalent of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention as claimed. Thus, it will be understood that although the present invention has been specifically disclosed by preferred embodiments and optional features, modification and variation of the concepts herein disclosed may be resorted to by those skilled in the art, and such modifications and variations are considered to be within the scope of this invention as defined by the appended claims.

[000442]The invention has been described broadly and generically herein. Each of the narrower species and subgeneric groupings falling within the generic disclosure also form part of the invention. This includes the generic description of the invention with a proviso or negative limitation removing any subject matter from the genus, regardless of whether or not the excised material is specifically recited herein.

Claims

1. An isolated antigen binding protein that binds HB-EGF, comprising:

A) one or more light chain complementary determining regions (CDRLs) selected from the group consisting of:

(i) a CDRL1 selected from the group consisting of SEQ ID NOs:189-217;

(ii) a CDRL2 selected from the group consisting of SEQ ID NOs:218-233;

(iii) a CDRL3 selected from the group consisting of SEQ ID NOs:234-274; and

(iv) a CDRL of (i), (ii) or (iii) that contains one or more amino acid substitutions, deletions or insertions of no more than four amino acids; or

B) one or more heavy chain complementary determining regions (CDRHs) selected from the group consisting of:

(i) a CDRH1 selected from the group consisting of SEQ ID NOs:275-299;

(ii) a CDRH2 selected from the group consisting of SEQ ID NOs:300-331;

(iii) a CDRH3 selected from the group consisting of SEQ ID NOs:332-372; and

(iv) a CDRH of (i), (ii) or (iii) that contains one or more amino acid substitutions, deletions or insertions of no more than four amino acids.

2. The isolated antigen binding protein of Claim 1, comprising one or more light chain CDRLs of A), and one or more heavy chain CDRHs of B).

3. The isolated antigen binding protein of Claim 1 that comprises at least two CDRLs of A) and at least two CDRHs of B).

4. The isolated antigen binding protein of Claim 1 that comprises said CDRH1, CDRH2, CDRH3, CDRL1, CDRL2 and CDRL3.

5. The isolated antigen binding protein of Claim 1, wherein

said CDRL of A) is selected from the group consisting of:

(i) a CDRL1 selected from the group consisting of SEQ ID NOs:189-217;

(ii) a CDRL2 selected from the group consisting of SEQ ID NOs:218-233;

(iii) a CDRL3 selected from the group consisting of SEQ ID NOs:234-274; and

(iv) a CDRL of (i), (ii) or (iii) that contains one or more amino acid substitutions, deletions or insertions of no more than two amino acids;

said CDRH of B) is selected from the group consisting of:

(i) a CDRH1 selected from the group consisting of SEQ ID NOs:275-299;

(ii) a CDRH2 selected from the group consisting of SEQ ID NOs:300-331;

(iii) a CDRH3 selected from the group consisting of SEQ ID NOs:332-372; and

(iv) a CDRH of (i), (ii) or (iii) that contains one or more amino acid substitutions, deletions or insertions of no more than two amino acids;

or

C) one or more light chain CDRLs of A) and one or more heavy chain CDRHs of B).

6. The isolated antigen binding protein of Claims 1, wherein said antigen binding protein comprises

A) a CDRL selected from the group consisting of

(i) a CDRL1 selected from the group consisting of SEQ ID NOs:189-217;

(ii) a CDRL2 selected from the group consisting of SEQ ID NOs:218-233; and

(iii) a CDRL3 selected from the group consisting of SEQ ID NOs:234-274;

B) a CDRH selected from the group consisting of

(i) a CDRH1 selected from the group consisting of SEQ ID NOs:275-299;

(ii) a CDRH2 selected from the group consisting of SEQ ID NOs:300-331;and

(iii) a CDRH3 selected from the group consisting of SEQ ID NOs:332-372;

or

C) one or more light chain CDRLs of A) and one or more heavy chain CDRHs of B).

7. The isolated antigen binding protein of Claims 6, wherein said antigen binding protein comprises

A) a CDRL1 of SEQ ID NOs:189-217, a CDRL2 of SEQ ID NOs:218-233, and a CDRL3 of SEQ ID NOs:234-274, and/or

B) a CDRH1 of SEQ ID NOs:275-299, a CDRH2 of SEQ ID NOs:300-331, and a CDRH3 of SEQ ID NOs:332-372.

8. The isolated antigen binding protein of Claim 1, wherein said antigen binding protein comprises a light chain variable region (V_L) having at least 80% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NOs:94-141, and/or a heavy chain variable region (V_H) having at least 80% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NOs:142-186.

9. The isolated antigen binding protein of Claim 8, wherein the V_L has at least 90% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NOs:94-141, and/or the V_H has at least 90% sequence identity with an amino acid sequence selected from the group consisting of SEQ ID NOs:142-186.

10. The isolated antigen binding protein of Claim 8, wherein the V_L is selected from the group consisting of SEQ ID NOs:94-141, and/or the V_H is selected from the group consisting of SEQ ID NOs:142-186.

11. An isolated antigen binding protein that specifically recognizes at least an IHGE-containing epitope and/or an EGF-like domain of HB-EGF.

12. An isolated antigen binding protein that competes for binding with the antigen binding protein of Claims 1.

13. An isolated antigen binding protein that binds HB-EGF, wherein said antigen binding protein comprises:

A) one or more light chain CDRs (CDRLs) selected from the group consisting of:

(i) a CDRL1 with at least 80% sequence identity to SEQ ID NOs:189-217;

(ii) a CDRL2 with at least 80% sequence identity to SEQ ID NOs:218-233; and

(iii) a CDRL3 with at least 80% sequence identity to SEQ ID NOs:234-274;

B) one or more heavy chain CDRs (CDRHs) selected from the group consisting of:

(i) a CDRH1 with at least 80% sequence identity to SEQ ID NOs:275-299;

(ii) a CDRH2 with at least 80% sequence identity to SEQ ID NOs:300-331; and

(iii) a CDRH3 with at least 80% sequence identity to SEQ ID NOs:332-372;

or

C) one or more light chain CDRLs of A) and one or more heavy chain CDRHs of B).

14. The isolated antigen binding protein of Claims 13, wherein said antigen binding protein comprises:

A) one or more CDRLs selected from the group consisting of:

(i) a CDRL1 with at least 90% sequence identity to SEQ ID NOs:189-217;

(ii) a CDRL2 with at least 90% sequence identity to SEQ ID NOs:218-233; and

(iii) a CDRL3 with at least 90% sequence identity to SEQ ID NOs:234-274;

B) one or more CDRHs selected from the group consisting of:

(i) a CDRH1 with at least 90% sequence identity to SEQ ID NOs:275-299;

(ii) a CDRH2 with at least 90% sequence identity to SEQ ID NOs:300-331; and

(iii) a CDRH3 with at least 90% sequence identity to SEQ ID NOs:332-372;

or

C) one or more light chain CDRLs of A) and one or more heavy chain CDRHs of B).

15. An isolated antigen binding protein that binds HB-EGF, the antigen binding protein comprising:

A) a light chain complementary determining region (CDRL) selected from the group consisting of

(i) a CDRL3 selected from the group consisting of SEQ ID NOs:234-274,

(ii) a CDRL3 that differs in amino acid sequence from the CDRL3 of (i) by an amino acid addition, deletion or substitution of not more than two amino acids; and

(iii) a CDRL3 amino acid sequence selected from the group consisting of

$X_1QX_2X_3X_4X_5PX_6X_7$ (SEQ ID NO:1046), wherein

X_1 is selected from the group consisting of I and M,

X_2 is selected from the group consisting of A, G and S,

X_3 is selected from the group consisting of I and T,

X_4 is selected from the group consisting of H and Q,

X_5 is selected from the group consisting of F, L and W,

$7X_6$ is selected from the group consisting of C, I, H, L and T,

X_7 is selected from the group consisting of S and T;

$QQX_1X_2X_3X_4X_5IT$ (SEQ ID NO:1047), wherein

X_1 is selected from the group consisting of I and S,

X_2 is selected from the group consisting of F and Y,

X_3 is selected from the group consisting of F, I, S and Y,

X_4 is selected from the group consisting of A, S and T,

X_5 is selected from the group consisting of P and S;

$X_1X_2X_3X_4X_5X_6X_7X_8T$ (SEQ ID NO:1048), wherein

X_1 is selected from the group consisting of L and Q,

X_2 is selected from the group consisting of K, N and Q,

X_3 is selected from the group consisting of A, H, S and Y,

X_4 is selected from the group consisting of H, N and Y,

X_5 is selected from the group consisting of N, S and T,

X_6 is selected from the group consisting of A, F, I, T, V and Y,

X_7 is selected from the group consisting of P and no amino acid,

X_8 is selected from the group consisting of F, L and P;

$QX_1X_2DX_3LPX_4X_5$ (SEQ ID NO:1049), wherein

X_1 is selected from the group consisting of H and Q,

X_2 is selected from the group consisting of C and Y,

X_3 is selected from the group consisting of D, I, N, S and Y,

X_4 is selected from the group consisting of F, I and L,

X_5 is selected from the group consisting of A, S and T;

$QQX_1X_2X_3X_4PX_5X_6X_7$ (SEQ ID NO:1050), wherein

X_1 is selected from the group consisting of H and Y,

X_2 is selected from the group consisting of G and N,

X_3 is selected from the group consisting of N and S,

X_4 is selected from the group consisting of S and W,

X_5 is selected from the group consisting of P and no amino acid,

X_6 is selected from the group consisting of R and W,

X_7 is selected from the group consisting of S and T; and

$X_1QYX_2X_3X_4X_5X_6X_7F$ (SEQ ID NO:1051), wherein

X_1 is selected from the group consisting of H and Q,

X_2 is selected from the group consisting of F and Y,

X_3 is selected from the group consisting of G, I and S,

X_4 is selected from the group consisting of F, I and T,

X_5 is selected from the group consisting of M, P, S and T,

X_6 is selected from the group consisting of F, L, R and W,

X_7 is selected from the group consisting of S and T; and/or

B) a heavy chain complementary determining region (CDRH) selected from the group consisting of

(i) a CDRH3 selected from the group consisting of SEQ ID NOs:332-372,

(ii) a CDRH3 that differs in amino acid sequence from the CDRH3 of (i) by an amino acid addition, deletion or substitution of not more than two amino acids; and

(iii) a CDRH3 amino acid sequence selected from the group consisting of

$X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}DX_{12}$ (SEQ ID NO:1065), wherein

X_1 is selected from the group consisting of E and S,

X_2 is selected from the group consisting of D, G and no amino acid,

X_3 is selected from the group consisting of D, N and no amino acid,

X_4 is selected from the group consisting of G and no amino acid,

X_5 is selected from the group consisting of G and no amino acid,

X_6 is selected from the group consisting of W, Y and no amino acid,

X_7 is selected from the group consisting of I, N and Y,

X_8 is selected from the group consisting of A and Y,

X_9 is selected from the group consisting of G, V and Y,

X_{10} is selected from the group consisting of A, F and G,

X_{11} is selected from the group consisting of F, L and M,

X_{12} is selected from the group consisting of V and Y;

$QX_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}YX_{12}X_{13}X_{14}DX_{15}$ (SEQ ID NO:1066), wherein

X_1 is selected from the group consisting of G and no amino acid,

X_2 is selected from the group consisting of K, L and Y,

X_3 is selected from the group consisting of A, G and S,

X_4 is selected from the group consisting of S, V and Y,

X_5 is selected from the group consisting of A and G,

X_6 is selected from the group consisting of G and no amino acid,

X_7 is selected from the group consisting of T and no amino acid,

X_8 is selected from the group consisting of S and no amino acid,

X_9 is selected from the group consisting of Y and no amino acid,

X_{10} is selected from the group consisting of W and Y,

X_{11} is selected from the group consisting of G, S and Y,

X_{12} is selected from the group consisting of F and Y,

X_{13} is selected from the group consisting of G and no amino acid,

X_{14} is selected from the group consisting of M and no amino acid,

X_{15} is selected from the group consisting of V and Y;

$X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}$ (SEQ ID NO:1067), wherein

X_1 is selected from the group consisting of D, G, L, S and no amino acid,

X_2 is selected from the group consisting of G, H, W, Y and no amino acid,

X_3 is selected from the group consisting of A, F, W, Y and no amino acid,

X_4 is selected from the group consisting of D, G, Q, T and no amino acid,

X_5 is selected from the group consisting of G, I, Q, S and no amino acid,

X_6 is selected from the group consisting of A, D, N, Q, S and no amino acid,

X_7 is selected from the group consisting of G, Y and no amino acid,

X_8 is selected from the group consisting of D, Y and no amino acid,

X_9 is selected from the group consisting of Y and no amino acid,

X_{10} is selected from the group consisting of A, E, N and Y,

X_{11} is selected from the group consisting of G, P, T, V and Y,

X_{12} is selected from the group consisting of F and I,

X_{13} is selected from the group consisting of D and Q,

X_{14} is selected from the group consisting of C, H, V and Y;

$X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}DX_{18}$ (SEQ ID NO:1068), wherein

X_1 is selected from the group consisting of E, D and no amino acid,

X_2 is selected from the group consisting of G, R and no amino acid,

X_3 is selected from the group consisting of I, V, Y and no amino acid,

X_4 is selected from the group consisting of A, G, L and N,

X_5 is selected from the group consisting of A, G, V and W,

X_6 is selected from the group consisting of A, N, R and T,

X_7 is selected from the group consisting of G, N, P and no amino acid,

X_8 is selected from the group consisting of G, T and no amino acid,

X_9 is selected from the group consisting of A and no amino acid,

X_{10} is selected from the group consisting of D, E and no amino acid,

X_{11} is selected from the group consisting of S, Y and no amino acid,

X_{12} is selected from the group consisting of G, Y and no amino acid,

X_{13} is selected from the group consisting of N, Y and no amino acid,

X_{14} is selected from the group consisting of Y and no amino acid,

X_{15} is selected from the group consisting of D, Y and no amino acid,

X_{16} is selected from the group consisting of A, G and no amino acid,

X_{17} is selected from the group consisting of F and M,

X_{18} is selected from the group consisting of I, V and Y;

$X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}X_{18}X_{19}X_{20}X_{21}X_{22}X_{23}$ (SEQ ID NO:1069), wherein

X_1 is selected from the group consisting of A, D, G, S and T,

X_2 is selected from the group consisting of A, E, G, L, N, R, Y and no amino acid,

X_3 is selected from the group consisting of A, G, L, N, R, T, Y and no amino acid,

X_4 is selected from the group consisting of D, G, R, S, V, Y and no amino acid,

X_5 is selected from the group consisting of A, G, I, S, V, Y and no amino acid,

X_6 is selected from the group consisting of F, G, L, R, V and no amino acid,

X_7 is selected from the group consisting of L, T, Y and no amino acid,

X_8 is selected from the group consisting of Y and no amino acid,

X_9 is selected from the group consisting of Y and no amino acid,

X_{10} is selected from the group consisting of D and no amino acid,

X_{11} is selected from the group consisting of S and no amino acid,

X_{12} is selected from the group consisting of S and no amino acid,

X_{13} is selected from the group consisting of G and no amino acid,

X_{14} is selected from the group consisting of D, L, M, S, Y and no amino acid,

X_{15} is selected from the group consisting of H, I, P, V, W and no amino acid,

X_{16} is selected from the group consisting of F, G, L, R, S, Y and no amino acid,

X_{17} is selected from the group consisting of D, F, V, W, Y and no amino acid,

X_{18} is selected from the group consisting of C, F, L, P, S and Y,

X_{19} is selected from the group consisting of D, F, G and Y,

X_{20} is selected from the group consisting of A, C, G, P, R, V and Y,

X_{21} is selected from the group consisting of F, L, M, S and no amino acid,

X_{22} is selected from the group consisting of A, D and no amino acid,

X_{23} is selected from the group consisting of I, L, V, Y and no amino acid;

$X_1YSSGWX_2X_3YGX_4X_5DX_6$ (SEQ ID NO:1070), wherein

X_1 is selected from the group consisting of M and V,

X_2 is selected from the group consisting of S and no amino acid,

X_3 is selected from the group consisting of F and no amino acid,

X_4 is selected from the group consisting of V and no amino acid,

X_5 is selected from the group consisting of F and M,

X_6 is selected from the group consisting of V and Y; and

$RX_1X_2X_3PFX_4Y$ (SEQ ID NO:1071), wherein

X_1 is selected from the group consisting of G, H, L, N and R,

X_2 is selected from the group consisting of E, T and W,

X_3 is selected from the group consisting of L, N, T and V,

X_4 is selected from the group consisting of D and E.

16. The isolated antigen binding protein of Claim 15, said antigen binding protein further comprising:

A) a CDRL selected from the group consisting of:

(i) a CDRL1 selected from the group consisting of SEQ ID NOs:189-217;

(ii) a CDRL1 that differs in amino acid sequence from the CDRL1 of (i) by an amino acid addition, deletion or substitution of not more than two amino acids;

(iii) a CDRL1 amino acid sequence selected from the group consisting of

$X_1SSQSLX_2X_3SDGX_4TYLX_5$ (SEQ ID NO:1035), wherein

X_1 is selected from the group consisting of K and R,

X_2 is selected from the group consisting of L and V,

X_3 is selected from the group consisting of H and Y,

X_4 is selected from the group consisting of K and N,

X_5 is selected from the group consisting of N, S and Y;

$RASQX_1ISX_2YLN$ (SEQ ID NO:1036), wherein

X_1 is selected from the group consisting of R, S and T,

X_2 is selected from the group consisting of R and S;

$RASQX_1IX_2X_3X_4LX_5$ (SEQ ID NO:1037), wherein

X_1 is selected from the group consisting of D, G, S and T,

X_2 is selected from the group consisting of A, R and S,

X_3 is selected from the group consisting of H, I, N, R, S and T,

X_4 is selected from the group consisting of D, W and Y,

X_5 is selected from the group consisting of A, G and N;

$QASQDIX_1X_2X_3LN$ (SEQ ID NO:1038), wherein

X_1 is selected from the group consisting of S and T,

X_2 is selected from the group consisting of D and N,

X_3 is selected from the group consisting of S and Y;

$RASQX_1VX_2X_3X_4X_5LA$ (SEQ ID NO:1039), wherein

X_1 is selected from the group consisting of S and T,

X_2 is selected from the group consisting of I and S,

X_3 is selected from the group consisting of R and S,

X_4 is selected from the group consisting of S, N and no amino acid,

X_5 is selected from the group consisting of Y and no amino acid; and

$KSSQX_1X_2LX_3X_4SNNKNYLX_5$ (SEQ ID NO:1040), wherein

X_1 is selected from the group consisting of N and S,

X_2 is selected from the group consisting of I and V,

X_3 is selected from the group consisting of D and Y,

X_4 is selected from the group consisting of N, R and S,

X_5 is selected from the group consisting of A and V;

(iv) a CDRL2 selected from the group consisting of SEQ ID NOs:218-233;

(v) a CDRL2 that differs in amino acid sequence from the CDRL2 of (iv) by an amino acid addition, deletion or substitution of not more than two amino acids; and

(vi) a CDRL2 amino acid sequence selected from the group consisting of

$X_1X_2SNX_3X_4S$ (SEQ ID NO:1041), wherein

X_1 is selected from the group consisting of E and K,

X_2 is selected from the group consisting of I and V,

X_3 is selected from the group consisting of R and W,

X_4 is selected from the group consisting of D and F;

$X_1X_2SX_3LQS$ (SEQ ID NO:1042), wherein

X_1 is selected from the group consisting of A and T,

X_2 is selected from the group consisting of A, E and V,

X_3 is selected from the group consisting of S and T;

X_1ASX_2LQS (SEQ ID NO:1043), wherein

X_1 is selected from the group consisting of A and V,

X_2 is selected from the group consisting of S and T;

$DASX_1LET$ (SEQ ID NO:1044), wherein

X_1 is selected from the group consisting of I and N;

GASSRAT (SEQ ID NO:223); and

$WASX_1RES$ (SEQ ID NO:1045), wherein

X_1 is selected from the group consisting of A and T; or

B) a CDRH selected from the group consisting of:

(i) a CDRH1 selected from the group consisting of SEQ ID NOs:275-299;

(ii) a CDRH1 that differs in amino acid sequence from the CDRH1 of (i) by an amino acid addition, deletion or substitution of not more than two amino acids;

(iii) a CDRH1 amino acid sequence selected from the group consisting of

$GYTX_1TX_2X_3X_4X_5X_6$ (SEQ ID NO:1052), wherein

X_1 is selected from the group consisting of F and L,

X_2 is selected from the group consisting of E, G and S,

X_3 is selected from the group consisting of H, L and Y,

X_4 is selected from the group consisting of G, S and Y,

X_5 is selected from the group consisting of I and M,

X_6 is selected from the group consisting of H and S;

$GYX_1FTSYWIG$ (SEQ ID NO:1053), wherein

X_1 is selected from the group consisting of R and S;

$GFTFX_1SX_2X_3MH$ (SEQ ID NO:1054), wherein

X_1 is selected from the group consisting of R and S,

X_2 is selected from the group consisting of H and Y,

X_3 is selected from the group consisting of D and G;

$GFX_1FSX_2YX_3MX_4$ (SEQ ID NO:1055), wherein

X_1 is selected from the group consisting of P and T,

X_2 is selected from the group consisting of A, R and S,

X_3 is selected from the group consisting of A and S,

X_4 is selected from the group consisting of N and S;

$GX_1SX_2SX_3X_4X_5X_6X_7WX_8$ (SEQ ID NO:1056), wherein

X_1 is selected from the group consisting of D and G,

X_2 is selected from the group consisting of F, I and V,

X_3 is selected from the group consisting of R, S and no amino acid,

X_4 is selected from the group consisting of G, Y and no amino acid,

X_5 is selected from the group consisting of D, G, S and no amino acid,

X_6 is selected from the group consisting of A, S and Y,

X_7 is selected from the group consisting of A and Y,

X_8 is selected from the group consisting of N and S;

GFSLSNARMGVS (SEQ ID NO:279); and

$GFSLX_1TGGVGVG$ (SEQ ID NO:1057), wherein

X_1 is selected from the group consisting of S and N;

(iv) a CDRH2 selected from the group consisting of SEQ ID NOs:300-331;

(v) a CDRH2 that differs in amino acid sequence from the CDRH2 of (iv) by an amino acid addition, deletion or substitution of not more than two amino acids; and

(vi) a CDRH2 amino acid sequence selected from the group consisting of

$X_1X_2X_3X_4X_5X_6GX_7TX_8X_9X_{10}QKX_{11}X_{12}$ (SEQ ID NO:1058), wherein

X_1 is selected from the group consisting of S and W,

X_2 is selected from the group consisting of F and I,

X_3 is selected from the group consisting of D, N and S,

X_4 is selected from the group consisting of A and P,

X_5 is selected from the group consisting of E, N and S,

X_6 is selected from the group consisting of D, N and S,

X_7 is selected from the group consisting of E, G and N,

X_8 is selected from the group consisting of I and N,

X_9 is selected from the group consisting of C, H and Y,

X_{10} is selected from the group consisting of A and T,

X_{11} is selected from the group consisting of F and L,

X_{12} is selected from the group consisting of D and G;

IIYPX_1DSDX_2RYSPSFQG (SEQ ID NO:1059), wherein

X_1 is selected from the group consisting of D and G,

X_2 is selected from the group consisting of A, I and T;

$X_1IX_2X_3DGSX_4X_5X_6YX_7DSVX_8G$ (SEQ ID NO:1060), wherein

X_1 is selected from the group consisting of F and V,

X_2 is selected from the group consisting of S and W,

X_3 is selected from the group consisting of D, S and Y,

X_4 is selected from the group consisting of I, N and T,

X_5 is selected from the group consisting of K and Q,

X_6 is selected from the group consisting of N, R and Y,

X_7 is selected from the group consisting of A, T and V,

X_8 is selected from the group consisting of K and R;

$X_1ISX_2SX_3X_4X_5X_6YYADSVKG$ (SEQ ID NO:1061), wherein

X_1 is selected from the group consisting of A, H and Y,

X_2 is selected from the group consisting of G, R and S,

X_3 is selected from the group consisting of G and S,

X_4 is selected from the group consisting of G, R and S,

X_5 is selected from the group consisting of S, T and Y,

X_6 is selected from the group consisting of I and T;

$X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}YX_{12}X_{13}SX_{14}KS$ (SEQ ID NO:1062), wherein

X_1 is selected from the group consisting of E, R and Y,

X_2 is selected from the group consisting of I and T,
X_3 is selected from the group consisting of H, N and Y,
X_4 is selected from the group consisting of C, H, S, T and Y,
X_5 is selected from the group consisting of S and R,
X_6 is selected from the group consisting of G and S,
X_7 is selected from the group consisting of G, K, S and T,
X_8 is selected from the group consisting of T and W,
X_9 is selected from the group consisting of N and Y,
X_{10} is selected from the group consisting of N and no amino acid,
X_{11} is selected from the group consisting of D and no amino acid,
X_{12} is selected from the group consisting of A and N,
X_{13} is selected from the group consisting of P and V,
X_{14} is selected from the group consisting of L and V;

X_1IFSNDEKSYSTSLKS (SEQ ID NO:1063), wherein

X_1 is selected from the group consisting of H and LI; and

LIYWNX_1X_2KRYSPSLX_3S (SEQ ID NO:1064), wherein

X_1 is selected from the group consisting of D and V,
X_2 is selected from the group consisting of D and E,
X_3 is selected from the group consisting of K and R.

17. The isolated antigen binding protein of Claim 16, wherein said antigen binding protein comprises said first amino acid sequence and said second amino acid sequence.

18. The isolated antigen binding protein of Claim 17, wherein said first amino acid sequence is covalently bonded to said second amino acid sequence.

19. The isolated antigen binding protein of Claim 17, wherein said first amino acid sequence comprises said CDRL3 of SEQ ID NOs:234-274, CDRL2 of SEQ ID NOs:218-233, and CDRL1 of SEQ ID NOs: 189-217, and said second amino acid sequence comprises said CDRH3 of SEQ ID NOs:332-372, CDRH2 of SEQ ID NOs:300-331, and CDRH1 of SEQ ID NOs:275-299.

20. The isolated antigen binding protein of any of Claim 1-19, wherein said antigen binding protein is a monoclonal antibody, a polyclonal antibody, a recombinant antibody, a human antibody, a humanized antibody, a chimeric antibody, a multispecific antibody, or an antibody fragment thereof.

21. The isolated antigen binding protein of Claim 20, wherein said antibody fragment is a Fab fragment, a Fab' fragment, a $F(ab')_2$ fragment, a Fv fragment, a diabody, or a single chain antibody molecule.

22. The isolated antigen binding protein of Claim 20, wherein said antigen binding protein is a human antibody.

23. The isolated antigen binding protein of Claim 20, wherein said antigen binding protein is a monoclonal antibody.

24. The isolated antigen binding protein of any of Claims 1-19 wherein said antigen binding protein is of the IgG1-, IgG2- IgG3- or IgG4-type.

25. The isolated antigen binding protein of Claim 24, wherein said antigen binding protein is of the IgG2- or IgG4-type.

26. The isolated antigen binding protein of any of Claims 1-19, wherein said antigen binding protein is coupled to a labeling group.

27. The isolate antigen binding protein of Claim 26, wherein the labeling group is a radioisotope, radionuclide, a fluorescent group, an enzymatic group, a chemiluminescent group, a biotinyl group, or a predetermined polypeptide group.

28. The isolated antigen binding protein of any of Claims 1-19, wherein said antigen binding protein is coupled to an effector group.

29. The isolated antigen binding protein of Claim 28, wherein said effector group is a radioisotope, a radionuclide, a toxin, a therapeutic group, or a chemotherapeutic group.

30. The isolated antigen binding protein of Claim 29, wherein said therapeutic group or chemotherapeutic group is calicheamicin, auristatin-PE, geldanamycin, maytanasine, or derivatives thereof.

31. An isolated antigen binding protein that competes for binding to human HB-EGF with an antigen binding protein of one of Claims 1-19.

32. The isolated antigen binding protein of Claim 31, wherein said antigen binding protein is a monoclonal antibody, a polyclonal antibody, a recombinant antibody, a human antibody, a humanized antibody, a chimeric antibody, a multispecific antibody, or an antibody fragment thereof.

33. The isolated antigen binding protein of Claim 32, wherein said antibody fragment is a Fab fragment, a Fab' fragment, a $F(ab')_2$ fragment, a Fv fragment, a diabody, or a single chain antibody molecule.

34. The isolated antigen binding protein of Claim 32, wherein said antigen binding protein is a human antibody.

35. The isolated antigen binding protein of Claim 32, wherein said antigen binding protein is a monoclonal antibody.

36. The isolated antigen binding protein of any of Claim 31, wherein said antigen binding protein is of the IgG1-, IgG2- IgG3- or IgG4-type.

37. The isolated antigen binding protein of Claim 36, wherein said antigen binding protein is of the IgG2- or the IgG4-type.

38. The isolated antigen binding protein of any of Claim 31, wherein said antigen binding protein is coupled to a labeling group.

39. The isolate antigen binding protein of Claim 38, wherein the labeling group is a radioisotope, radionuclide, a fluorescent group, an enzymatic group, a chemiluminescent group, a biotinyl group, or a predetermined polypeptide group.

40. The isolated antigen binding protein of Claim 31, wherein said antigen binding protein is coupled to an effector group.

41. The isolated antigen binding protein of Claim 40, wherein said effector group is a radioisotope, a radionuclide, a toxin, a therapeutic group, or a chemotherapeutic group.

42. The isolated antigen binding protein of Claim 41, wherein said therapeutic group or chemotherapeutic group is calicheamicin, auristatin-PE, geldanamycin, maytanasine, or derivatives thereof.

43. The isolated antigen binding protein of one of Claims 1-19, wherein said antigen binding protein reduces at least partially HB-EGF-mediated signal transduction..

44. A nucleic acid molecule encoding the antigen binding protein according to any one of Claims 1-19.

45. The nucleic acid molecule according to Claim 44, wherein said nucleic acid molecule is operably linked to a control sequence.

46. A vector comprising a nucleic acid molecule according to Claim 44.

47. A vector comprising a nucleic acid molecule according to Claim 45.

48. A host cell comprising the nucleic acid molecule according to Claim 45.

49. A host cell comprising the vector according to one of Claim 46 or 47.

50. A method of making the antigen binding protein according to any one of Claims 1-19, comprising the step of preparing said antigen binding protein from a host cell that secretes said antigen binding protein.

51. A pharmaceutical composition comprising at least one antigen binding protein according to any one of Claims 1-19, and pharmaceutically acceptable carrier, diluents and/or adjuvants.

52. The pharmaceutical composition of Claim 51, further comprises an additional active agent.

53. The pharmaceutical composition according to Claim 52, wherein the at least one further active agent is an anti-neoplastic agent.

54. The pharmaceutical composition of Claim 53, wherein the anti-neoplastic agent is an anti-tumor antibody.

55. The pharmaceutical composition of Claim 54, wherein the anti-tumor antibody is an antibody directed against a receptor tyrosine kinase.

56. The pharmaceutical composition of Claim 53, wherein the anti-tumor antibody is directed against EGFR.

57. The pharmaceutical composition of Claim 51, for the diagnosis, prevention or treatment of a hyperproliferative disease.

58. The pharmaceutical composition to Claim 57, wherein said hyperproliferative disease is associated with HB-EGF expression.

59. The pharmaceutical composition according to Claim 57, wherein said hyperproliferative disease is associated with or accompanied by a disturbed, *e.g.*, pathologically enhanced growth factor receptor activation.

60. The pharmaceutical composition of Claim 59, wherein said pathologically enhanced growth factor receptor activation is associated with or caused by a pathological increase in the activity of a G protein and/or a G protein coupled receptor.

61. The pharmaceutical composition of Claim 51 for the diagnosis, prevention or treatment of cancer.

62. The pharmaceutical composition Claim 61, wherein said cancer is selected from the group consisting of breast cancer, gastrointestinal cancer, pancreas cancer, prostate cancer, ovarian cancer, stomach cancer, endometrial cancer, salivary gland cancer, lung cancer, kidney cancer, colon cancer, colorectal cancer, thyroid cancer, bladder cancer, glioma, melanoma, carcinoma, in particular epithelial or squamous carcinoma, other HB-EGF expressing or overexpressing cancers, and formation of tumor metastases.

63. Use of at least one antigen binding protein of Claims 1-19, for the manufacture of a pharmaceutical composition for the diagnosis, prevention or treatment of a hyperproliferative disease.

64. The use according to Claim 63, wherein said hyperproliferative disease is a hyperproliferative disease as defined in Claim 58.

65. A method for diagnosing a condition associated with the expression of HB-EGF, comprising contacting a sample with an antigen binding protein of Claims 1-19, and determining the presence of HB-EGF in said sample.

66. The method according to Claim 65, wherein the condition is a hyperproliferative disease as defined in Claim 58.

67. A method for preventing or treating a condition associated with the expression of HB-EGF in a patient, comprising administering to a patient in need thereof an effective amount of at least one antigen binding protein of Claims 1-19.

68. The method according to Claim 62, wherein the condition is a hyperproliferative disease as defined in any one of Claims 57-60.

69. The method of Claim 57, wherein the patient is a mammalian patient.

70. A kit comprising a antigen binding protein of Claims 1-19, a nucleic acid molecule of Claim 44 or 45 or a vector according to Claim 46 or 47.

71. The kit of Claim 70 comprising at least one further active agent.

72. The kit of Claim 71, wherein the further active agent is an anti-neoplastic agent.

73. The pharmaceutical composition according to claim 53, wherein the the anti-neoplastic agent id Cisplatin or Avastin.

74. The pharmaceutical composition according to any of the claims 51 to 62 which is to be administered as a monotherapy or in combination with a further pharmaceutical composition preferably comprising an anti-neoplastic agent such as cisplatin or Avastin.

U-V_L-1 light-chain variable region amino acid sequence (SEQ ID NO:94)

DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWFQQRPGQSPRRLIYKVSNWDSGVPDRFNGSGSGTDFTLKISRVEAEDVG
CDR1 CDR2

VYYCMQSTHWPITFGQGTRLEIK
CDR3

U-V_L-2 light-chain variable region amino acid sequence (SEQ ID NO:95)

DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWFQQRPGQSPRRLIYKVSNWDSGVPDRFSGSGSGTDFTLKISRVEAEDVG
CDR1 CDR2

VYYCIQGTHWPTTFGQGTRLEIK
CDR3

U-V_L-3 light-chain variable region amino acid sequence (SEQ ID NO:96)

DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWLQQRPGQSPRRLIYKVSNWDSGVPDRFSGSGSGTDFTLKISRVEAEDVG
CDR1 CDR2

VYYCMQGTHWPITFGQGTRLEIK
CDR3

U-V_L-4 light-chain variable region amino acid sequence (SEQ ID NO:96)

DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWLQQRPGQSPRRLIYKVSNWDSGVPDRFSGSGSGTDFTLKISRVEAEDVG
CDR1 CDR2

VYYCMQGTHWPITFGQGTRLEIK
CDR3

FIGURE 1A

U-V_L-5 light-chain variable region amino acid sequence (SEQ ID NO:97)

DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWYLQKPGQPPQLLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVG
CDR1 CDR2

VYYCMQGIQLPCSFGQGTKLEIK
CDR3

U-V_L-6 light-chain variable region amino acid sequence (SEQ ID NO:98)

DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWYLQKPGQPPQLLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVG
CDR1 CDR2

VYYCMQSIQLPLTFGGGTKVEIK
CDR3

U-V_L-7 light-chain variable region amino acid sequence (SEQ ID NO:98)

DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWYLQKPGQPPQLLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVG
CDR1 CDR2

VYYCMQSIQLPLTFGGGTKVEIK
CDR3

U-V_L-8 light-chain variable region amino acid sequence (SEQ ID NO:99)

DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWFLQKPGQPPQPLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVG
CDR1 CDR2

VYYCMQSIQLPITFGHGTRLEIK
CDR3

FIGURE 1B

U-V_L-9 light-chain variable region amino acid sequence (SEQ ID NO:99)

DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWFLQKPGQPPQPLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVG
CDR1 CDR2

VYYCMQSIQLPITFGHGTRLEIK
CDR3

U-V_L-11 light-chain variable region amino acid sequence (SEQ ID NO:100)

DIQMTQSPSSLSASVGDRVTITCRASQGIANYLAWYQQKPGKVPKLLIYVASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQ
CDR1 CDR2

NYNSAPFTFGPGTKVDIK
CDR3

U-V_L-12 light-chain variable region amino acid sequence (SEQ ID NO:101)

DIQMTQSPSSLSASVGDRVTIICRASQGISNDLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQ
CDR1 CDR2

KYNSVPLTFGGGTKVEIK
CDR3

U-V_L-13 light-chain variable region amino acid sequence (SEQ ID NO:102)

NIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYKISNRFSGVPDRFSGSGAGTDFTLKISRVEAEDVG
CDR1 CDR2

VYYCMQATQFPHTFGPGTKVDIK
CDR3

FIGURE 1C

U-V_L-14 light-chain variable region amino acid sequence (SEQ ID NO:102)

NIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYKISNRFSGVPDRFSGSGAGTDFTLKISRVEAEDVG
CDR1 CDR2

VYYCMQATQFPHTFGPGTKVDIK
CDR3

U-V_L-15 light-chain variable region amino acid sequence (SEQ ID NO:103)

EIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYKISNRFSGVPDRFSGTGAGTDFTLKISRVEAEDVG
CDR1 CDR2

VYYCMQATQFPHTFGGGTKVEIK
CDR3

U-V_L-16 light-chain variable region amino acid sequence (SEQ ID NO:104)

EIVLTQSPGTLSLSPGERATLSCRASQTVISSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC
CDR1 CDR2

QQYGSSPRTFGQGTKVEIK
CDR3

U-V_L-17 light-chain variable region amino acid sequence (SEQ ID NO:105)

EIVLTQSPGTLSLSPGERATLSCRASQSVSRLAWYQQKPGQAPRLLIYGASRRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQ
CDR1 CDR2

YGSSPRSFGQGTKLEIK
CDR3

FIGURE 1D

U-V_L-18 light-chain variable region amino acid sequence (SEQ ID NO:106)

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCL
CDR1 CDR2

QHNSYPPTFGQGTKVEIK
CDR3

U-V_L-19 light-chain variable region amino acid sequence (SEQ ID NO:107)

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLVWYQQKPGQPPKLFIYWASTRESGVPDRFTGSGSGTDFTLTISSLQAEDV
CDR1 CDR2

AVYYCQQYYSFPWTFGQGTKVEIK
CDR3

U-V_L-20 light-chain variable region amino acid sequence (SEQ ID NO:107)

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLVWYQQKPGQPPKLFIYWASTRESGVPDRFTGSGSGTDFTLTISSLQAEDV
CDR1 CDR2

AVYYCQQYYSFPWTFGQGTKVEIK
CDR3

U-V_L-21 light-chain variable region amino acid sequence (SEQ ID NO:108)

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDV
CDR1 CDR2

AVYYCQQYYSTTWTFGQGTKVEIK
CDR3

FIGURE 1E

U-V_L-22 light-chain variable region amino acid sequence (SEQ ID NO:109)

DIVMTQSPDSLAVSLGERATINCKSSQNVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDV
CDR1 CDR2

AVYFCQQYYGTPRTFGQGTKVEIK
CDR3

U-V_L-23 light-chain variable region amino acid sequence (SEQ ID NO:110)

DIVMTQSPDSLAVSLGERATINCKSSQNVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDV
CDR1 CDR2

AVYFCQQYYGTPRTFGQGTKVEIK
CDR3

U-V_L-24 light-chain variable region amino acid sequence (SEQ ID NO:111)

DIVMTQSPDSLTVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFGGSGSGTDFTLTISSLQAEDV
CDR1 CDR2

AVYYCQQYYSISRTFGQGTKVEIK
CDR3

U-V_L-25 light-chain variable region amino acid sequence (SEQ ID NO:111)

DIVMTQSPDSLTVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFGGSGSGTDFTLTISSLQAEDV
CDR1 CDR2

AVYYCQQYYSISRTFGQGTKVEIK
CDR3

FIGURE 1F

U-V_L-26 light-chain variable region amino acid sequence (SEQ ID NO:112)

DIVMTQSPDSLAVSLGERATINCKSSQSVLYNSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQADDV
CDR1 CDR2

AVYYCQQYYSTTWTFGPGTKVEIK
CDR3

U-V_L-27 light-chain variable region amino acid sequence (SEQ ID NO:113)

DIVMTQSPDSLAVSLGERATINCKSSQSVLYNSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQADDV
CDR1 CDR2

AVYYCQQYYSTTWTFGPGTKVEIK
CDR3

U-V_L-28 light-chain variable region amino acid sequence (SEQ ID NO:114)

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKVLIYWASTRKSGVPDRFSGSGSGTDFTLTISGLQAEDV
CDR1 CDR2

ALYYCQQYYSTMFSFGQGTKLEIK
CDR3

U-V_L-29 light-chain variable region amino acid sequence (SEQ ID NO:114)

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKVLIYWASTRKSGVPDRFSGSGSGTDFTLTISGLQAEDV
CDR1 CDR2

ALYYCQQYYSTMFSFGQGTKLEIK
CDR3

FIGURE 1G

U-V_L-30 light-chain variable region amino acid sequence (SEQ ID NO:115)

DIVMTQSPDSLAVSLGERATINCKSSQSVLDSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDV
CDR1 CDR2

AVFYCHQYYSTPLTFGGGTKVAIK
CDR3

U-V_L-31 light-chain variable region amino acid sequence (SEQ ID NO:115)

DIVMTQSPDSLAVSLGERATINCKSSQSVLDSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDV
CDR1 CDR2

AVFYCHQYYSTPLTFGGGTKVAIK
CDR3

U-V_L-32 light-chain variable region amino acid sequence (SEQ ID NO:116)

DIVMTQSPDSLAVSLGERATINCKSSQSILYRSNNKNYLAWYQQKPGQPPKLLIYWASARESGVPDRFSGSGSGTDFTLTISSLQAEDV
CDR1 CDR2

AVYFCQQYFITPLTFGGGTKVEIK
CDR3

U-V_L-33 light-chain variable region amino acid sequence (SEQ ID NO:116)

DIVMTQSPDSLAVSLGERATINCKSSQSILYRSNNKNYLAWYQQKPGQPPKLLIYWASARESGVPDRFSGSGSGTDFTLTISSLQAEDV
CDR1 CDR2

AVYFCQQYFITPLTFGGGTKVEIK
CDR3

FIGURE 1H

U-V_L-34 light-chain variable region amino acid sequence (SEQ ID NO:117)

DIQMTQSPSSLSASVGDRVTITCRASQDISHYLAWFQQKPGKAPKSLIYAASSLQSGVPSKFSGSGSGTDFTLTISSLQPEDFATYYCQ
CDR1 CDR2

QYNNYPFTFGPGTKVDIK
CDR3

U-V_L-35 light-chain variable region amino acid sequence (SEQ ID NO:118)

DIQMTQSPSSLSASVGDRVAITCRASQDISNYLAWLQQKPGKAPKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ
CDR1 CDR2

QYNTYPFTFGPGTKMDIK
CDR3

U-V_L-36 light-chain variable region amino acid sequence (SEQ ID NO:119)

EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQDPGQAPRLLIYGASRRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQ
CDR1 CDR2

QHNNWPPWTFGQGTKVEIK
CDR3

U-V_L-37 light-chain variable region amino acid sequence (SEQ ID NO:119)

EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQDPGQAPRLLIYGASRRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQ
CDR1 CDR2

QHNNWPPWTFGQGTKVEIK
CDR3

FIGURE 1I

U-V_L-38 light-chain variable region amino acid sequence (SEQ ID NO:120)

DIQMTQSPSSVSASVGDRVTITCRASQDISRWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ
CDR1 CDR2

QANSFPPTFGQGTKVEFK
CDR3

U-V_L-39 light-chain variable region amino acid sequence (SEQ ID NO:121)

DIQMTQSPSSLSASVGDRVTITCRASQSISTYLNWYQQKPGKAPKFLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFAAYYCQ
CDR1 CDR2

QSHSAPFTFGPGTKVDIK
CDR3

U-V_L-40 light-chain variable region amino acid sequence (SEQ ID NO:122)

DIQMTQSPSSLSASLGDRVTITCRASQTISIYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ
CDR1 CDR2

QSYSTLTFGGGTKVEIK
CDR3

U-V_L-41 light-chain variable region amino acid sequence (SEQ ID NO:123)

DIQMTQSPSSLSASVGDRVTITCRASQSIRSYLNWYQQRPGNAPKLLIYAASSLQSGVPSRVSGSGSGTDFTLTIRSLQPEDFATYYCQ
CDR1 CDR2

QSYSIPLTFGGGTKVEIK
CDR3

FIGURE 1J

U-V_L-42 light-chain variable region amino acid sequence (SEQ ID NO:124)

DIQMTQSPSSRSASVGDRVTITCRASQTISRYLNWYQQKPGKAPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTLSSLQPEDFATYYCQ
CDR1 CDR2

QIYSTSITFGQGTRLEIK
CDR3

U-V_L-43 light-chain variable region amino acid sequence (SEQ ID NO:125)

DIQMTQSPSSLSASVGDRVTITCRASQRISSYLNWYQQKPGKAPKVLIYAESSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ
CDR1 CDR2

QSYITPITFGQGTRLEII
CDR3

U-V_L-44 light-chain variable region amino acid sequence (SEQ ID NO:126)

DIQMTQSPSSLSASVGDRVTITCRASQSISRYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTISSLQPENFATYYCQ
CDR1 CDR2

QSYFTPITFGQGTRLEIK
CDR3

U-V_L-45 light-chain variable region amino acid sequence (SEQ ID NO:127)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTFSSLQPEDFATYYCQ
CDR1 CDR2

QSYFSPITFGQGTRLEIK
CDR3

FIGURE 1K

U-V_L-46 light-chain variable region amino acid sequence (SEQ ID NO:128)

```
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTLSSLQPEDFASYYCQ
                        CDR1                    CDR2

QSFYTPITFGQGTRLEIK
 CDR3
```

U-V_L-47 light-chain variable region amino acid sequence (SEQ ID NO:128)

```
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTLSSLQPEDFASYYCQ
                        CDR1                    CDR2

QSFYTPITFGQGTRLEIK
 CDR3
```

U-V_L-48 light-chain variable region amino acid sequence (SEQ ID NO:129)

```
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTVSSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ
                        CDR1                    CDR2

QSYFTPITFGQGTRLEIK
 CDR3
```

U-V_L-49 light-chain variable region amino acid sequence (SEQ ID NO:129)

```
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTVSSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ
                        CDR1                    CDR2

QSYFTPITFGQGTRLEIK
 CDR3
```

FIGURE 1L

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U-V_L-50 light-chain variable region amino acid sequence (SEQ ID NO:129)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTVSSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ
CDR1 CDR2

QSYFTPITFGQGTRLEIK
CDR3

U-V_L-51 light-chain variable region amino acid sequence (SEQ ID NO:130)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFASYYCQ
CDR1 CDR2

QSFYAPITFGQGTRLEIK
CDR3

U-V_L-52 light-chain variable region amino acid sequence (SEQ ID NO:130)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFASYYCQ
CDR1 CDR2

QSFYAPITFGQGTRLEIK
CDR3

U-V_L-53 light-chain variable region amino acid sequence (SEQ ID NO:131)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ
CDR1 CDR2

QSYFTPITFGQGTRLEIK
CDR3

FIGURE 1M

U-V_L-54 light-chain variable region amino acid sequence (SEQ ID NO:132)

DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQ
CDR1 CDR2

QYDYLPFTFGPGTKVDIK
CDR3

U-V_L-55 light-chain variable region amino acid sequence (SEQ ID NO:132)

DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQ
CDR1 CDR2

QYDYLPFTFGPGTKVDIK
CDR3

U-V_L-56 light-chain variable region amino acid sequence (SEQ ID NO:133)

DIQMTQSPSSLSASVGDRVTITCQASQDISNSLNWYQQKPGKAPELLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQ
CDR1 CDR2

QCDDLPLTFGGGTKVEIK
CDR3

U-V_L-57 light-chain variable region amino acid sequence (SEQ ID NO:134)

DIQMTQSPSSLSASVGDRVTITCQASQDISDYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQ
CDR1 CDR2

HYDNLPLTFGGGTKVEIK
CDR3

FIGURE 1N

U-V_L-58 light-chain variable region amino acid sequence (SEQ ID NO:135)

DIQMTQSPSSLSASVGDRVAITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQ
CDR1 CDR2

QYDNLPLTFGGGTKVEIK
CDR3

U-V_L-59 light-chain variable region amino acid sequence (SEQ ID NO:135)

DIQMTQSPSSLSASVGDRVAITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQ
CDR1 CDR2

QYDNLPLTFGGGTKVEIK
CDR3

U-V_L-60 light-chain variable region amino acid sequence (SEQ ID NO:136)

DIQMTQSPSSLSASVGDRVTITCQASQDISNSLNWYQQKPGKAPKLLIYDASILETGVPSRFSGSGSETDFTFTISSLQPEDIATYYCQ
CDR1 CDR2

QCDILPLSFGGGTKVEIK
CDR3

U-V_L-61 light-chain variable region amino acid sequence (SEQ ID NO:137)

DIQMTQSPSSLSASVGDRVTITCQASQDISNSLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQ
CDR1 CDR2

QYDNLPLAFGGGTKVEIR
CDR3

FIGURE 1O

U-V_L-62 light-chain variable region amino acid sequence (SEQ ID NO:138)

DIQMTQSPSSLSASVGDGVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQ
CDR1 CDR2

QYDSLPITFGQGTRLEIK
CDR3

U-V_L-63 light-chain variable region amino acid sequence (SEQ ID NO:139)

DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKLGKAPKLLIHDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQ
CDR1 CDR2

QYDNLPITFGQGTRLEIK
CDR3

U-V_L-64 light-chain variable region amino acid sequence (SEQ ID NO:140)

DIQMTQSPSSLSASVGDRVTITCQASQDISDYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQ
CDR1 CDR2

HYDNLPITFGQGTRLEIK
CDR3

U-V_L-65 light-chain variable region amino acid sequence (SEQ ID NO:141)

DIQMTQSPSSLSASVGDRVTITCQASQDISNSLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQ
CDR1 CDR2

HYDNLPITFGQGTRLEIK
CDR3

FIGURE 1P

U-V_H-1 heavy chain variable region amino acid sequence (SEQ ID NO:142)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISASNGNTNYAQKLQDRVTMTTDTSTSTAYMELRSLRSD
CDR1 CDR2

DTAVYYCAREDNWNYGFFDYWGQGTLVTVSS
CDR3

U-V_H-2 heavy chain variable region amino acid sequence (SEQ ID NO:142)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISASNGNTNYAQKLQDRVTMTTDTSTSTAYMELRSLRSD
CDR1 CDR2

DTAVYYCAREDNWNYGFFDYWGQGTLVTVSS
CDR3

U-V_H-3 heavy chain variable region amino acid sequence (SEQ ID NO:143)

QVHLVQSGAEVKKPGASVKVSCKVSGYTFTGHYMHWVRQAPGQGLEWMGWINPNSGGTNCAQKFQGRVTMTRDTSISTAYMELSRLRSD
CDR1 CDR2

DTAVYYCARSIAVALDYWGQGTLVTVSS
CDR3

U-V_H-4 heavy chain variable region amino acid sequence (SEQ ID NO:144)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNHTQKFQGRVTMTRDTSISTAYMELSRLRSD
CDR1 CDR2

DTAVYYCARSIAVALDYWGQGTLVTVSS
CDR3

FIGURE 2A

U-V_H-5 heavy chain variable region amino acid sequence (SEQ ID NO:145)

QVQLVQSGAEVRKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGSFDPEDGETIYAQKFQGRVTMLEDTSTDTAYMELSSLRSE
CDR1 CDR2

DTAVYYCATEGDGGYYYYGMDVWGQGTTVTVSS
CDR3

U-V_H-6 heavy chain variable region amino acid sequence (SEQ ID NO:145)

QVQLVQSGAEVRKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGSFDPEDGETIYAQKFQGRVTMLEDTSTDTAYMELSSLRSE
CDR1 CDR2

DTAVYYCATEGDGGYYYYGMDVWGQGTTVTVSS
CDR3

U-V_H-7 heavy chain variable region amino acid sequence (SEQ ID NO:146)

QVTLKESGPVLVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQVVLTMTNMDP
CDR1 CDR2

VDTATYYCARMYSSGWYGVFDYWGQGTLVTVSS
CDR3

U-V_H-8 heavy chain variable region amino acid sequence (SEQ ID NO:147)

QVTLKESGPVLVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKALEWLVLIFSNDEKSYSTSLKSRLTISKDTSKSQVVLTMTNMDP
CDR1 CDR2

VDTATYYCARVYSSGWSFYGMDVWGQGTTVTVSS
CDR3

FIGURE 2B

U-V_H-9 heavy chain variable region amino acid sequence (SEQ ID NO:148)

QITLKESGPTLVKPTQTLTLTCTFSGFSLSTGGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSRLTITKDTSKNQVVLTMTNMDP
CDR1 CDR2

VDTATYYCAHRRELPFDYWGQGTLVTVSS
CDR3

U-V_H-10 heavy chain variable region amino acid sequence (SEQ ID NO:149)

QITLKESGPTLVKPTQTLTLTCTFSGFSLSTGGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSRLTITKDTSKTQVVLTVTDMDP
CDR1 CDR2

VDTATYYCAHRNWTPFDYWGQGTLVTVSS
CDR3

U-V_H-11 heavy chain variable region amino acid sequence (SEQ ID NO:150)

QITLKESGPTLVKPTQTLTLTCTFSGFSLNTGGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSRLTITKDTSKNQVVLTMTNMDP
CDR1 CDR2

VDTATYYCAHRLELPFDYWGQGTLVTVSS
CDR3

U-V_H-12 heavy chain variable region amino acid sequence (SEQ ID NO:151)

QITLKESGPTLVKPTQTLTLTCTFSGFSLSTGGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSRLTITKDTSKNQVVLTMTNLDP
CDR1 CDR2

VDTATYYCAHRREVPFDYWGQGTLVTVSS
CDR3

FIGURE 2C

U-V_H-13 heavy chain variable region amino acid sequence (SEQ ID NO:152)

QITLKESGPTLVKPTQTLTLTCTFSGFSLSTGGVGVGWIRQPPGKALEWLALIYWNVEKRYSPSLRSRLTITKATSKNQVVLTMTNMDP
CDR1 CDR2

VDTATYYCAHRHTNPFEYWGQGTLVTVSS
CDR3

U-V_H-14 heavy chain variable region amino acid sequence (SEQ ID NO:153)

QITLKESGPTLVKPTQTLTLTCTFSGFSLSTGGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSRLTITKDTSKNQVVLTMTNMDP
CDR1 CDR2

VDTATYYCAHRGELPFDYWGQGTLVTVSS
CDR3

U-V_H-15 heavy chain variable region amino acid sequence (SEQ ID NO:153)

QITLKESGPTLVKPTQTLTLTCTFSGFSLSTGGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSRLTITKDTSKNQVVLTMTNMDP
CDR1 CDR2

VDTATYYCAHRGELPFDYWGQGTLVTVSS
CDR3

U-V_H-16 heavy chain variable region amino acid sequence (SEQ ID NO:154)

EVQLVESGGGLVKPGGSLRLSCAASGFPFSRYSMNWVRQAPGKGLEWVSAISSSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRAE
CDR1 CDR2

DTAVYYCARDRVGATPDAFDIWGQGTMVTVSS
CDR3

FIGURE 2D

U-V_H-17 heavy chain variable region amino acid sequence (SEQ ID NO:155)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAE
CDR1 CDR2

DTAVYYCAKEGIAVAGTAEYYYYYAMDVWGQGTTVTVSS
CDR3

U-V_H-18 heavy chain variable region amino acid sequence (SEQ ID NO:156)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAE
CDR1 CDR2

DTAVYYCAKEGIAARDSYYYYAMDVWGQGTTVTVSS
CDR3

U-V_H-19 heavy chain variable region amino acid sequence (SEQ ID NO:157)

EVQLLESGGGLVQPGGSLRLSCTASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAE
CDR1 CDR2

DTAEYYCAKEGIAGRDSYYYYGMDVWGQGTTVTVSS
CDR3

U-V_H-20 heavy chain variable region amino acid sequence (SEQ ID NO:157)

EVQLLESGGGLVQPGGSLRLSCTASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAE
CDR1 CDR2

DTAEYYCAKEGIAGRDSYYYYGMDVWGQGTTVTVSS
CDR3

FIGURE 2E

U-V_H-21 heavy chain variable region amino acid sequence (SEQ ID NO:158)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFISDDGSTKYYADSVKGRFTISRDNSMNTLYLQMNSLRAE
CDR1 CDR2

DTAVYYCARSYYDSSGYYYGFDYWGQGTLVTVSS
CDR3

U-V_H-22 heavy chain variable region amino acid sequence (SEQ ID NO:158)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFISDDGSTKYYADSVKGRFTISRDNSMNTLYLQMNSLRAE
CDR1 CDR2

DTAVYYCARSYYDSSGYYYGFDYWGQGTLVTVSS
CDR3

U-V_H-23 heavy chain variable region amino acid sequence (SEQ ID NO:159)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAE
CDR1 CDR2

DTAVYYCARNVIDYWGQGTLVTVSS
CDR3

U-V_H-24 heavy chain variable region amino acid sequence (SEQ ID NO:160)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVIWYDGSIKYYADSVKGRFTISRDNSKNTLYLQMNSLRAE
CDR1 CDR2

DTAVYYCARGGATGAEYFQHWGQGTLVTVSS
CDR3

FIGURE 2F

U-V_H-25 heavy chain variable region amino acid sequence (SEQ ID NO:160)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVIWYDGSIKYYADSVKGRFTISRDNSKNTLYLQMNSLRAE
CDR1 CDR2

DTAVYYCARGGATGAEYFQHWGQGTLVTVSS
CDR3

U-V_H-26 heavy chain variable region amino acid sequence (SEQ ID NO:161)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAE
CDR1 CDR2

DTAVYYCVLLWFGETFDYWGQGSLVTVSP
CDR3

U-V_H-27 heavy chain variable region amino acid sequence (SEQ ID NO:162)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWSDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAE
CDR1 CDR2

DTAVYYCARNLPFDYWGQGTLVTVSS
CDR3

U-V_H-28 heavy chain variable region amino acid sequence (SEQ ID NO:163)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWDDGSNQYYTDSVKGRFTVSRDNSKNTLFLQMNSLRAE
CDR1 CDR2

DTAVYYCARSHYGGDYDYYGMDVWGQGTTVTVSS
CDR3

FIGURE 2G

U-V_H-29 heavy chain variable region amino acid sequence (SEQ ID NO:164)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKRYVDSVKGRFTISRDNSKNTLYLQMNSLRAE
CDR1 CDR2

DTAVYYCARDGWQQQAPFDYWGQGTLVTVSS
CDR3

U-V_H-30 heavy chain variable region amino acid sequence (SEQ ID NO:165)

QVQLVESGGGVVQPGRSLRLSCAASGFTFRSHGMHWVRQAPGKGLEWVAVIWYDGSNKNYADSVRGRFTISRDNSKNTLDLQMNSLRAE
CDR1 CDR2

DTAVYYCARWGISAPFDCWGQGTLVTVSS
CDR3

U-V_H-31 heavy chain variable region amino acid sequence (SEQ ID NO:166)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYSMNWVRQAPGKGLEWVSYISSSGRTIYYADSVKGRFTISRDNAKNSLFLQMNSLRDE
CDR1 CDR2

DTAVYYCALWAPFDYWGQGTLVTVSS
CDR3

U-V_H-32 heavy chain variable region amino acid sequence (SEQ ID NO:167)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSHISSSSRTIYYADSVKGRFTISRDNAKNSVYLQMNSLRDE
CDR1 CDR2

DTAVYYCARDGYNWNGGGNYYGMDVWGQGTTVTVSS
CDR3

FIGURE 2H

U-V_H-33 heavy chain variable region amino acid sequence (SEQ ID NO:168)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSHISRSSRTIYYADSVKGRFTISRDNAKNSLYLQMNSLRDE
CDR1 CDR2

DTAVYYCARDGYNWNNGGYYYGMDVWGQGTTVTVSS
CDR3

U-V_H-34 heavy chain variable region amino acid sequence (SEQ ID NO:168)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSHISRSSRTIYYADSVKGRFTISRDNAKNSLYLQMNSLRDE
CDR1 CDR2

DTAVYYCARDGYNWNNGGYYYGMDVWGQGTTVTVSS
CDR3

U-V_H-35 heavy chain variable region amino acid sequence (SEQ ID NO:169)

QVQLQESGPGLVKPSQTLSLTCTVSGGSVSSGGYYWSWIRQHPGKGLEWIGYIHSSGSTYYNPSLKSRVTISVDTSKNQFSLNLSSVTA
CDR1 CDR2

ADTAVYYCARGPYYGMDVWGQGTTVTVSS
CDR3

U-V_H-36 heavy chain variable region amino acid sequence (SEQ ID NO:170)

QVQLQESGPGLVKPSQTLSLTCTVSGGSISRGGYYWSWIRQHPGKGLEWIGYIYHSGSTYYNPSLKSRVNMSVDTSKNQFSLKLSSVTA
CDR1 CDR2

ADTAVYYCARALRGIVLMVYVLGALDIWGQGTKVTVSS
CDR3

FIGURE 2I

U-V_H-37 heavy chain variable region amino acid sequence (SEQ ID NO:170)

QVQLQESGPGLVKPSQTLSLTCTVSGGSISRGGYYWSWIRQHPGKGLEWIGYIYHSGSTYYNPSLKSRVNMSVDTSKNQFSLKLSSVTA
CDR1 CDR2

ADTAVYYCARALRGIVLMVYVLGALDIWGQGTKVTVSS
CDR3

U-V_H-38 heavy chain variable region amino acid sequence (SEQ ID NO:171)

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTA
CDR1 CDR2

ADTAVYYCARDETVVRGLIRYCYGMDVWGQGTTVTVSS
CDR3

U-V_H-39 heavy chain variable region amino acid sequence (SEQ ID NO:172)

QVQLQESGPGLVKPSQTLSLNCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIHYSGSTYYNPSLKSRITISADTSKNQFSLKLNSVTA
CDR1 CDR2

ADTAVYYCARDRGGGDYGRMDVWGQGTTVTVSS
CDR3

U-V_H-40 heavy chain variable region amino acid sequence (SEQ ID NO:173)

QVQLQESGPGLVKPSQTLSLNCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIHYSGSTYYNPSLKSRITISADTSKNQFSLKLNSVTA
CDR1 CDR2

ADTAVYYCARDRGGGDYGRMDVWGQGTTVTVSS
CDR3

FIGURE 2J

U-V_H-41 heavy chain variable region amino acid sequence (SEQ ID NO:174)

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIHSSGSTYYNPSLKSRITKSVDTSKNQFSLKLSSVTA
CDR1 CDR2

ADTAVYYCARSNNYGCFALWGRGTLVTVSS
CDR3

U-V_H-42 heavy chain variable region amino acid sequence (SEQ ID NO:175)

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIHSSGSTYYNPSLKSRITKSVDTSKNQFSLKLSSVTA
CDR1 CDR2

ADTAVYYCARSNNYGCFALWGRGTLVTVSS
CDR3

U-V_H-43 heavy chain variable region amino acid sequence (SEQ ID NO:176)

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIHYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTA
CDR1 CDR2

ADTAVYYCASGYNYGLYYYDSSGYPSYYYGMDVWGQGTTVTVSS
CDR3

U-V_H-44 heavy chain variable region amino acid sequence (SEQ ID NO:177)

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGDYYWNWVRQHPGKGLEWIGYIYYSGGTYYNPSLKSRVTISVDTSKNQFSLKLFSVTA
CDR1 CDR2

ADTAVYFCARTYYDILTGYPFYFDYWGQGTLVTVSS
CDR3

FIGURE 2K

U-V_H-45 heavy chain variable region amino acid sequence (SEQ ID NO:178)

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGDYYWNWVRQHPGKGLEWIGYIYYSGGTYYNPSLKSRVTISVDTSKNQFSLKLFSVTA
CDR1 CDR2

ADTAVYFCARTYYDILTGYPFYFDYWGQGTLVTVSS
CDR3

U-V_H-46 heavy chain variable region amino acid sequence (SEQ ID NO:179)

QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAAD
CDR1 CDR2

TAVYYCARGGYSSSWYWFDPWGQGTLVTVSS
CDR3

U-V_H-47 heavy chain variable region amino acid sequence (SEQ ID NO:180)

QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAAD
CDR1 CDR2

TAVYYCARGGYSSSWFWFDPWGQGTLVTVSS
CDR3

U-V_H-48 heavy chain variable region amino acid sequence (SEQ ID NO:180)

QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAAD
CDR1 CDR2

TAVYYCARGGYSSSWFWFDPWGQGTLVTVSS
CDR3

FIGURE 2L

U-V_H-49 heavy chain variable region amino acid sequence (SEQ ID NO:180)

QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAAD
CDR1 CDR2

TAVYYCARGGYSSSWFWFDPWGQGTLVTVSS
CDR3

U-V_H-50 heavy chain variable region amino acid sequence (SEQ ID NO:180)

QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAAD
CDR1 CDR2

TAVYYCARGGYSSSWFWFDPWGQGTLVTVSS
CDR3

U-V_H-51 heavy chain variable region amino acid sequence (SEQ ID NO:181)

QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPAGKGLEWIGRIYTSGTTNYNPSLKSRVTMSVDTSKNQFSLKLSSVTAAD
CDR1 CDR2

TAVYYCARDGYSYGHYYYYGMDVWGQGTTVTVSS
CDR3

U-V_H-52 heavy chain variable region amino acid sequence (SEQ ID NO:182)

QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGGSYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISIVTSRNQFSLKLSSVTA
CDR1 CDR2

ADTAVYYCARSALRYFDWLFSDVSDIWGQGTMVTVSS
CDR3

FIGURE 2M

U-V_H-53 heavy chain variable region amino acid sequence (SEQ ID NO:182)

QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGGSYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISIVTSRNQFSLKLSSVTA
CDR1 CDR2

ADTAVYYCARSALRYFDWLFSDVSDIWGQGTMVTVSS
CDR3

U-V_H-54 heavy chain variable region amino acid sequence (SEQ ID NO:183)

EVQLVQSGAELKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIIYPDDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKAS
CDR1 CDR2

DTAMYYCARQKSYGYSYFDYWGQGTLVTVSS
CDR3

U-V_H-55 heavy chain variable region amino acid sequence (SEQ ID NO:184)

EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPDDSDARYSPSFQGQVTISADKSINTAYLQWSSLKAS
CDR1 CDR2

DTAMYYCARQGYGSGWGYFDYWGQGTLVTVSS
CDR3

U-V_H-56 heavy chain variable region amino acid sequence (SEQ ID NO:185)

EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDIRYSPSFQGQVTISADKSISTAYLQWSSLKAS
CDR1 CDR2

DTAMYYCARQGLAVAGTSYYYYYGMDVWGQGTTVTVSS
CDR3

FIGURE 2N

U-V_H-57 heavy chain variable region amino acid sequence (SEQ ID NO:186)

QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSYSAAWNWIRQSPSRGLEWLGRTYCRSKWYNDYAVSVKSRITINPDTSKNQFSLQLNSV
CDR1 CDR2

TPEDTAVYYCARDRAVAGYYYGMDVWGQGTTVTVSS
CDR3

U-V_H-58 heavy chain variable region amino acid sequence (SEQ ID NO:166)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYSMNWVRQAPGKGLEWVSYISSSGRTIYYADSVKGRFTISRDNAKNSLFLQMNSLRDE
CDR1 CDR2

DTAVYYCALWAPFDYWGQGTLVTVSS
CDR3

FIGURE 2O

U_L-1 light chain amino acid sequence (SEQ ID NO:1)

DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWFQQRPGQSPRRLIYKVSNWDSGVP
DRFNGSGSGTDFTLKISRVEAEDVGVYYCMQSTHWPITFGQGTRLEIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-2 light chain amino acid sequence (SEQ ID NO:2)

DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWFQQRPGQSPRRLIYKVSNWDSGVP
DRFSGSGSGTDFTLKISRVEAEDVGVYYCIQGTHWPTTFGQGTRLEIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-3 light chain amino acid sequence (SEQ ID NO:3)

DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWLQQRPGQSPRRLIYKVSNWDSGVP
DRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWPITFGQGTRLEIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-4 light chain amino acid sequence (SEQ ID NO:3)

DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWLQQRPGQSPRRLIYKVSNWDSGVP
DRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWPITFGQGTRLEIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-5 light chain amino acid sequence (SEQ ID NO:4)

DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWYLQKPGQPPQLLIYEVSNRFSGVP
DRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGIQLPCSFGQGTKLEIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-6 light chain amino acid sequence (SEQ ID NO:5)

DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWYLQKPGQPPQLLIYEVSNRFSGVP
DRFSGSGSGTDFTLKISRVEAEDVGVYYCMQSIQLPLTFGGGTKVEIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURE 3A

U_L-7 light chain amino acid sequence (SEQ ID NO:5)

DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWYLQKPGQPPQLLIYEVSNRFSGVP
DRFSGSGSGTDFTLKISRVEAEDVGVYYCMQSIQLPLTFGGGTKVEIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-8 light chain amino acid sequence (SEQ ID NO:6)

DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWFLQKPGQPPQPLIYEVSNRFSGVP
DRFSGSGSGTDFTLKISRVEAEDVGVYYCMQSIQLPITFGHGTRLEIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-9 light chain amino acid sequence (SEQ ID NO:6)

DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWFLQKPGQPPQPLIYEVSNRFSGVP
DRFSGSGSGTDFTLKISRVEAEDVGVYYCMQSIQLPITFGHGTRLEIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-11 light chain amino acid sequence (SEQ ID NO:7)

DIQMTQSPSSLSASVGDRVTITCRASQGIANYLAWYQQKPGKVPKLLIYVASTLQSGVPSRFSG
SGSGTDFTLTISSLQPEDVATYYCQNYNSAPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-12 light chain amino acid sequence (SEQ ID NO:8)

DIQMTQSPSSLSASVGDRVTIICRASQGISNDLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSG
SGSGTDFTLTISSLQPEDVATYYCQKYNSVPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-13 light chain amino acid sequence (SEQ ID NO:9)

NIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYKISNRFSGVP
DRFSGSGAGTDFTLKISRVEAEDVGVYYCMQATQFPHTFGPGTKVDIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURE 3B

U_L-14 light chain amino acid sequence (SEQ ID NO:9)

NIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYKISNRFSGVP
DRFSGSGAGTDFTLKISRVEAEDVGVYYCMQATQFPHTFGPGTKVDIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-15 light chain amino acid sequence (SEQ ID NO:10)

EIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYKISNRFSGVP
DRFSGTGAGTDFTLKISRVEAEDVGVYYCMQATQFPHTFGGGTKVEIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-16 light chain amino acid sequence (SEQ ID NO:11)

EIVLTQSPGTLSLSPGERATLSCRASQTVISSYLAWYQQKPGQAPRLLISGASSRATGIPDRFS
GSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPRTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKS
GTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKV
YACEVTHQGLSSPVTKSFNRGEC

U_L-17 light chain amino acid sequence (SEQ ID NO:12)

EIVLTQSPGTLSLSPGERATLSCRASQSVSRLAWYQQKPGQAPRLLIYGASRRATGIPDRFSGS
GSGTDFTLTISRLEPEDFAVYYCQQYGSSPRSFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGT
ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYA
CEVTHQGLSSPVTKSFNRGEC

U_L-18 light chain amino acid sequence (SEQ ID NO:13)

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSG
SGSGTEFTLTISSLQPEDFATYYCLQHNSYPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-19 light chain amino acid sequence (SEQ ID NO:14)

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLVWYQQKPGQPPKLFIYWASTRESGV
PDRFTGSGSGTDFTLTISSLQAEDVAVYYCQQYYSFPWTFGQGTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURE 3C

U_L-20 light chain amino acid sequence (SEQ ID NO:14)

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLVWYQQKPGQPPKLFIYWASTRESGV
PDRFTGSGSGTDFTLTISSLQAEDVAVYYCQQYYSFPWTFGQGTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-21 light chain amino acid sequence (SEQ ID NO:15)

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGV
PDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTTWTFGQGTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-22 light chain amino acid sequence (SEQ ID NO:16)

DIVMTQSPDSLAVSLGERATINCKSSQNVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGV
PDRFSGSGSGTDFTLTISSLQAEDVAVYFCQQYYGTPRTFGQGTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-23 light chain amino acid sequence (SEQ ID NO:17)

DIVMTQSPDSLAVSLGERATINCKSSQNVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGV
PDRFSGSGSGTDFTLTISSLQAEDVAVYFCQQYYGTPRTFGQGTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-24 light chain amino acid sequence (SEQ ID NO:18)

DIVMTQSPDSLTVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGV
PDRFGGSGSGTDFTLTISSLQAEDVAVYYCQQYYSISRTFGQGTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-25 light chain amino acid sequence (SEQ ID NO:18)

DIVMTQSPDSLTVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGV
PDRFGGSGSGTDFTLTISSLQAEDVAVYYCQQYYSISRTFGQGTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURE 3D

U_L-26 light chain amino acid sequence (SEQ ID NO:19)

DIVMTQSPDSLAVSLGERATINCKSSQSVLYNSNNKNYLAWYQQKPGQPPKLLIYWASTRESGV
PDRFSGSGSGTDFTLTISSLQADDVAVYYCQQYYSTTWTFGPGTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-27 light chain amino acid sequence (SEQ ID NO:20)

DIVMTQSPDSLAVSLGERATINCKSSQSVLYNSNNKNYLAWYQQKPGQPPKLLIYWASTRESGV
PDRFSGSGSGTDFTLTISSLQADDVAVYYCQQYYSTTWTFGPGTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-28 light chain amino acid sequence (SEQ ID NO:21)

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKVLIYWASTRKSGV
PDRFSGSGSGTDFTLTISGLQAEDVALYYCQQYYSTMFSFGQGTKLEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-29 light chain amino acid sequence (SEQ ID NO:21)

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKVLIYWASTRKSGV
PDRFSGSGSGTDFTLTISGLQAEDVALYYCQQYYSTMFSFGQGTKLEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-30 light chain amino acid sequence (SEQ ID NO:22)

DIVMTQSPDSLAVSLGERATINCKSSQSVLDSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGV
PDRFSGSGSGTDFTLTISSLQAEDVAVFYCHQYYSTPLTFGGGTKVAIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-31 light chain amino acid sequence (SEQ ID NO:22)

DIVMTQSPDSLAVSLGERATINCKSSQSVLDSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGV
PDRFSGSGSGTDFTLTISSLQAEDVAVFYCHQYYSTPLTFGGGTKVAIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURE 3E

U_L-32 light chain amino acid sequence (SEQ ID NO:23)

DIVMTQSPDSLAVSLGERATINCKSSQSILYRSNNKNYLAWYQQKPGQPPKLLIYWASARESGV
PDRFSGSGSGTDFTLTISSLQAEDVAVYFCQQYFITPLTFGGGTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-33 light chain amino acid sequence (SEQ ID NO:23)

DIVMTQSPDSLAVSLGERATINCKSSQSILYRSNNKNYLAWYQQKPGQPPKLLIYWASARESGV
PDRFSGSGSGTDFTLTISSLQAEDVAVYFCQQYFITPLTFGGGTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-34 light chain amino acid sequence (SEQ ID NO:24)

DIQMTQSPSSLSASVGDRVTITCRASQDISHYLAWFQQKPGKAPKSLIYAASSLQSGVPSKFSG
SGSGTDFTLTISSLQPEDFATYYCQQYNNYPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-35 light chain amino acid sequence (SEQ ID NO:25)

DIQMTQSPSSLSASVGDRVAITCRASQDISNYLAWLQQKPGKAPKSLIYAASSLQSGVPSRFSG
SGSGTDFTLTISSLQPEDFATYYCQQYNTYPFTFGPGTKMDIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-36 light chain amino acid sequence (SEQ ID NO:26)

EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQDPGQAPRLLIYGASRRATGIPARFSG
SGSGTEFTLTISSLQSEDFAVYYCQQHNNWPPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKS
GTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKV
YACEVTHQGLSSPVTKSFNRGEC

U_L-37 light chain amino acid sequence (SEQ ID NO:26)

EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQDPGQAPRLLIYGASRRATGIPARFSG
SGSGTEFTLTISSLQSEDFAVYYCQQHNNWPPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKS
GTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKV
YACEVTHQGLSSPVTKSFNRGEC

FIGURE 3F

U_L-38 light chain amino acid sequence (SEQ ID NO:27)

DIQMTQSPSSVSASVGDRVTITCRASQDISRWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSG
SGSGTDFTLTISSLQPEDFATYYCQQANSFPPTFGQGTKVEFKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-39 light chain amino acid sequence (SEQ ID NO:28)

DIQMTQSPSSLSASVGDRVTITCRASQSISTYLNWYQQKPGKAPKFLIYAASSLQSGVPSRFSG
SGSGTDFTLTISSLQPEDFAAYYCQQSHSAPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-40 light chain amino acid sequence (SEQ ID NO:29)

DIQMTQSPSSLSASLGDRVTITCRASQTISIYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSG
SGSGTDFTLTISSLQPEDFATYYCQQSYSTLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGT
ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYA
CEVTHQGLSSPVTKSFNRGEC

U_L-41 light chain amino acid sequence (SEQ ID NO:30)

DIQMTQSPSSLSASVGDRVTITCRASQSIRSYLNWYQQRPGNAPKLLIYAASSLQSGVPSRVSG
SGSGTDFTLTIRSLQPEDFATYYCQQSYSIPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-42 light chain amino acid sequence (SEQ ID NO:31)

DIQMTQSPSSRSASVGDRVTITCRASQTISRYLNWYQQKPGKAPKLLIYAASTLQSGVPSRFSG
SGSGTDFTLTLSSLQPEDFATYYCQQIYSTSITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-43 light chain amino acid sequence (SEQ ID NO:32)

DIQMTQSPSSLSASVGDRVTITCRASQRISSYLNWYQQKPGKAPKVLIYAESSLQSGVPSRFSG
SGSGTDFTLTISSLQPEDFATYYCQQSYITPITFGQGTRLEIIRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

FIGURE 3G

U_L-44 light chain amino acid sequence (SEQ ID NO:33)

DIQMTQSPSSLSASVGDRVTITCRASQSISRYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSG
SGSGTDFTLTISSLQPENFATYYCQQSYFTPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-45 light chain amino acid sequence (SEQ ID NO:34)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSG
SGSGTDFTLTFSSLQPEDFATYYCQQSYFSPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-46 light chain amino acid sequence (SEQ ID NO:35)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSG
SGSGTDFTLTLSSLQPEDFASYYCQQSFYTPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-47 light chain amino acid sequence (SEQ ID NO:35)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSG
SGSGTDFTLTLSSLQPEDFASYYCQQSFYTPITFGQGTRLEIKASTKGPSVFPLAPCSRSTSES
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNV
DHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
PEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEK
TISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPML
DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_L-48 light chain amino acid sequence (SEQ ID NO:36)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTVSSLQSGVPSRFSG
SGSGTDFTLTISSLQPEDFATYYCQQSYFTPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-49 light chain amino acid sequence (SEQ ID NO:36)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTVSSLQSGVPSRFSG
SGSGTDFTLTISSLQPEDFATYYCQQSYFTPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

FIGURE 3H

U_L-50 light chain amino acid sequence (SEQ ID NO:36)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTVSSLQSGVPSRFSG
SGSGTDFTLTISSLQPEDFATYYCQQSYFTPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-51 light chain amino acid sequence (SEQ ID NO:37)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSG
SGSGTDFTLTISSLQPEDFASYYCQQSFYAPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-52 light chain amino acid sequence (SEQ ID NO:37)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSG
SGSGTDFTLTISSLQPEDFASYYCQQSFYAPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-53 light chain amino acid sequence (SEQ ID NO:38)

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSG
SGSGTDFTLTISSLQPEDFATYYCQQSYFTPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-54 light chain amino acid sequence (SEQ ID NO:39)

DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSG
SGSGTDFTFTISSLQPEDIATYYCQQYDYLPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-55 light chain amino acid sequence (SEQ ID NO:39)

DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSG
SGSGTDFTFTISSLQPEDIATYYCQQYDYLPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

FIGURE 3I

U_L-56 light chain amino acid sequence (SEQ ID NO:40)

DIQMTQSPSSLSASVGDRVTITCQASQDISNSLNWYQQKPGKAPELLIYDASNLETGVPSRFSG
SGSGTDFTFTISSLQPEDIATYYCQQCDDLPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-57 light chain amino acid sequence (SEQ ID NO:41)

DIQMTQSPSSLSASVGDRVTITCQASQDISDYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSG
SGSGTDFTFTISSLQPEDIATYYCQHYDNLPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-58 light chain amino acid sequence (SEQ ID NO:42)

DIQMTQSPSSLSASVGDRVAITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSG
SGSGTDFTFTISSLQPEDIATYYCQQYDNLPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-59 light chain amino acid sequence (SEQ ID NO:42)

DIQMTQSPSSLSASVGDRVAITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSG
SGSGTDFTFTISSLQPEDIATYYCQQYDNLPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-60 light chain amino acid sequence (SEQ ID NO:43)

DIQMTQSPSSLSASVGDRVTITCQASQDISNSLNWYQQKPGKAPKLLIYDASILETGVPSRFSG
SGSETDFTFTISSLQPEDIATYYCQQCDILPLSFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-61 light chain amino acid sequence (SEQ ID NO:44)

DIQMTQSPSSLSASVGDRVTITCQASQDISNSLNWYQQKPGKAPKLLIYDASNLETGVPSRFSG
SGSGTDFTFTISSLQPEDIATYYCQQYDNLPLAFGGGTKVEIRRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

FIGURE 3J

U_L-62 light chain amino acid sequence (SEQ ID NO:45)

DIQMTQSPSSLSASVGDGVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSG
SGSGTDFTFTISSLQPEDIATYYCQQYDSLPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-63 light chain amino acid sequence (SEQ ID NO:46)

DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKLGKAPKLLIHDASNLETGVPSRFSG
SGSGTDFTFTISSLQPEDIATYYCQQYDNLPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-64 light chain amino acid sequence (SEQ ID NO:47)

DIQMTQSPSSLSASVGDRVTITCQASQDISDYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSG
SGSGTDFTFTISSLQPEDIATYYCQHYDNLPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-65 light chain amino acid sequence (SEQ ID NO:48)

DIQMTQSPSSLSASVGDRVTITCQASQDISNSLNWYQQKPGKAPKLLIYDASNLETGVPSRFSG
SGSGTDFTFTISSLQPEDIATYYCQHYDNLPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

FIGURE 3K

U_B-1 heavy chain amino acid sequence (SEQ ID NO:49)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISASNGNTNYAQKL
QDRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAREDNWNYGFFDYWGQGTLVTVSSASTKGPSV
FPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTP
EVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC
KVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-2 heavy chain amino acid sequence (SEQ ID NO:49)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISASNGNTNYAQKL
QDRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAREDNWNYGFFDYWGQGTLVTVSSASTKGPSV
FPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTP
EVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC
KVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-3 heavy chain amino acid sequence (SEQ ID NO:50)

QVHLVQSGAEVKKPGASVKVSCKVSGYTFTGHYMHWVRQAPGQGLEWMGWINPNSGGTNCAQKF
QGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARSIAVALDYWGQGTLVTVSSASTKGPSVFPL
APCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSN
FGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVT
CVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVS
NKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
NNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-4 heavy chain amino acid sequence (SEQ ID NO:51)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNHTQKF
QGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARSIAVALDYWGQGTLVTVSSASTKGPSVFPL
APCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSN
FGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVT
CVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVS
NKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
NNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

FIGURE 4A

U_B-5 heavy chain amino acid sequence (SEQ ID NO:52)

QVQLVQSGAEVRKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGSFDPEDGETIYAQKF
QGRVTMLEDTSTDTAYMELSSLRSEDTAVYYCATEGDGGYYYYGMDVWGQGTTVTVSSASTKGP
SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT
VPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISR
TPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEY
KCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-6 heavy chain amino acid sequence (SEQ ID NO:52)

QVQLVQSGAEVRKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGSFDPEDGETIYAQKF
QGRVTMLEDTSTDTAYMELSSLRSEDTAVYYCATEGDGGYYYYGMDVWGQGTTVTVSSASTKGP
SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT
VPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISR
TPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEY
KCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-7 heavy chain amino acid sequence (SEQ ID NO:53)

QVTLKESGPVLVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTS
LKSRLTISKDTSKSQVVLTMTNMDPVDTATYYCARMYSSGWYGVFDYWGQGTLVTVSSASTKGP
SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT
VPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISR
TPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEY
KCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-8 heavy chain amino acid sequence (SEQ ID NO:54)

QVTLKESGPVLVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKALEWLVLIFSNDEKSYSTS
LKSRLTISKDTSKSQVVLTMTNMDPVDTATYYCARVYSSGWSFYGMDVWGQGTTVTVSSASTKG
PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV
TVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMIS
RTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKE
YKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

FIGURE 4B

U_R-9 heavy chain amino acid sequence (SEQ ID NO:55)

QITLKESGPTLVKPTQTLTLTCTFSGFSLSTGGVGVGWIRQPPGKALEWLALIYWNDDKRYSPS
LKSRLTITKDTSKNQVVLTMTNMDPVDTATYYCAHRRELPFDYWGQGTLVTVSSASTKGPSVFP
LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
NFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV
SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_R-10 heavy chain amino acid sequence (SEQ ID NO:56)

QITLKESGPTLVKPTQTLTLTCTFSGFSLSTGGVGVGWIRQPPGKALEWLALIYWNDDKRYSPS
LKSRLTITKDTSKTQVVLTVTDMDPVDTATYYCAHRNWTPFDYWGQGTLVTVSSASTKGPSVFP
LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
NFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV
SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_R-11 heavy chain amino acid sequence (SEQ ID NO:57)

QITLKESGPTLVKPTQTLTLTCTFSGFSLNTGGVGVGWIRQPPGKALEWLALIYWNDDKRYSPS
LKSRLTITKDTSKNQVVLTMTNMDPVDTATYYCAHRLELPFDYWGQGTLVTVSSASTKGPSVFP
LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
NFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV
SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_R-12 heavy chain amino acid sequence (SEQ ID NO:58)

QITLKESGPTLVKPTQTLTLTCTFSGFSLSTGGVGVGWIRQPPGKALEWLALIYWNDDKRYSPS
LKSRLTITKDTSKNQVVLTMTNLDPVDTATYYCAHRREVPFDYWGQGTLVTVSSASTKGPSVFP
LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
NFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV
SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

FIGURE 4C

U_B-13 heavy chain amino acid sequence (SEQ ID NO:59)

QITLKESGPTLVKPTQTLTLTCTFSGFSLSTGGVGVGWIRQPPGKALEWLALIYWNVEKRYSPS
LRSRLTITKATSKNQVVLTMTNMDPVDTATYYCAHRHTNPFEYWGQGTLVTVSSASTKGPSVFP
LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
NFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV
SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-14 heavy chain amino acid sequence (SEQ ID NO:60)

QITLKESGPTLVKPTQTLTLTCTFSGFSLSTGGVGVGWIRQPPGKALEWLALIYWNDDKRYSPS
LKSRLTITKDTSKNQVVLTMTNMDPVDTATYYCAHRGELPFDYWGQGTLVTVSSASTKGPSVFP
LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
NFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV
SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-15 heavy chain amino acid sequence (SEQ ID NO:60)

QITLKESGPTLVKPTQTLTLTCTFSGFSLSTGGVGVGWIRQPPGKALEWLALIYWNDDKRYSPS
LKSRLTITKDTSKNQVVLTMTNMDPVDTATYYCAHRGELPFDYWGQGTLVTVSSASTKGPSVFP
LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
NFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV
SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-16 heavy chain amino acid sequence (SEQ ID NO:61)

EVQLVESGGGLVKPGGSLRLSCAASGFPFSRYSMNWVRQAPGKGLEWVSAISSSSSYIYYADSV
KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDRVGATPDAFDIWGQGTMVTVSSASTKGPS
VFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTV
PSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRT
PEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYK
CKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN
GQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

FIGURE 4D

U_B-17 heavy chain amino acid sequence (SEQ ID NO:62)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSAISGSGGSTYYADSV
KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKEGIAVAGTAEYYYYYAMDVWGQGTTVTVSS
ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS
LSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKD
TLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDW
LNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI
AVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

U_B-18 heavy chain amino acid sequence (SEQ ID NO:63)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSV
KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKEGIAARDSYYYYAMDVWGQGTTVTVSSASTK
GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV
VTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGK
EYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

U_B-19 heavy chain amino acid sequence (SEQ ID NO:64)

EVQLLESGGGLVQPGGSLRLSCTASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSV
KGRFTISRDNSKNTLYLQMNSLRAEDTAEYYCAKEGIAGRDSYYYYGMDVWGQGTTVTVSSASTK
GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV
VTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGK
EYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

U_B-20 heavy chain amino acid sequence (SEQ ID NO:64)

EVQLLESGGGLVQPGGSLRLSCTASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSV
KGRFTISRDNSKNTLYLQMNSLRAEDTAEYYCAKEGIAGRDSYYYYGMDVWGQGTTVTVSSASTK
GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV
VTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGK
EYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

FIGURE 4E

U_H-21 heavy chain amino acid sequence (SEQ ID NO:65)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFISDDGSTKYYADSV
KGRFTISRDNSMNTLYLQMNSLRAEDTAVYYCARSYYDSSGYYYGFDYWGQGTLVTVSSASTKG
PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV
TVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMIS
RTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKE
YKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_H-22 heavy chain amino acid sequence (SEQ ID NO:65)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFISDDGSTKYYADSV
KGRFTISRDNSMNTLYLQMNSLRAEDTAVYYCARSYYDSSGYYYGFDYWGQGTLVTVSSASTKG
PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV
TVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMIS
RTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKE
YKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_H-23 heavy chain amino acid sequence (SEQ ID NO:66)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYYADSV
KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARNVIDYWGQGTLVTVSSASTKGPSVFPLAPC
SRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGT
QTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVV
VDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKG
LPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
KTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_H-24 heavy chain amino acid sequence (SEQ ID NO:67)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVIWYDGSIKYYADSV
KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGGATGAEYFQHWGQGTLVTVSSASTKGPSV
FPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTP
EVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC
KVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

FIGURE 4F

U_H-25 heavy chain amino acid sequence (SEQ ID NO:67)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVIWYDGSIKYYADSV
KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGGATGAEYFQHWGQGTLVTVSSASTKGPSV
FPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTP
EVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC
KVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_H-26 heavy chain amino acid sequence (SEQ ID NO:68)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYYADSV
KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVLLWFGETFDYWGQGSLVTVSPASTKGPSVFP
LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
NFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV
SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_H-27 heavy chain amino acid sequence (SEQ ID NO:69)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWSDGSNKYYADSV
KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARNLPFDYWGQGTLVTVSSASTKGPSVFPLAP
CSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFG
TQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNK
GLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN
YKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_H-28 heavy chain amino acid sequence (SEQ ID NO:70)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWDDGSNQYYTDSV
KGRFTVSRDNSKNTLFLQMNSLRAEDTAVYYCARSHYGGDYDYYGMDVWGQGTTVTVSSASTKG
PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV
TVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMIS
RTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKE
YKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

FIGURE 4G

U_B-29 heavy chain amino acid sequence (SEQ ID NO:71)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKRYVDSV
KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGWQQQAPFDYWGQGTLVTVSSASTKGPSV
FPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTP
EVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC
KVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-30 heavy chain amino acid sequence (SEQ ID NO:72)

QVQLVESGGGVVQPGRSLRLSCAASGFTFRSHGMHWVRQAPGKGLEWVAVIWYDGSNKNYADSV
RGRFTISRDNSKNTLDLQMNSLRAEDTAVYYCARWGISAPFDCWGQGTLVTVSSASTKGPSVFP
LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
NFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV
SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-31 heavy chain amino acid sequence (SEQ ID NO:73)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYSMNWVRQAPGKGLEWVSYISSSGRTIYYADSV
KGRFTISRDNAKNSLFLQMNSLRDEDTAVYYCALWAPFDYWGQGTLVTVSSASTKGPSVFPLAP
CSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFG
TQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNK
GLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN
YKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-32 heavy chain amino acid sequence (SEQ ID NO:74)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSHISSSSRTIYYADSV
KGRFTISRDNAKNSVYLQMNSLRDEDTAVYYCARDGYNWNGGGNYYGMDVWGQGTTVTVSSASTK
GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV
VTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGK
EYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

FIGURE 4H

U_H-33 heavy chain amino acid sequence (SEQ ID NO:75)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSHISRSSRTIYYADSV
KGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCARDGYNWNNGGYYYGMDVWGQGTTVTVSSASTK
GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV
VTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGK
EYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

U_H-34 heavy chain amino acid sequence (SEQ ID NO:75)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSHISRSSRTIYYADSV
KGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCARDGYNWNNGGYYYGMDVWGQGTTVTVSSASTK
GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV
VTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGK
EYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

U_H-35 heavy chain amino acid sequence (SEQ ID NO:76)

QVQLQESGPGLVKPSQTLSLTCTVSGGSVSSGGYYWSWIRQHPGKGLEWIGYIHSSGSTYYNPS
LKSRVTISVDTSKNQFSLNLSSVTAADTAVYYCARGPYYGMDVWGQGTTVTVSSASTKGPSVFP
LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
NFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV
SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_H-36 heavy chain amino acid sequence (SEQ ID NO:77)

QVQLQESGPGLVKPSQTLSLTCTVSGGSISRGGYYWSWIRQHPGKGLEWIGYIYHSGSTYYNPS
LKSRVNMSVDTSKNQFSLKLSSVTAADTAVYYCARALRGIVLMVYVLGALDIWGQGTKVTVSSA
STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL
SSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDT
LMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWL
NGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
LSPGK

FIGURE 4I

U_B-37 heavy chain amino acid sequence (SEQ ID NO:77)

QVQLQESGPGLVKPSQTLSLTCTVSGGSISRGGYYWSWIRQHPGKGLEWIGYIYHSGSTYYNPS
LKSRVNMSVDTSKNQFSLKLSSVTAADTAVYYCARALRGIVLMVYVLGALDIWGQGTKVTVSSA
STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL
SSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDT
LMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWL
NGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
LSPGK

U_B-38 heavy chain amino acid sequence (SEQ ID NO:78)

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPS
LKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDETVVRGLIRYCYGMDVWGQGTTVTVSSA
STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL
SSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDT
LMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWL
NGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
LSPGK

U_B-39 heavy chain amino acid sequence (SEQ ID NO:79)

QVQLQESGPGLVKPSQTLSLNCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIHYSGSTYYNPS
LKSRITISADTSKNQFSLKLNSVTAADTAVYYCARDRGGGDYGRMDVWGQGTTVTVSSASTKGP
SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT
VPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISR
TPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEY
KCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-40 heavy chain amino acid sequence (SEQ ID NO:80)

QVQLQESGPGLVKPSQTLSLNCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIHYSGSTYYNPS
LKSRITISADTSKNQFSLKLNSVTAADTAVYYCARDRGGGDYGRMDVWGQGTTVTVSSASTKGP
SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT
VPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISR
TPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEY
KCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

FIGURE 4J

U_R-41 heavy chain amino acid sequence (SEQ ID NO:81)

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWI81RQHPGKGLEWIGYIHSSGSTYYN
PSLKSRITKSVDTSKNQFSLKLSSVTAADTAVYYCARSNNYGCFALWGRGTLVTVSSASTKGPS
VFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTV
PSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRT
PEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYK
CKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN
GQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_R-42 heavy chain amino acid sequence (SEQ ID NO:82)

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIHSSGSTYYNPS
LKSRITKSVDTSKNQFSLKLSSVTAADTAVYYCARSNNYGCFALWGRGTLVTVSSASTKGPSVF
PLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS
SNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
VTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCK
VSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ
PENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_R-43 heavy chain amino acid sequence (SEQ ID NO:83)

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIHYSGSTYYNPS
LKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCASGYNYGLYYYDSSGYPSYYYGMDVWGQGTT
VTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
SGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFP
PKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTV
VHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY
TQKSLSLSPGK

U_R-44 heavy chain amino acid sequence (SEQ ID NO:84)

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGDYYWNWVRQHPGKGLEWIGYIYYSGGTYYNPS
LKSRVTISVDTSKNQFSLKLFSVTAADTAVYFCARTYYDILTGYPFYFDYWGQGTLVTVSSASTK
GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV
VTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGK
EYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

FIGURE 4K

U_H-45 heavy chain amino acid sequence (SEQ ID NO:85)

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGDYYWNWVRQHPGKGLEWIGYIYYSGGTYYNPS
LKSRVTISVDTSKNQFSLKLFSVTAADTAVYFCARTYYDILTGYPFYFDYWGQGTLVTVSSASTK
GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV
VTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGK
EYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

U_H-46 heavy chain amino acid sequence (SEQ ID NO:86)

QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLK
SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGYSSSWYWFDPWGQGTLVTVSSASTKGPSV
FPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTP
EVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC
KVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_H-47 heavy chain amino acid sequence (SEQ ID NO:87)

QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLK
SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGYSSSWFWFDPWGQGTLVTVSSASTKGPSV
FPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTP
EVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC
KVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_H-48 heavy chain amino acid sequence (SEQ ID NO:87)

QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLK
SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGYSSSWFWFDPWGQGTLVTVSSASTKGPSV
FPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTP
EVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC
KVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

FIGURE 4L

U_B-49 heavy chain amino acid sequence (SEQ ID NO:87)

QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLK
SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGYSSSWFWFDPWGQGTLVTVSSASTKGPSV
FPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTP
EVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC
KVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-50 heavy chain amino acid sequence (SEQ ID NO:87)

QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLK
SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGYSSSWFWFDPWGQGTLVTVSSASTKGPSV
FPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTP
EVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC
KVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-51 heavy chain amino acid sequence (SEQ ID NO:88)

QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPAGKGLEWIGRIYTSGTTNYNPSLK
SRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARDGYSYGHYYYYGMDVWGQGTTVTVSSASTKG
PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV
TVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMIS
RTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKE
YKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-52 heavy chain amino acid sequence (SEQ ID NO:89)

QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGGSYWSWIRQPPGKGLEWIGYIYYSGSTNYNPS
LKSRVTISIVTSRNQFSLKLSSVTAADTAVYYCARSALRYFDWLFSDVSDIWGQGTMVTVSSAS
TKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLS
SVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTL
MISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLN
GKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV
EWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
SPGK

FIGURE 4M

U_B-53 heavy chain amino acid sequence (SEQ ID NO:89)

QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGGSYWSWIRQPPGKGLEWIGYIYYSGSTNYNPS
LKSRVTISIVTSRNQFSLKLSSVTAADTAVYYCARSALRYFDWLFSDVSDIWGQGTMVTVSSAS
TKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLS
SVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTL
MISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLN
GKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV
EWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
SPGK

U_B-54 heavy chain amino acid sequence (SEQ ID NO:90)

EVQLVQSGAELKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIIYPDDSDTRYSPSF
QGQVTISADKSISTAYLQWSSLKASDTAMYYCARQKSYGYSYFDYWGQGTLVTVSSASTKGPSV
FPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTP
EVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC
KVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-55 heavy chain amino acid sequence (SEQ ID NO:91)

EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPDDSDARYSPSF
QGQVTISADKSINTAYLQWSSLKASDTAMYYCARQGYGSGWGYFDYWGQGTLVTVSSASTKGPS
VFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTV
PSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRT
PEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYK
CKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN
GQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-56 heavy chain amino acid sequence (SEQ ID NO:92)

EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDIRYSPSF
QGQVTISADKSISTAYLQWSSLKASDTAMYYCARQGLAVAGTSYYYYYGMDVWGQGTTVTVSSA
STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL
SSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDT
LMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWL
NGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
LSPGK

FIGURE 4N

U_B-57 heavy chain amino acid sequence (SEQ ID NO:93)

QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSYSAAWNWIRQSPSRGLEWLGRTYCRSKWYNDYA
VSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARDRAVAGYYYGMDVWGQGTTVTVSSASTK
GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV
VTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGK
EYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

U_B-58 heavy chain amino acid sequence (SEQ ID NO:73)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYSMNWVRQAPGKGLEWVSYISSSGRTIYYADSV
KGRFTISRDNAKNSLFLQMNSLRDEDTAVYYCALWAPFDYWGQGTLVTVSSASTKGPSVFPLAP
CSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFG
TQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNK
GLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN
YKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

FIGURE 4O

CONSTANT REGION: LIGHT CHAIN AMINO ACID SEQUENCE

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKA
DYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:187)

FIGURE 5A

CONSTANT REGION: HEAVY CHAIN AMINO ACID SEQUENCE

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFG
TQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF
NWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLP
PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPGK (SEQ ID NO:188)

FIGURE 5B

LIGHT CHAIN CDRS

NAME	SEQUENCE	SEQ ID NO:
CDRL1-1	RSSQSLVYSDGNTYLN	189
CDRL1-2	RSSQSLVYSDGNTYLN	189
CDRL1-3	RSSQSLVYSDGNTYLN	189
CDRL1-4	RSSQSLVYSDGNTYLN	189
CDRL1-5	KSSQSLLHSDGKTYLY	190
CDRL1-6	KSSQSLLHSDGKTYLY	190
CDRL1-7	KSSQSLLHSDGKTYLY	190
CDRL1-8	KSSQSLLHSDGKTYLY	190
CDRL1-9	KSSQSLLHSDGKTYLY	190
CDRL1-11	RASQGIANYLA	191
CDRL1-12	RASQGISNDLA	192
CDRL1-13	RSSQSLVHSDGNTYLS	193
CDRL1-14	RSSQSLVHSDGNTYLS	193
CDRL1-15	RSSQSLVHSDGNTYLS	193
CDRL1-16	RASQTVISSYLA	194
CDRL1-17	RASQSVSRLA	195
CDRL1-18	RASQGIRNDLG	196
CDRL1-19	KSSQSVLYSSNNKNYLV	197
CDRL1-20	KSSQSVLYSSNNKNYLV	197
CDRL1-21	KSSQSVLYSSNNKNYLA	198
CDRL1-22	KSSQNVLYSSNNKNYLA	199
CDRL1-23	KSSQNVLYSSNNKNYLA	199
CDRL1-24	KSSQSVLYSSNNKNYLA	198
CDRL1-25	KSSQSVLYSSNNKNYLA	198
CDRL1-26	KSSQSVLYNSNNKNYLA	200
CDRL1-27	KSSQSVLYNSNNKNYLA	200
CDRL1-28	KSSQSVLYSSNNKNYLA	198
CDRL1-29	KSSQSVLYSSNNKNYLA	198
CDRL1-30	KSSQSVLDSSNNKNYLA	201
CDRL1-31	KSSQSVLDSSNNKNYLA	201
CDRL1-32	KSSQSILYRSNNKNYLA	202
CDRL1-33	KSSQSILYRSNNKNYLA	202
CDRL1-34	RASQDISHYLA	203
CDRL1-35	RASQDISNYLA	204

FIGURE 6A

NAME	SEQUENCE	SEQ ID NO:
CDRL1-36	RASQSVSSNLA	205
CDRL1-37	RASQSVSSNLA	205
CDRL1-38	RASQDISRWLA	206
CDRL1-39	RASQSISTYLN	207
CDRL1-40	RASQTISIYLN	208
CDRL1-41	RASQSIRSYLN	209
CDRL1-42	RASQTISRYLN	210
CDRL1-43	RASQRISSYLN	211
CDRL1-44	RASQSISRYLN	212
CDRL1-45	RASQSISSYLN	213
CDRL1-46	RASQSISSYLN	213
CDRL1-47	RASQSISSYLN	213
CDRL1-48	RASQSISSYLN	213
CDRL1-49	RASQSISSYLN	213
CDRL1-50	RASQSISSYLN	213
CDRL1-51	RASQSISSYLN	213
CDRL1-52	RASQSISSYLN	213
CDRL1-53	RASQSISSYLN	213
CDRL1-54	QASQDISNYLN	214
CDRL1-55	QASQDISNYLN	214
CDRL1-56	QASQDISNSLN	215
CDRL1-57	QASQDISDYLN	216
CDRL1-58	QASQDISNYLN	214
CDRL1-59	QASQDISNYLN	214
CDRL1-60	QASQDISNSLN	215
CDRL1-61	QASQDISNSLN	215
CDRL1-62	QASQDITNYLN	217
CDRL1-63	QASQDISNYLN	214
CDRL1-64	QASQDISDYLN	216
CDRL1-65	QASQDISNSLN	215
CDRL2-1	KVSNWDS	218
CDRL2-2	KVSNWDS	218
CDRL2-3	KVSNWDS	218
CDRL2-4	KVSNWDS	218
CDRL2-5	EVSNRFS	219
CDRL2-6	EVSNRFS	219

FIGURE 6B

NAME	SEQUENCE	SEQ ID NO:
CDRL2-7	EVSNRFS	219
CDRL2-8	EVSNRFS	219
CDRL2-9	EVSNRFS	219
CDRL2-11	VASTLQS	220
CDRL2-12	AASTLQS	221
CDRL2-13	KISNRFS	222
CDRL2-14	KISNRFS	222
CDRL2-15	KISNRFS	222
CDRL2-16	GASSRAT	223
CDRL2-17	GASRRAT	224
CDRL2-18	AASSLQS	225
CDRL2-19	WASTRES	226
CDRL2-20	WASTRES	226
CDRL2-21	WASTRES	226
CDRL2-22	WASTRES	226
CDRL2-23	WASTRES	226
CDRL2-24	WASTRES	226
CDRL2-25	WASTRES	226
CDRL2-26	WASTRES	226
CDRL2-27	WASTRES	226
CDRL2-28	WASTRKS	227
CDRL2-29	WASTRKS	227
CDRL2-30	WASTRES	226
CDRL2-31	WASTRES	226
CDRL2-32	WASARES	228
CDRL2-33	WASARES	228
CDRL2-34	AASSLQS	225
CDRL2-35	AASSLQS	225
CDRL2-36	GASRRAT	224
CDRL2-37	GASRRAT	224
CDRL2-38	AASSLQS	225
CDRL2-39	AASSLQS	225
CDRL2-40	AASSLQS	225
CDRL2-41	AASSLQS	225
CDRL2-42	AASTLQS	221
CDRL2-43	AESSLQS	229

FIGURE 6C

NAME	SEQUENCE	SEQ ID NO:
CDRL2-44	TASSLQS	230
CDRL2-45	TASSLQS	230
CDRL2-46	TASSLQS	230
CDRL2-47	TASSLQS	230
CDRL2-48	TVSSLQS	231
CDRL2-49	TVSSLQS	231
CDRL2-50	TVSSLQS	231
CDRL2-51	TASSLQS	230
CDRL2-52	TASSLQS	230
CDRL2-53	TASSLQS	230
CDRL2-54	DASNLET	232
CDRL2-55	DASNLET	232
CDRL2-56	DASNLET	232
CDRL2-57	DASNLET	232
CDRL2-58	DASNLET	232
CDRL2-59	DASNLET	232
CDRL2-60	DASILET	233
CDRL2-61	DASNLET	232
CDRL2-62	DASNLET	232
CDRL2-63	DASNLET	232
CDRL2-64	DASNLET	232
CDRL2-65	DASNLET	232
CDRL3-1	MQSTHWPIT	234
CDRL3-2	IQGTHWPTT	235
CDRL3-3	MQGTHWPIT	236
CDRL3-4	MQGTHWPIT	236
CDRL3-5	MQGIQLPCS	237
CDRL3-6	MQSIQLPLT	238
CDRL3-7	MQSIQLPLT	238
CDRL3-8	MQSIQLPIT	239
CDRL3-9	MQSIQLPIT	239
CDRL3-11	QNYNSAPFT	240
CDRL3-12	QKYNSVPLT	241
CDRL3-13	MQATQFPHT	242
CDRL3-14	MQATQFPHT	242
CDRL3-15	MQATQFPHT	242

FIGURE 6D

NAME	SEQUENCE	SEQ ID NO:
CDRL3-16	QQYGSSPRT	243
CDRL3-17	QQYGSSPRS	244
CDRL3-18	LQHNSYPPT	245
CDRL3-19	QQYYSFPWT	246
CDRL3-20	QQYYSFPWT	246
CDRL3-21	QQYYSTTWT	247
CDRL3-22	QQYYGTPRT	248
CDRL3-23	QQYYGTPRT	248
CDRL3-24	QQYYSISRT	249
CDRL3-25	QQYYSISRT	249
CDRL3-26	QQYYSTTWT	247
CDRL3-27	QQYYSTTWT	247
CDRL3-28	QQYYSTMFS	250
CDRL3-29	QQYYSTMFS	250
CDRL3-30	HQYYSTPLT	251
CDRL3-31	HQYYSTPLT	251
CDRL3-32	QQYFITPLT	252
CDRL3-33	QQYFITPLT	252
CDRL3-34	QQYNNYPFT	253
CDRL3-35	QQYNTYPFT	254
CDRL3-36	QQHNNWPPWT	255
CDRL3-37	QQHNNWPPWT	255
CDRL3-38	QQANSFPPT	256
CDRL3-39	QQSHSAPFT	257
CDRL3-40	QQSYSTLT	258
CDRL3-41	QQSYSIPLT	259
CDRL3-42	QQIYSTSIT	260
CDRL3-43	QQSYITPIT	261
CDRL3-44	QQSYFTPIT	262
CDRL3-45	QQSYFSPIT	263
CDRL3-46	QQSFYTPIT	264
CDRL3-47	QQSFYTPIT	264
CDRL3-48	QQSYFTPIT	262
CDRL3-49	QQSYFTPIT	262
CDRL3-50	QQSYFTPIT	262
CDRL3-51	QQSFYAPIT	265

FIGURE 6E

NAME	SEQUENCE	SEQ ID NO:
CDRL3-52	QQSFYAPIT	265
CDRL3-53	QQSYFTPIT	262
CDRL3-54	QQYDYLPFT	266
CDRL3-55	QQYDYLPFT	266
CDRL3-56	QQCDDLPLT	267
CDRL3-57	QHYDNLPLT	268
CDRL3-58	QQYDNLPLT	269
CDRL3-59	QQYDNLPLT	269
CDRL3-60	QQCDILPLS	270
CDRL3-61	QQYDNLPLA	271
CDRL3-62	QQYDSLPIT	272
CDRL3-63	QQYDNLPIT	273
CDRL3-64	QHYDNLPIT	274
CDRL3-65	QHYDNLPIT	274

FIGURE 6F

HEAVY CHAIN CDRS

NAME	NAME	SEQUENCE	SEQ ID NO:
CDRH1-1	CDRH1-10.1	GYTFTSYGIS	275
CDRH1-2	CDRH1-10	GYTFTSYGIS	275
CDRH1-3	CDRH1-42	GYTFTGHYMH	276
CDRH1-4	CDRH1-40	GYTFTGYYMH	277
CDRH1-5	CDRH1-30	GYTLTELSMH	278
CDRH1-6	CDRH1-31	GYTLTELSMH	278
CDRH1-7	CDRH1-29	GFSLSNARMGVS	279
CDRH1-8	CDRH1-20	GFSLSNARMGVS	279
CDRH1-9	CDRH1-65	GFSLSTGGVGVG	280
CDRH1-10	CDRH1-56	GFSLSTGGVGVG	280
CDRH1-11	CDRH1-62	GFSLNTGGVGVG	281
CDRH1-12	CDRH1-2	GFSLSTGGVGVG	280
CDRH1-13	CDRH1-59	GFSLSTGGVGVG	280
CDRH1-14	CDRH1-57	GFSLSTGGVGVG	280
CDRH1-15	CDRH1-64	GFSLSTGGVGVG	280
CDRH1-16	CDRH1-41	GFPFSRYSMN	282
CDRH1-17	CDRH1-45	GFTFSSYAMN	283
CDRH1-18	CDRH1-47	GFTFSSYAMS	284
CDRH1-19	CDRH1-51	GFTFSSYAMS	284
CDRH1-20	CDRH1-52	GFTFSSYAMS	284
CDRH1-21	CDRH1-13	GFTFSSYGMH	285
CDRH1-22	CDRH1-14	GFTFSSYGMH	285
CDRH1-23	CDRH1-1	GFTFSSYGMH	285
CDRH1-24	CDRH1-22	GFTFSSYDMH	286
CDRH1-25	CDRH1-23	GFTFSSYDMH	286
CDRH1-26	CDRH1-12	GFTFSSYGMH	285
CDRH1-27	CDRH1-5	GFTFSSYGMH	285
CDRH1-28	CDRH1-15	GFTFSSYGMH	285
CDRH1-29	CDRH1-7	GFTFSSYGMH	285
CDRH1-30	CDRH1-61	GFTFRSHGMH	287
CDRH1-31	CDRH1-39	GFTFSAYSMN	288
CDRH1-32	CDRH1-34	GFTFSSYSMN	289
CDRH1-33	CDRH1-6	GFTFSSYSMN	289
CDRH1-34	CDRH1-35	GFTFSSYSMN	289
CDRH1-35	CDRH1-21	GGSVSSGGYYWS	290
CDRH1-36	CDRH1-8	GGSISRGGYYWS	291
CDRH1-37	CDRH1-9	GGSISRGGYYWS	291
CDRH1-38	CDRH1-18	GGSISSGGYYWS	292

FIGURE 7A

NAME	NAME	SEQUENCE	SEQ ID NO:
CDRH1-39	CDRH1-24	GGSISSGGYYWS	292
CDRH1-40	CDRH1-25	GGSISSGGYYWS	292
CDRH1-41	CDRH1-26	GGSISSGGYYWS	292
CDRH1-42	CDRH1-27	GGSISSGGYYWS	292
CDRH1-43	CDRH1-38	GGSISSGGYYWS	292
CDRH1-44	CDRH1-54	GGSISSGDYYWN	293
CDRH1-45	CDRH1-55	GGSISSGDYYWN	293
CDRH1-46	CDRH1-43	GGSFSGYYWS	294
CDRH1-47	CDRH1-44	GGSFSGYYWS	294
CDRH1-48	CDRH1-49	GGSFSGYYWS	294
CDRH1-49	CDRH1-50	GGSFSGYYWS	294
CDRH1-50	CDRH1-53	GGSFSGYYWS	294
CDRH1-51	CDRH1-33	GGSISSYYWS	295
CDRH1-52	CDRH1-3	GGSVSSGGSYWS	296
CDRH1-53	CDRH1-4	GGSVSSGGSYWS	296
CDRH1-54	CDRH1-16	GYRFTSYWIG	297
CDRH1-55	CDRH1-17	GYSFTSYWIG	298
CDRH1-56	CDRH1-11	GYSFTSYWIG	298
CDRH1-57	CDRH1-37	GDSVSSYSAAWN	299
CDRH1-58	CDRH1-39.1	GFTFSAYSMN	288
CDRH2-1	CDRH2-10.1	WISASNGNTNYAQKLQD	300
CDRH2-2	CDRH2-10	WISASNGNTNYAQKLQD	300
CDRH2-3	CDRH2-42	WINPNSGGTNCAQKFQG	301
CDRH2-4	CDRH2-40	WINPNSGGTNHTQKFQG	302
CDRH2-5	CDRH2-30	SFDPEDGETIYAQKFQG	303
CDRH2-6	CDRH2-31	SFDPEDGETIYAQKFQG	303
CDRH2-7	CDRH2-29	HIFSNDEKSYSTSLKS	304
CDRH2-8	CDRH2-20	LIFSNDEKSYSTSLKS	305
CDRH2-9	CDRH2-65	LIYWNDDKRYSPSLKS	306
CDRH2-10	CDRH2-56	LIYWNDDKRYSPSLKS	306
CDRH2-11	CDRH2-62	LIYWNDDKRYSPSLKS	306
CDRH2-12	CDRH2-2	LIYWNDDKRYSPSLKS	306
CDRH2-13	CDRH2-59	LIYWNVEKRYSPSLRS	307
CDRH2-14	CDRH2-57	LIYWNDDKRYSPSLKS	306
CDRH2-15	CDRH2-64	LIYWNDDKRYSPSLKS	306
CDRH2-16	CDRH2-41	AISSSSSYIYYADSVKG	308
CDRH2-17	CDRH2-45	AISGSGGSTYYADSVKG	309
CDRH2-18	CDRH2-47	AISGSGGSTYYADSVKG	309
CDRH2-19	CDRH2-51	AISGSGGSTYYADSVKG	309
CDRH2-20	CDRH2-52	AISGSGGSTYYADSVKG	309

FIGURE 7B

NAME	NAME	SEQUENCE	SEQ ID NO:
CDRH2-21	CDRH2-13	FISDDGSTKYYADSVKG	310
CDRH2-22	CDRH2-14	FISDDGSTKYYADSVKG	310
CDRH2-23	CDRH2-1	VIWYDGSNKYYADSVKG	311
CDRH2-24	CDRH2-22	VIWYDGSIKYYADSVKG	312
CDRH2-25	CDRH2-23	VIWYDGSIKYYADSVKG	312
CDRH2-26	CDRH2-12	VIWYDGSNKYYADSVKG	311
CDRH2-27	CDRH2-5	VIWSDGSNKYYADSVKG	313
CDRH2-28	CDRH2-15	VIWDDGSNQYYTDSVKG	314
CDRH2-29	CDRH2-7	VIWYDGSNKRYVDSVKG	315
CDRH2-30	CDRH2-61	VIWYDGSNKNYADSVRG	316
CDRH2-31	CDRH2-39	YISSSGRTIYYADSVKG	317
CDRH2-32	CDRH2-34	HISSSSRTIYYADSVKG	318
CDRH2-33	CDRH2-6	HISRSSRTIYYADSVKG	319
CDRH2-34	CDRH2-35	HISRSSRTIYYADSVKG	319
CDRH2-35	CDRH2-21	YIHSSGSTYYNPSLKS	320
CDRH2-36	CDRH2-8	YIYHSGSTYYNPSLKS	321
CDRH2-37	CDRH2-9	YIYHSGSTYYNPSLKS	321
CDRH2-38	CDRH2-18	YIYYSGSTYYNPSLKS	322
CDRH2-39	CDRH2-24	YIHYSGSTYYNPSLKS	323
CDRH2-40	CDRH2-25	YIHYSGSTYYNPSLKS	323
CDRH2-41	CDRH2-26	YIHSSGSTYYNPSLKS	320
CDRH2-42	CDRH2-27	YIHSSGSTYYNPSLKS	320
CDRH2-43	CDRH2-38	YIHYSGSTYYNPSLKS	323
CDRH2-44	CDRH2-54	YIYYSGGTYYNPSLKS	324
CDRH2-45	CDRH2-55	YIYYSGGTYYNPSLKS	324
CDRH2-46	CDRH2-43	EINHSGSTNYNPSLKS	325
CDRH2-47	CDRH2-44	EINHSGSTNYNPSLKS	325
CDRH2-48	CDRH2-49	EINHSGSTNYNPSLKS	325
CDRH2-49	CDRH2-50	EINHSGSTNYNPSLKS	325
CDRH2-50	CDRH2-53	EINHSGSTNYNPSLKS	325
CDRH2-51	CDRH2-33	RIYTSGTTNYNPSLKS	326
CDRH2-52	CDRH2-3	YIYYSGSTNYNPSLKS	327
CDRH2-53	CDRH2-4	YIYYSGSTNYNPSLKS	327
CDRH2-54	CDRH2-16	IIYPDDSDTRYSPSFQG	328
CDRH2-55	CDRH2-17	IIYPDDSDARYSPSFQG	329
CDRH2-56	CDRH2-11	IIYPGDSDIRYSPSFQG	330
CDRH2-57	CDRH2-37	RTYCRSKWYNDYAVSVKS	331
CDRH2-58	CDRH2-39.1	YISSSGRTIYYADSVKG	317
CDRH3-1	CDRH3-10.1	EDNWNYGFFDY	332
CDRH3-2	CDRH3-10	EDNWNYGFFDY	332

FIGURE 7C

NAME	NAME	SEQUENCE	SEQ ID NO:
CDRH3-3	CDRH3-42	SIAVALDY	333
CDRH3-4	CDRH3-40	SIAVALDY	333
CDRH3-5	CDRH3-30	EGDGGYYYYGMDV	334
CDRH3-6	CDRH3-31	EGDGGYYYYGMDV	334
CDRH3-7	CDRH3-29	MYSSGWYGVFDY	335
CDRH3-8	CDRH3-20	VYSSGWSFYGMDV	336
CDRH3-9	CDRH3-65	RRELPFDY	337
CDRH3-10	CDRH3-56	RNWTPFDY	338
CDRH3-11	CDRH3-62	RLELPFDY	339
CDRH3-12	CDRH3-2	RREVPFDY	340
CDRH3-13	CDRH3-59	RHTNPFEY	341
CDRH3-14	CDRH3-57	RGELPFDY	342
CDRH3-15	CDRH3-64	RGELPFDY	342
CDRH3-16	CDRH3-41	DRVGATPDAFDI	343
CDRH3-17	CDRH3-45	EGIAVAGTAEYYYYYAMDV	344
CDRH3-18	CDRH3-47	EGIAARDSYYYYAMDV	345
CDRH3-19	CDRH3-51	EGIAGRDSYYYYGMDV	346
CDRH3-20	CDRH3-52	EGIAGRDSYYYYGMDV	346
CDRH3-21	CDRH3-13	SYYDSSGYYYGFDY	347
CDRH3-22	CDRH3-14	SYYDSSGYYYGFDY	347
CDRH3-23	CDRH3-1	NVIDY	348
CDRH3-24	CDRH3-22	GGATGAEYFQH	349
CDRH3-25	CDRH3-23	GGATGAEYFQH	349
CDRH3-26	CDRH3-12	LWFGETFDY	350
CDRH3-27	CDRH3-5	NLPFDY	351
CDRH3-28	CDRH3-15	SHYGGDYDYYGMDV	352
CDRH3-29	CDRH3-7	DGWQQQAPFDY	353
CDRH3-30	CDRH3-61	WGISAPFDC	354
CDRH3-31	CDRH3-39	WAPFDY	355
CDRH3-32	CDRH3-34	DGYNWNGGGNYYGMDV	356
CDRH3-33	CDRH3-6	DGYNWNNGGYYYGMDV	357
CDRH3-34	CDRH3-35	DGYNWNNGGYYYGMDV	357
CDRH3-35	CDRH3-21	GPYYGMDV	358
CDRH3-36	CDRH3-8	ALRGIVLMVYVLGALDI	359
CDRH3-37	CDRH3-9	ALRGIVLMVYVLGALDI	359
CDRH3-38	CDRH3-18	DETVVRGLIRYCYGMDV	360
CDRH3-39	CDRH3-24	DRGGGDYGRMDV	361
CDRH3-40	CDRH3-25	DRGGGDYGRMDV	361
CDRH3-41	CDRH3-26	SNNYGCFAL	362
CDRH3-42	CDRH3-27	SNNYGCFAL	362

FIGURE 7D

NAME	NAME	SEQUENCE	SEQ ID NO:
CDRH3-43	CDRH3-38	GYNYGLYYYDSSGYPSYYYGMDV	363
CDRH3-44	CDRH3-54	TYYDILTGYPFYFDY	364
CDRH3-45	CDRH3-55	TYYDILTGYPFYFDY	364
CDRH3-46	CDRH3-43	GGYSSSWYWFDP	365
CDRH3-47	CDRH3-44	GGYSSSWFWFDP	366
CDRH3-48	CDRH3-49	GGYSSSWFWFDP	366
CDRH3-49	CDRH3-50	GGYSSSWFWFDP	366
CDRH3-50	CDRH3-53	GGYSSSWFWFDP	366
CDRH3-51	CDRH3-33	DGYSYGHYYYYGMDV	367
CDRH3-52	CDRH3-3	SALRYFDWLFSDVSDI	368
CDRH3-53	CDRH3-4	SALRYFDWLFSDVSDI	368
CDRH3-54	CDRH3-16	QKSYGYSYFDY	369
CDRH3-55	CDRH3-17	QGYGSGWGYFDY	370
CDRH3-56	CDRH3-11	QGLAVAGTSYYYYYGMDV	371
CDRH3-57	CDRH3-37	DRAVAGYYYGMDV	372
CDRH3-58	CDRH3-39.1	WAPFDY	355

FIGURE 7E

LIGHT CHAIN FRS

NAME	SEQUENCE	SEQ ID NO:
FRL1-1	DVVMTQSPLSLPVTLGQPASISC	388
FRL1-2	DVVMTQSPLSLPVTLGQPASISC	388
FRL1-3	DVVMTQSPLSLPVTLGQPASISC	389
FRL1-4	DVVMTQSPLSLPVTLGQPASISC	389
FRL1-5	DIVMTQTPLSLSVTPGQPASISC	390
FRL1-6	DIVMTQTPLSLSVTPGQPASISC	390
FRL1-7	DIVMTQTPLSLSVTPGQPASISC	390
FRL1-8	DIVMTQTPLSLSVTPGQPASISC	391
FRL1-9	DIVMTQTPLSLSVTPGQPASISC	391
FRL1-11	DIQMTQSPSSLSASVGDRVTITC	392
FRL1-12	DIQMTQSPSSLSASVGDRVTIIC	392
FRL1-13	NIVMTQTPLSSPVTLGQPASISC	393
FRL1-14	NIVMTQTPLSSPVTLGQPASISC	393
FRL1-15	EIVMTQTPLSSPVTLGQPASISC	393
FRL1-16	EIVLTQSPGTLSLSPGERATLSC	394
FRL1-17	EIVLTQSPGTLSLSPGERATLSC	395
FRL1-18	DIQMTQSPSSLSASVGDRVTITC	396
FRL1-19	DIVMTQSPDSLAVSLGERATINC	397
FRL1-20	DIVMTQSPDSLAVSLGERATINC	397
FRL1-21	DIVMTQSPDSLAVSLGERATINC	398
FRL1-22	DIVMTQSPDSLAVSLGERATINC	398
FRL1-23	DIVMTQSPDSLAVSLGERATINC	398
FRL1-24	DIVMTQSPDSLTVSLGERATINC	398
FRL1-25	DIVMTQSPDSLTVSLGERATINC	398
FRL1-26	DIVMTQSPDSLAVSLGERATINC	398
FRL1-27	DIVMTQSPDSLAVSLGERATINC	398
FRL1-28	DIVMTQSPDSLAVSLGERATINC	399
FRL1-29	DIVMTQSPDSLAVSLGERATINC	399
FRL1-30	DIVMTQSPDSLAVSLGERATINC	398
FRL1-31	DIVMTQSPDSLAVSLGERATINC	398
FRL1-32	DIVMTQSPDSLAVSLGERATINC	398
FRL1-33	DIVMTQSPDSLAVSLGERATINC	398
FRL1-34	DIQMTQSPSSLSASVGDRVTITC	400
FRL1-35	DIQMTQSPSSLSASVGDRVAITC	401

FIGURE 8A

NAME	SEQUENCE	SEQ ID NO:
FRL1-36	EIVMTQSPATLSVSPGERATLSC	402
FRL1-37	EIVMTQSPATLSVSPGERATLSC	402
FRL1-38	DIQMTQSPSSVSASVGDRVTITC	403
FRL1-39	DIQMTQSPSSLSASVGDRVTITC	404
FRL1-40	DIQMTQSPSSLSASLGDRVTITC	403
FRL1-41	DIQMTQSPSSLSASVGDRVTITC	405
FRL1-42	DIQMTQSPSSRSASVGDRVTITC	403
FRL1-43	DIQMTQSPSSLSASVGDRVTITC	406
FRL1-44	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-45	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-46	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-47	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-48	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-49	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-50	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-51	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-52	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-53	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-54	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-55	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-56	DIQMTQSPSSLSASVGDRVTITC	407
FRL1-57	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-58	DIQMTQSPSSLSASVGDRVAITC	403
FRL1-59	DIQMTQSPSSLSASVGDRVAITC	403
FRL1-60	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-61	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-62	DIQMTQSPSSLSASVGDGVTITC	403
FRL1-63	DIQMTQSPSSLSASVGDRVTITC	408
FRL1-64	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-65	DIQMTQSPSSLSASVGDRVTITC	403
FRL2-1	WFQQRPGQSPRRLIY	408
FRL2-2	WFQQRPGQSPRRLIY	408
FRL2-3	WLQQRPGQSPRRLIY	409
FRL2-4	WLQQRPGQSPRRLIY	409
FRL2-5	WYLQKPGQPPQLLIY	410
FRL2-6	WYLQKPGQPPQLLIY	410

FIGURE 8B

NAME	SEQUENCE	SEQ ID NO:
FRL2-7	WYLQKPGQPPQLLIY	410
FRL2-8	WFLQKPGQPPQPLIY	411
FRL2-9	WFLQKPGQPPQPLIY	411
FRL2-11	WYQQKPGKVPKLLIY	412
FRL2-12	WYQQKPGKVPKLLIY	412
FRL2-13	WLQQRPGQPPRLLIY	413
FRL2-14	WLQQRPGQPPRLLIY	413
FRL2-15	WLQQRPGQPPRLLIY	413
FRL2-16	WYQQKPGQAPRLLIS	414
FRL2-17	WYQQKPGQAPRLLIY	415
FRL2-18	WYQQKPGKAPKRLIY	416
FRL2-19	WYQQKPGQPPKLFIY	417
FRL2-20	WYQQKPGQPPKLFIY	417
FRL2-21	WYQQKPGQPPKLLIY	418
FRL2-22	WYQQKPGQPPKLLIY	418
FRL2-23	WYQQKPGQPPKLLIY	418
FRL2-24	WYQQKPGQPPKLLIY	418
FRL2-25	WYQQKPGQPPKLLIY	418
FRL2-26	WYQQKPGQPPKLLIY	418
FRL2-27	WYQQKPGQPPKLLIY	418
FRL2-28	WYQQKPGQPPKVLIY	419
FRL2-29	WYQQKPGQPPKVLIY	419
FRL2-30	WYQQKPGQPPKLLIY	418
FRL2-31	WYQQKPGQPPKLLIY	418
FRL2-32	WYQQKPGQPPKLLIY	418
FRL2-33	WYQQKPGQPPKLLIY	418
FRL2-34	WFQQKPGKAPKSLIY	420
FRL2-35	WLQQKPGKAPKSLIY	421
FRL2-36	WYQQDPGQAPRLLIY	422
FRL2-37	WYQQDPGQAPRLLIY	422
FRL2-38	WYQQKPGKAPKLLIY	423
FRL2-39	WYQQKPGKAPKFLIY	424
FRL2-40	WYQQKPGKAPKLLIY	423
FRL2-41	WYQQRPGNAPKLLIY	425
FRL2-42	WYQQKPGKAPKLLIY	423
FRL2-43	WYQQKPGKAPKVLIY	426

FIGURE 8C

NAME	SEQUENCE	SEQ ID NO:
FRL2-44	WYQQKPGKAPKLLIY	423
FRL2-45	WYQQKPGKAPKLLIY	423
FRL2-46	WYQQKPGKAPKLLIY	423
FRL2-47	WYQQKPGKAPKLLIY	423
FRL2-48	WYQQKPGKAPKLLIY	423
FRL2-49	WYQQKPGKAPKLLIY	423
FRL2-50	WYQQKPGKAPKLLIY	423
FRL2-51	WYQQKPGKAPKLLIY	423
FRL2-52	WYQQKPGKAPKLLIY	423
FRL2-53	WYQQKPGKAPKLLIY	423
FRL2-54	WYQQKPGKAPKLLIY	423
FRL2-55	WYQQKPGKAPKLLIY	423
FRL2-56	WYQQKPGKAPELLIY	427
FRL2-57	WYQQKPGKAPKLLIY	423
FRL2-58	WYQQKPGKAPKLLIY	423
FRL2-59	WYQQKPGKAPKLLIY	423
FRL2-60	WYQQKPGKAPKLLIY	423
FRL2-61	WYQQKPGKAPKLLIY	423
FRL2-62	WYQQKPGKAPKLLIY	423
FRL2-63	WYQQKLGKAPKLLIH	428
FRL2-64	WYQQKPGKAPKLLIY	423
FRL2-65	WYQQKPGKAPKLLIY	423
FRL3-1	GVPDRFNGSGSGTDFTLKISRVEAEDVGVYYC	429
FRL3-2	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	430
FRL3-3	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	430
FRL3-4	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	430
FRL3-5	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	430
FRL3-6	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	430
FRL3-7	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	430
FRL3-8	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	430
FRL3-9	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	430
FRL3-11	GVPSRFSGSGSGTDFTLTISSLQPEDVATYYC	431
FRL3-12	GVPSRFSGSGSGTDFTLTISSLQPEDVATYYC	431
FRL3-13	GVPDRFSGSGAGTDFTLKISRVEAEDVGVYYC	432
FRL3-14	GVPDRFSGSGAGTDFTLKISRVEAEDVGVYYC	432

FIGURE 8D

NAME	SEQUENCE	SEQ ID NO:
FRL3-15	GVPDRFSGTGAGTDFTLKISRVEAEDVGVYYC	433
FRL3-16	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	434
FRL3-17	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	434
FRL3-18	GVPSRFSGSGSGTEFTLTISSLQPEDFATYYC	435
FRL3-19	GVPDRFTGSGSGTDFTLTISSLQAEDVAVYYC	436
FRL3-20	GVPDRFTGSGSGTDFTLTISSLQAEDVAVYYC	436
FRL3-21	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC	437
FRL3-22	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYFC	438
FRL3-23	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYFC	438
FRL3-24	GVPDRFGGSGSGTDFTLTISSLQAEDVAVYYC	439
FRL3-25	GVPDRFGGSGSGTDFTLTISSLQAEDVAVYYC	439
FRL3-26	GVPDRFSGSGSGTDFTLTISSLQADDVAVYYC	440
FRL3-27	GVPDRFSGSGSGTDFTLTISSLQADDVAVYYC	440
FRL3-28	GVPDRFSGSGSGTDFTLTISGLQAEDVALYYC	441
FRL3-29	GVPDRFSGSGSGTDFTLTISGLQAEDVALYYC	441
FRL3-30	GVPDRFSGSGSGTDFTLTISSLQAEDVAVFYC	442
FRL3-31	GVPDRFSGSGSGTDFTLTISSLQAEDVAVFYC	442
FRL3-32	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYFC	438
FRL3-33	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYFC	438
FRL3-34	GVPSKFSGSGSGTDFTLTISSLQPEDFATYYC	443
FRL3-35	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	444
FRL3-36	GIPARFSGSGSGTEFTLTISSLQSEDFAVYYC	445
FRL3-37	GIPARFSGSGSGTEFTLTISSLQSEDFAVYYC	445
FRL3-38	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	444
FRL3-39	GVPSRFSGSGSGTDFTLTISSLQPEDFAAYYC	446
FRL3-40	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	444
FRL3-41	GVPSRVSGSGSGTDFTLTIRSLQPEDFATYYC	447
FRL3-42	GVPSRFSGSGSGTDFTLTLSSLQPEDFATYYC	448
FRL3-43	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	444
FRL3-44	GVPSRFSGSGSGTDFTLTISSLQPENFATYYC	449
FRL3-45	GVPSRFSGSGSGTDFTLTFSSLQPEDFATYYC	450
FRL3-46	GVPSRFSGSGSGTDFTLTLSSLQPEDFASYYC	451
FRL3-47	GVPSRFSGSGSGTDFTLTLSSLQPEDFASYYC	451
FRL3-48	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	444
FRL3-49	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	444
FRL3-50	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	444

FIGURE 8E

NAME	SEQUENCE	SEQ ID NO:
FRL3-51	GVPSRFSGSGSGTDFTLTISSLQPEDFASYYC	452
FRL3-52	GVPSRFSGSGSGTDFTLTISSLQPEDFASYYC	452
FRL3-53	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	444
FRL3-54	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	453
FRL3-55	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	453
FRL3-56	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	453
FRL3-57	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	453
FRL3-58	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	453
FRL3-59	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	453
FRL3-60	GVPSRFSGSGSETDFTFTISSLQPEDIATYYC	454
FRL3-61	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	453
FRL3-62	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	453
FRL3-63	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	453
FRL3-64	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	453
FRL3-65	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	453
FRL4-1	FGQGTRLEIK	455
FRL4-2	FGQGTRLEIK	455
FRL4-3	FGQGTRLEIK	455
FRL4-4	FGQGTRLEIK	455
FRL4-5	FGQGTKLEIK	457
FRL4-6	FGGGTKVEIK	458
FRL4-7	FGGGTKVEIK	458
FRL4-8	FGHGTRLEIK	459
FRL4-9	FGHGTRLEIK	459
FRL4-11	FGPGTKVDIK	460
FRL4-12	FGGGTKVEIK	458
FRL4-13	FGPGTKVDIK	460
FRL4-14	FGPGTKVDIK	460
FRL4-15	FGGGTKVEIK	458
FRL4-16	FGQGTKVEIK	461
FRL4-17	FGQGTKLEIK	457
FRL4-18	FGQGTKVEIK	461
FRL4-19	FGQGTKVEIK	461
FRL4-20	FGQGTKVEIK	461
FRL4-21	FGQGTKVEIK	461
FRL4-22	FGQGTKVEIK	461

FIGURE 8F

NAME	SEQUENCE	SEQ ID NO:
FRL4-23	FGQGTKVEIK	461
FRL4-24	FGQGTKVEIK	461
FRL4-25	FGQGTKVEIK	461
FRL4-26	FGPGTKVEIK	462
FRL4-27	FGPGTKVEIK	462
FRL4-28	FGQGTKLEIK	457
FRL4-29	FGQGTKLEIK	457
FRL4-30	FGGGTKVAIK	463
FRL4-31	FGGGTKVAIK	463
FRL4-32	FGGGTKVEIK	458
FRL4-33	FGGGTKVEIK	458
FRL4-34	FGPGTKVDIK	460
FRL4-35	FGPGTKMDIK	464
FRL4-36	FGQGTKVEIK	461
FRL4-37	FGQGTKVEIK	461
FRL4-38	FGQGTKVEFK	465
FRL4-39	FGPGTKVDIK	460
FRL4-40	FGGGTKVEIK	458
FRL4-41	FGGGTKVEIK	458
FRL4-42	FGQGTRLEIK	455
FRL4-43	FGQGTRLEII	456
FRL4-44	FGQGTRLEIK	455
FRL4-45	FGQGTRLEIK	455
FRL4-46	FGQGTRLEIK	455
FRL4-47	FGQGTRLEIK	455
FRL4-48	FGQGTRLEIK	455
FRL4-49	FGQGTRLEIK	455
FRL4-50	FGQGTRLEIK	455
FRL4-51	FGQGTRLEIK	455
FRL4-52	FGQGTRLEIK	455
FRL4-53	FGQGTRLEIK	455
FRL4-54	FGPGTKVDIK	460
FRL4-55	FGPGTKVDIK	460
FRL4-56	FGGGTKVEIK	458
FRL4-57	FGGGTKVEIK	458
FRL4-58	FGGGTKVEIK	458

FIGURE 8G

NAME	SEQUENCE	SEQ ID NO:
FRL4-59	FGGGTKVEIK	458
FRL4-60	FGGGTKVEIK	458
FRL4-61	FGGGTKVEIR	466
FRL4-62	FGQGTRLEIK	455
FRL4-63	FGQGTRLEIK	455
FRL4-64	FGQGTRLEIK	455
FRL4-65	FGQGTRLEIK	455

FIGURE 8H

HEAVY CHAIN FRS

NAME	NAME	SEQUENCE	SEQ ID NO:
FRH1-1	FRH1-10.1	QVQLVQSGAEVKKPGASVKVSCKAS	467
FRH1-2	FRH1-10	QVQLVQSGAEVKKPGASVKVSCKAS	467
FRH1-3	FRH1-42	QVHLVQSGAEVKKPGASVKVSCKVS	468
FRH1-4	FRH1-40	QVQLVQSGAEVKKPGASVKVSCKAS	467
FRH1-5	FRH1-30	QVQLVQSGAEVRKPGASVKVSCKVS	469
FRH1-6	FRH1-31	QVQLVQSGAEVRKPGASVKVSCKVS	469
FRH1-7	FRH1-29	QVTLKESGPVLVKPTETLTLTCTVS	470
FRH1-8	FRH1-20	QVTLKESGPVLVKPTETLTLTCTVS	470
FRH1-9	FRH1-65	QITLKESGPTLVKPTQTLTLTCTFS	471
FRH1-10	FRH1-56	QITLKESGPTLVKPTQTLTLTCTFS	471
FRH1-11	FRH1-62	QITLKESGPTLVKPTQTLTLTCTFS	471
FRH1-12	FRH1-2	QITLKESGPTLVKPTQTLTLTCTFS	471
FRH1-13	FRH1-59	QITLKESGPTLVKPTQTLTLTCTFS	471
FRH1-14	FRH1-57	QITLKESGPTLVKPTQTLTLTCTFS	471
FRH1-15	FRH1-64	QITLKESGPTLVKPTQTLTLTCTFS	471
FRH1-16	FRH1-41	EVQLVESGGGLVKPGGSLRLSCAAS	472
FRH1-17	FRH1-45	EVQLLESGGGLVQPGGSLRLSCAAS	473
FRH1-18	FRH1-47	EVQLLESGGGLVQPGGSLRLSCAAS	473
FRH1-19	FRH1-51	EVQLLESGGGLVQPGGSLRLSCTAS	474
FRH1-20	FRH1-52	EVQLLESGGGLVQPGGSLRLSCTAS	474
FRH1-21	FRH1-13	QVQLVESGGGVVQPGRSLRLSCAAS	475
FRH1-22	FRH1-14	QVQLVESGGGVVQPGRSLRLSCAAS	475
FRH1-23	FRH1-1	QVQLVESGGGVVQPGRSLRLSCAAS	475
FRH1-24	FRH1-22	QVQLVESGGGVVQPGRSLRLSCAAS	475
FRH1-25	FRH1-23	QVQLVESGGGVVQPGRSLRLSCAAS	475
FRH1-26	FRH1-12	QVQLVESGGGVVQPGRSLRLSCAAS	475
FRH1-27	FRH1-5	QVQLVESGGGVVQPGRSLRLSCAAS	475
FRH1-28	FRH1-15	QVQLVESGGGVVQPGRSLRLSCAAS	475
FRH1-29	FRH1-7	QVQLVESGGGVVQPGRSLRLSCAAS	475
FRH1-30	FRH1-61	QVQLVESGGGVVQPGRSLRLSCAAS	475
FRH1-31	FRH1-39	EVQLVESGGGLVQPGGSLRLSCAAS	476
FRH1-32	FRH1-34	EVQLVESGGGLVQPGGSLRLSCAAS	476
FRH1-33	FRH1-6	EVQLVESGGGLVQPGGSLRLSCAAS	476
FRH1-34	FRH1-35	EVQLVESGGGLVQPGGSLRLSCAAS	476
FRH1-35	FRH1-21	QVQLQESGPGLVKPSQTLSLTCTVS	477
FRH1-36	FRH1-8	QVQLQESGPGLVKPSQTLSLTCTVS	477
FRH1-37	FRH1-9	QVQLQESGPGLVKPSQTLSLTCTVS	477

FIGURE 9A

NAME	NAME	SEQUENCE	SEQ ID NO:
FRH1-38	FRH1-18	QVQLQESGPGLVKPSQTLSLTCTVS	477
FRH1-39	FRH1-24	QVQLQESGPGLVKPSQTLSLNCTVS	478
FRH1-40	FRH1-25	QVQLQESGPGLVKPSQTLSLNCTVS	478
FRH1-41	FRH1-26	QVQLQESGPGLVKPSQTLSLTCTVS	477
FRH1-42	FRH1-27	QVQLQESGPGLVKPSQTLSLTCTVS	477
FRH1-43	FRH1-38	QVQLQESGPGLVKPSQTLSLTCTVS	477
FRH1-44	FRH1-54	QVQLQESGPGLVKPSQTLSLTCTVS	477
FRH1-45	FRH1-55	QVQLQESGPGLVKPSQTLSLTCTVS	477
FRH1-46	FRH1-43	QVQLQQWGAGLLKPSETLSLTCAVY	479
FRH1-47	FRH1-44	QVQLQQWGAGLLKPSETLSLTCAVY	479
FRH1-48	FRH1-49	QVQLQQWGAGLLKPSETLSLTCAVY	479
FRH1-49	FRH1-50	QVQLQQWGAGLLKPSETLSLTCAVY	479
FRH1-50	FRH1-53	QVQLQQWGAGLLKPSETLSLTCAVY	479
FRH1-51	FRH1-33	QVQLQESGPGLVKPSETLSLTCTVS	480
FRH1-52	FRH1-3	QVQLQESGPGLVKPSETLSLTCTVS	480
FRH1-53	FRH1-4	QVQLQESGPGLVKPSETLSLTCTVS	480
FRH1-54	FRH1-16	EVQLVQSGAELKKPGESLKISCKGS	481
FRH1-55	FRH1-17	EVQLVQSGAEVKKPGESLKISCKGS	482
FRH1-56	FRH1-11	EVQLVQSGAEVKKPGESLKISCKGS	482
FRH1-57	FRH1-37	QVQLQQSGPGLVKPSQTLSLTCAIS	483
FRH1-58	FRH1-39.1	EVQLVESGGGLVQPGGSLRLSCAAS	476
FRH2-1	FRH2-10.1	WVRQAPGQGLEWMG	484
FRH2-2	FRH2-10	WVRQAPGQGLEWMG	484
FRH2-3	FRH2-42	WVRQAPGQGLEWMG	484
FRH2-4	FRH2-40	WVRQAPGQGLEWMG	484
FRH2-5	FRH2-30	WVRQAPGKGLEWMG	485
FRH2-6	FRH2-31	WVRQAPGKGLEWMG	485
FRH2-7	FRH2-29	WIRQPPGKALEWLA	486
FRH2-8	FRH2-20	WIRQPPGKALEWLV	487
FRH2-9	FRH2-65	WIRQPPGKALEWLA	486
FRH2-10	FRH2-56	WIRQPPGKALEWLA	486
FRH2-11	FRH2-62	WIRQPPGKALEWLA	486
FRH2-12	FRH2-2	WIRQPPGKALEWLA	486
FRH2-13	FRH2-59	WIRQPPGKALEWLA	486
FRH2-14	FRH2-57	WIRQPPGKALEWLA	486
FRH2-15	FRH2-64	WIRQPPGKALEWLA	486
FRH2-16	FRH2-41	WVRQAPGKGLEWVS	488
FRH2-17	FRH2-45	WVRQAPGKGLEWVS	488
FRH2-18	FRH2-47	WVRQAPGKGLEWVS	488
FRH2-19	FRH2-51	WVRQAPGKGLEWVS	488

FIGURE 9B

NAME	NAME	SEQUENCE	SEQ ID NO:
FRH2-20	FRH2-52	WVRQAPGKGLEWVS	488
FRH2-21	FRH2-13	WVRQAPGKGLEWVA	489
FRH2-22	FRH2-14	WVRQAPGKGLEWVA	489
FRH2-23	FRH2-1	WVRQAPGKGLEWVA	489
FRH2-24	FRH2-22	WVRQAPGKGLEWVA	489
FRH2-25	FRH2-23	WVRQAPGKGLEWVA	489
FRH2-26	FRH2-12	WVRQAPGKGLEWVA	489
FRH2-27	FRH2-5	WVRQAPGKGLEWVA	489
FRH2-28	FRH2-15	WVRQAPGKGLEWVA	489
FRH2-29	FRH2-7	WVRQAPGKGLEWVA	489
FRH2-30	FRH2-61	WVRQAPGKGLEWVA	489
FRH2-31	FRH2-39	WVRQAPGKGLEWVS	488
FRH2-32	FRH2-34	WVRQAPGKGLEWVS	488
FRH2-33	FRH2-6	WVRQAPGKGLEWVS	488
FRH2-34	FRH2-35	WVRQAPGKGLEWVS	488
FRH2-35	FRH2-21	WIRQHPGKGLEWIG	490
FRH2-36	FRH2-8	WIRQHPGKGLEWIG	490
FRH2-37	FRH2-9	WIRQHPGKGLEWIG	490
FRH2-38	FRH2-18	WIRQHPGKGLEWIG	490
FRH2-39	FRH2-24	WIRQHPGKGLEWIG	490
FRH2-40	FRH2-25	WIRQHPGKGLEWIG	490
FRH2-41	FRH2-26	WIRQHPGKGLEWIG	490
FRH2-42	FRH2-27	WIRQHPGKGLEWIG	490
FRH2-43	FRH2-38	WIRQHPGKGLEWIG	490
FRH2-44	FRH2-54	WVRQHPGKGLEWIG	491
FRH2-45	FRH2-55	WVRQHPGKGLEWIG	491
FRH2-46	FRH2-43	WIRQPPGKGLEWIG	492
FRH2-47	FRH2-44	WIRQPPGKGLEWIG	492
FRH2-48	FRH2-49	WIRQPPGKGLEWIG	492
FRH2-49	FRH2-50	WIRQPPGKGLEWIG	492
FRH2-50	FRH2-53	WIRQPPGKGLEWIG	492
FRH2-51	FRH2-33	WIRQPAGKGLEWIG	493
FRH2-52	FRH2-3	WIRQPPGKGLEWIG	492
FRH2-53	FRH2-4	WIRQPPGKGLEWIG	492
FRH2-54	FRH2-16	WVRQMPGKGLEWMG	494
FRH2-55	FRH2-17	WVRQMPGKGLEWMG	494
FRH2-56	FRH2-11	WVRQMPGKGLEWMG	494
FRH2-57	FRH2-37	WIRQSPSRGLEWLG	495
FRH2-58	FRH2-39.1	WVRQAPGKGLEWVS	488
FRH3-1	FRH3-10.1	RVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR	496

FIGURE 9C

NAME	NAME	SEQUENCE	SEQ ID NO:
FRH3-2	FRH3-10	RVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR	496
FRH3-3	FRH3-42	RVTMTRDTSISTAYMELSRLRSDDTAVYYCAR	497
FRH3-4	FRH3-40	RVTMTRDTSISTAYMELSRLRSDDTAVYYCAR	497
FRH3-5	FRH3-30	RVTMLEDTSTDTAYMELSSLRSEDTAVYYCAT	498
FRH3-6	FRH3-31	RVTMLEDTSTDTAYMELSSLRSEDTAVYYCAT	498
FRH3-7	FRH3-29	RLTISKDTSKSQVVLTMTNMDPVDTATYYCAR	499
FRH3-8	FRH3-20	RLTISKDTSKSQVVLTMTNMDPVDTATYYCAR	499
FRH3-9	FRH3-65	RLTITKDTSKNQVVLTMTNMDPVDTATYYCAH	500
FRH3-10	FRH3-56	RLTITKDTSKTQVVLTVTDMDPVDTATYYCAH	501
FRH3-11	FRH3-62	RLTITKDTSKNQVVLTMTNMDPVDTATYYCAH	500
FRH3-12	FRH3-2	RLTITKDTSKNQVVLTMTNLDPVDTATYYCAH	502
FRH3-13	FRH3-59	RLTITKATSKNQVVLTMTNMDPVDTATYYCAH	503
FRH3-14	FRH3-57	RLTITKDTSKNQVVLTMTNMDPVDTATYYCAH	500
FRH3-15	FRH3-64	RLTITKDTSKNQVVLTMTNMDPVDTATYYCAH	500
FRH3-16	FRH3-41	RFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR	504
FRH3-17	FRH3-45	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK	505
FRH3-18	FRH3-47	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK	505
FRH3-19	FRH3-51	RFTISRDNSKNTLYLQMNSLRAEDTAEYYCAK	506
FRH3-20	FRH3-52	RFTISRDNSKNTLYLQMNSLRAEDTAEYYCAK	506
FRH3-21	FRH3-13	RFTISRDNSMNTLYLQMNSLRAEDTAVYYCAR	507
FRH3-22	FRH3-14	RFTISRDNSMNTLYLQMNSLRAEDTAVYYCAR	507
FRH3-23	FRH3-1	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	508
FRH3-24	FRH3-22	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	508
FRH3-25	FRH3-23	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	508
FRH3-26	FRH3-12	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCVL	509
FRH3-27	FRH3-5	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	508
FRH3-28	FRH3-15	RFTVSRDNSKNTLFLQMNSLRAEDTAVYYCAR	510
FRH3-29	FRH3-7	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	508
FRH3-30	FRH3-61	RFTISRDNSKNTLDLQMNSLRAEDTAVYYCAR	510
FRH3-31	FRH3-39	RFTISRDNAKNSLFLQMNSLRDEDTAVYYCAL	511
FRH3-32	FRH3-34	RFTISRDNAKNSVYLQMNSLRDEDTAVYYCAR	512
FRH3-33	FRH3-6	RFTISRDNAKNSLYLQMNSLRDEDTAVYYCAR	513
FRH3-34	FRH3-35	RFTISRDNAKNSLYLQMNSLRDEDTAVYYCAR	513
FRH3-35	FRH3-21	RVTISVDTSKNQFSLNLSSVTAADTAVYYCAR	514
FRH3-36	FRH3-8	RVNMSVDTSKNQFSLKLSSVTAADTAVYYCAR	515
FRH3-37	FRH3-9	RVNMSVDTSKNQFSLKLSSVTAADTAVYYCAR	515
FRH3-38	FRH3-18	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	516
FRH3-39	FRH3-24	RITISADTSKNQFSLKLNSVTAADTAVYYCAR	517
FRH3-40	FRH3-25	RITISADTSKNQFSLKLNSVTAADTAVYYCAR	517
FRH3-41	FRH3-26	RITKSVDTSKNQFSLKLSSVTAADTAVYYCAR	518

FIGURE 9D

NAME	NAME	SEQUENCE	SEQ ID NO:
FRH3-42	FRH3-27	RITKSVDTSKNQFSLKLSSVTAADTAVYYCAR	518
FRH3-43	FRH3-38	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAS	519
FRH3-44	FRH3-54	RVTISVDTSKNQFSLKLFSVTAADTAVYFCAR	520
FRH3-45	FRH3-55	RVTISVDTSKNQFSLKLFSVTAADTAVYFCAR	520
FRH3-46	FRH3-43	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	516
FRH3-47	FRH3-44	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	516
FRH3-48	FRH3-49	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	516
FRH3-49	FRH3-50	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	516
FRH3-50	FRH3-53	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	516
FRH3-51	FRH3-33	RVTMSVDTSKNQFSLKLSSVTAADTAVYYCAR	521
FRH3-52	FRH3-3	RVTISIVTSRNQFSLKLSSVTAADTAVYYCAR	522
FRH3-53	FRH3-4	RVTISIVTSRNQFSLKLSSVTAADTAVYYCAR	522
FRH3-54	FRH3-16	QVTISADKSISTAYLQWSSLKASDTAMYYCAR	523
FRH3-55	FRH3-17	QVTISADKSINTAYLQWSSLKASDTAMYYCAR	524
FRH3-56	FRH3-11	QVTISADKSISTAYLQWSSLKASDTAMYYCAR	523
FRH3-57	FRH3-37	RITINPDTSKNQFSLQLNSVTPEDTAVYYCAR	525
FRH3-58	FRH3-39.1	RFTISRDNAKNSLFLQMNSLRDEDTAVYYCAL	511
FRH4-1	FRH4-10.1	WGQGTLVTVSS	526
FRH4-2	FRH4-10	WGQGTLVTVSS	526
FRH4-3	FRH4-42	WGQGTLVTVSS	526
FRH4-4	FRH4-40	WGQGTLVTVSS	526
FRH4-5	FRH4-30	WGQGTTVTVSS	527
FRH4-6	FRH4-31	WGQGTTVTVSS	527
FRH4-7	FRH4-29	WGQGTLVTVSS	526
FRH4-8	FRH4-20	WGQGTTVTVSS	527
FRH4-9	FRH4-65	WGQGTLVTVSS	526
FRH4-10	FRH4-56	WGQGTLVTVSS	526
FRH4-11	FRH4-62	WGQGTLVTVSS	526
FRH4-12	FRH4-2	WGQGTLVTVSS	526
FRH4-13	FRH4-59	WGQGTLVTVSS	526
FRH4-14	FRH4-57	WGQGTLVTVSS	526
FRH4-15	FRH4-64	WGQGTLVTVSS	526
FRH4-16	FRH4-41	WGQGTMVTVSS	528
FRH4-17	FRH4-45	WGQGTTVTVSS	527
FRH4-18	FRH4-47	WGQGTTVTVSS	527
FRH4-19	FRH4-51	WGQGTTVTVSS	527
FRH4-20	FRH4-52	WGQGTTVTVSS	527
FRH4-21	FRH4-13	WGQGTLVTVSS	526
FRH4-22	FRH4-14	WGQGTLVTVSS	526
FRH4-23	FRH4-1	WGQGTLVTVSS	526

FIGURE 9E

NAME	NAME	SEQUENCE	SEQ ID NO:
FRH4-24	FRH4-22	WGQGTLVTVSS	526
FRH4-25	FRH4-23	WGQGTLVTVSS	526
FRH4-26	FRH4-12	WGQGSLVTVSP	529
FRH4-27	FRH4-5	WGQGTLVTVSS	526
FRH4-28	FRH4-15	WGQGTTVTVSS	527
FRH4-29	FRH4-7	WGQGTLVTVSS	526
FRH4-30	FRH4-61	WGQGTLVTVSS	526
FRH4-31	FRH4-39	WGQGTLVTVSS	526
FRH4-32	FRH4-34	WGQGTTVTVSS	527
FRH4-33	FRH4-6	WGQGTTVTVSS	527
FRH4-34	FRH4-35	WGQGTTVTVSS	527
FRH4-35	FRH4-21	WGQGTTVTVSS	527
FRH4-36	FRH4-8	WGQGTKVTVSS	530
FRH4-37	FRH4-9	WGQGTKVTVSS	530
FRH4-38	FRH4-18	WGQGTTVTVSS	527
FRH4-39	FRH4-24	WGQGTTVTVSS	527
FRH4-40	FRH4-25	WGQGTTVTVSS	527
FRH4-41	FRH4-26	WGRGTLVTVSS	531
FRH4-42	FRH4-27	WGRGTLVTVSS	531
FRH4-43	FRH4-38	WGQGTTVTVSS	527
FRH4-44	FRH4-54	WGQGTLVTVSS	526
FRH4-45	FRH4-55	WGQGTLVTVSS	526
FRH4-46	FRH4-43	WGQGTLVTVSS	526
FRH4-47	FRH4-44	WGQGTLVTVSS	526
FRH4-48	FRH4-49	WGQGTLVTVSS	526
FRH4-49	FRH4-50	WGQGTLVTVSS	526
FRH4-50	FRH4-53	WGQGTLVTVSS	526
FRH4-51	FRH4-33	WGQGTTVTVSS	527
FRH4-52	FRH4-3	WGQGTMVTVSS	528
FRH4-53	FRH4-4	WGQGTMVTVSS	528
FRH4-54	FRH4-16	WGQGTLVTVSS	526
FRH4-55	FRH4-17	WGQGTLVTVSS	526
FRH4-56	FRH4-11	WGQGTTVTVSS	527
FRH4-57	FRH4-37	WGQGTTVTVSS	527
FRH4-58	FRH4-39.1	WGQGTLVTVSS	526

FIGURE 9F

FIGURE 10A: Light Chain Variable Regions

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          1                   20                  40                  60                  80
U2-1      DVVMTQSPLS LPVTLGQPAS ISCRSSQSLV YSDGN.TYLN WFQQRPGQSP RRLIYKVSNW DSGVPDRFNG SGSGTDFTLK
U2-2      DVVMTQSPLS LPVTLGQPAS ISCRSSQSLV YSDGN.TYLN WFQQRPGQSP RRLIYKVSNW DSGVPDRFSG SGSGTDFTLK
U2-3      DVVMTQSPLS LPVTLGQPAS ISCRSSQSLV YSDGN.TYLN WLQQRPGQSP RRLIYKVSNW DSGVPDRFSG SGSGTDFTLK
U2-4      DVVMTQSPLS LPVTLGQPAS ISCRSSQSLV YSDGN.TYLN WLQQRPGQSP RRLIYKVSNW DSGVPDRFSG SGSGTDFTLK
U2-5      DIVMTQTPLS LSVTPGQPAS ISCKSSQSLL HSDGK.TYLY WYLQKPGQPP QLLIYEVSNR FSGVPDRFSG SGSGTDFTLK
U2-6      DIVMTQTPLS LSVTPGQPAS ISCKSSQSLL HSDGK.TYLY WYLQKPGQPP QLLIYEVSNR FSGVPDRFSG SGSGTDFTLK
U2-7      DIVMTQTPLS LSVTPGQPAS ISCKSSQSLL HSDGK.TYLY WYLQKPGQPP QLLIYEVSNR FSGVPDRFSG SGSGTDFTLK
U2-8      DIVMTQTPLS LSVTPGQPAS ISCKSSQSLL HSDGK.TYLY WFLQKPGQPP QPLIYEVSNR FSGVPDRFSG SGSGTDFTLK
U2-9      DIVMTQTPLS LSVTPGQPAS ISCKSSQSLL HSDGK.TYLY WFLQKPGQPP QPLIYEVSNR FSGVPDRFSG SGSGTDFTLK
U2-11     DIQMTQSPSS LSASVGDRVT ITCRASQGIA ....N..YLA WYQQKPGKVP KLLIYVASTL QSGVPSRFSG SGSGTDFTLT
U2-12     DIQMTQSPSS LSASVGDRVT IICRASQGIS .ND.....LA WYQQKPGKVP KLLIYAASTL QSGVPSRFSG SGSGTDFTLT
U2-13     NIVMTQTPLS SPVTLGQPAS ISCRSSQSLV HSDGN.TYLS WLQQRPGQPP RLLIYKISNR FSGVPDRFSG SGAGTDFTLK
U2-14     NIVMTQTPLS SPVTLGQPAS ISCRSSQSLV HSDGN.TYLS WLQQRPGQPP RLLIYKISNR FSGVPDRFSG SGAGTDFTLK
U2-15     EIVMTQTPLS SPVTLGQPAS ISCRSSQSLV HSDGN.TYLS WLQQRPGQPP RLLIYKISNR FSGVPDRFSG TGAGTDFTLK
U2-16     EIVLTQSPGT LSLSPGERAT LSCRASQTVI SS.....YLA WYQQKPGQAP RLLISGASSR ATGIPDRFSG SGSGTDFTLT
U2-17     EIVLTQSPGT LSLSPGERAT LSCRASQSVS R.......LA WYQQKPGQAP RLLIYGASRR ATGIPDRFSG SGSGTDFTLT
U2-18     DIQMTQSPSS LSASVGDRVT ITCRASQGIR .ND.....LG WYQQKPGKAP KRLIYAASSL QSGVPSRFSG SGSGTEFTLT
U2-19     DIVMTQSPDS LAVSLGERAT INCKSSQSVL YSSNNKNYLV WYQQKPGQPP KLFIYWASTR ESGVPDRFTG SGSGTDFTLT
U2-20     DIVMTQSPDS LAVSLGERAT INCKSSQSVL YSSNNKNYLV WYQQKPGQPP KLFIYWASTR ESGVPDRFTG SGSGTDFTLT
U2-21     DIVMTQSPDS LAVSLGERAT INCKSSQSVL YSSNNKNYLA WYQQKPGQPP KLLIYWASTR ESGVPDRFSG SGSGTDFTLT
U2-22     DIVMTQSPDS LAVSLGERAT INCKSSQNVL YSSNNKNYLA WYQQKPGQPP KLLIYWASTR ESGVPDRFSG SGSGTDFTLT
U2-23     DIVMTQSPDS LAVSLGERAT INCKSSQNVL YSSNNKNYLA WYQQKPGQPP KLLIYWASTR ESGVPDRFSG SGSGTDFTLT
U2-24     DIVMTQSPDS LTVSLGERAT INCKSSQSVL YSSNNKNYLA WYQQKPGQPP KLLIYWASTR ESGVPDRFGG SGSGTDFTLT
U2-25     DIVMTQSPDS LTVSLGERAT INCKSSQSVL YSSNNKNYLA WYQQKPGQPP KLLIYWASTR ESGVPDRFGG SGSGTDFTLT
U2-26     DIVMTQSPDS LAVSLGERAT INCKSSQSVL YNSNNKNYLA WYQQKPGQPP KLLIYWASTR ESGVPDRFSG SGSGTDFTLT
U2-27     DIVMTQSPDS LAVSLGERAT INCKSSQSVL YNSNNKNYLA WYQQKPGQPP KLLIYWASTR ESGVPDRFSG SGSGTDFTLT
U2-28     DIVMTQSPDS LAVSLGERAT INCKSSQSVL YSSNNKNYLA WYQQKPGQPP KVLIYWASTR KSGVPDRFSG SGSGTDFTLT
U2-29     DIVMTQSPDS LAVSLGERAT INCKSSQSVL YSSNNKNYLA WYQQKPGQPP KVLIYWASTR KSGVPDRFSG SGSGTDFTLT
U2-30     DIVMTQSPDS LAVSLGERAT INCKSSQSVL DSSNNKNYLA WYQQKPGQPP KLLIYWASTR ESGVPDRFSG SGSGTDFTLT
U2-31     DIVMTQSPDS LAVSLGERAT INCKSSQSVL DSSNNKNYLA WYQQKPGQPP KLLIYWASTR ESGVPDRFSG SGSGTDFTLT
U2-32     DIVMTQSPDS LAVSLGERAT INCKSSQSIL YRSNNKNYLA WYQQKPGQPP KLLIYWASAR ESGVPDRFSG SGSGTDFTLT
U2-33     DIVMTQSPDS LAVSLGERAT INCKSSQSIL YRSNNKNYLA WYQQKPGQPP KLLIYWASAR ESGVPDRFSG SGSGTDFTLT
U2-34     DIQMTQSPSS LSASVGDRVT ITCRASQDIS H.......YLA WFQQKPGKAP KSLIYAASSL QSGVPSKFSG SGSGTDFTLT
U2-35     DIQMTQSPSS LSASVGDRVA ITCRASQDIS ......NYLA WLQQKPGKAP KSLIYAASSL QSGVPSRFSG SGSGTDFTLT
U2-36     EIVMTQSPAT LSVSPGERAT LSCRASQSVS ..SN....LA WYQQDPGQAP RLLIYGASRR ATGIPARFSG SGSGTEFTLT
U2-37     EIVMTQSPAT LSVSPGERAT LSCRASQSVS ..SN....LA WYQQDPGQAP RLLIYGASRR ATGIPARFSG SGSGTEFTLT
U2-38     DIQMTQSPSS VSASVGDRVT ITCRASQDIS ..RW....LA WYQQKPGKAP KLLIYAASSL QSGVPSRFSG SGSGTDFTLT
U2-39     DIQMTQSPSS LSASVGDRVT ITCRASQSIS ......TYLN WYQQKPGKAP KFLIYAASSL QSGVPSRFSG SGSGTDFTLT
U2-40     DIQMTQSPSS LSASLGDRVT ITCRASQTIS ......IYLN WYQQKPGKAP KLLIYAASSL QSGVPSRFSG SGSGTDFTLT
U2-41     DIQMTQSPSS LSASVGDRVT ITCRASQSIR ..S....YLN WYQQRPGNAP KLLIYAASSL QSGVPSRVSG SGSGTDFTLT
U2-42     DIQMTQSPSS RSASVGDRVT ITCRASQTIS ......RYLN WYQQKPGKAP KLLIYAASTL QSGVPSRFSG SGSGTDFTLT
U2-43     DIQMTQSPSS LSASVGDRVT ITCRASQRIS ..S....YLN WYQQKPGKAP KVLIYAESSL QSGVPSRFSG SGSGTDFTLT
U2-44     DIQMTQSPSS LSASVGDRVT ITCRASQSIS ......RYLN WYQQKPGKAP KLLIYTASSL QSGVPSRFSG SGSGTDFTLT
U2-45     DIQMTQSPSS LSASVGDRVT ITCRASQSIS ..S....YLN WYQQKPGKAP KLLIYTASSL QSGVPSRFSG SGSGTDFTLT
U2-46     DIQMTQSPSS LSASVGDRVT ITCRASQSIS ..S....YLN WYQQKPGKAP KLLIYTASSL QSGVPSRFSG SGSGTDFTLT
U2-47     DIQMTQSPSS LSASVGDRVT ITCRASQSIS ..S....YLN WYQQKPGKAP KLLIYTASSL QSGVPSRFSG SGSGTDFTLT
U2-48     DIQMTQSPSS LSASVGDRVT ITCRASQSIS ..S....YLN WYQQKPGKAP KLLIYTVSSL QSGVPSRFSG SGSGTDFTLT
U2-49     DIQMTQSPSS LSASVGDRVT ITCRASQSIS ..S....YLN WYQQKPGKAP KLLIYTVSSL QSGVPSRFSG SGSGTDFTLT
U2-50     DIQMTQSPSS LSASVGDRVT ITCRASQSIS ..S....YLN WYQQKPGKAP KLLIYTVSSL QSGVPSRFSG SGSGTDFTLT
U2-51     DIQMTQSPSS LSASVGDRVT ITCRASQSIS ..S....YLN WYQQKPGKAP KLLIYTASSL QSGVPSRFSG SGSGTDFTLT
U2-52     DIQMTQSPSS LSASVGDRVT ITCRASQSIS ..S....YLN WYQQKPGKAP KLLIYTASSL QSGVPSRFSG SGSGTDFTLT
U2-53     DIQMTQSPSS LSASVGDRVT ITCRASQSIS ..S....YLN WYQQKPGKAP KLLIYTASSL QSGVPSRFSG SGSGTDFTLT
U2-54     DIQMTQSPSS LSASVGDRVT ITCQASQDIS ......NYLN WYQQKPGKAP KLLIYDASNL ETGVPSRFSG SGSGTDFTFT
U2-55     DIQMTQSPSS LSASVGDRVT ITCQASQDIS ......NYLN WYQQKPGKAP KLLIYDASNL ETGVPSRFSG SGSGTDFTFT
U2-56     DIQMTQSPSS LSASVGDRVT ITCQASQDIS ......NSLN WYQQKPGKAP ELLIYDASNL ETGVPSRFSG SGSGTDFTFT
U2-57     DIQMTQSPSS LSASVGDRVT ITCQASQDIS ..D....YLN WYQQKPGKAP KLLIYDASNL ETGVPSRFSG SGSGTDFTFT
U2-58     DIQMTQSPSS LSASVGDRVA ITCQASQDIS ......NYLN WYQQKPGKAP KLLIYDASNL ETGVPSRFSG SGSGTDFTFT
U2-59     DIQMTQSPSS LSASVGDRVA ITCQASQDIS ......NYLN WYQQKPGKAP KLLIYDASNL ETGVPSRFSG SGSGTDFTFT
U2-60     DIQMTQSPSS LSASVGDRVT ITCQASQDIS ......NSLN WYQQKPGKAP KLLIYDASIL ETGVPSRFSG SGSETDFTFT
U2-61     DIQMTQSPSS LSASVGDRVT ITCQASQDIS ......NSLN WYQQKPGKAP KLLIYDASNL ETGVPSRFSG SGSGTDFTFT
U2-62     DIQMTQSPSS LSASVGDGVT ITCQASQDIT ......NYLN WYQQKPGKAP KLLIYDASNL ETGVPSRFSG SGSGTDFTFT
U2-63     DIQMTQSPSS LSASVGDRVT ITCQASQDIS ......NYLN WYQQKLGKAP KLLIHDASNL ETGVPSRFSG SGSGTDFTFT
U2-64     DIQMTQSPSS LSASVGDRVT ITCQASQDIS ..D....YLN WYQQKPGKAP KLLIYDASNL ETGVPSRFSG SGSGTDFTFT
U2-65     DIQMTQSPSS LSASVGDRVT ITCQASQDIS ......NSLN WYQQKPGKAP KLLIYDASNL ETGVPSRFSG SGSGTDFTFT
                                  CDR1                                  CDR2
```

FIGURE 10B

			100		114	
U2-1	ISRVEAEDVG	VYYC	MQSTHW	.PIT	FGQGTR LEIK	(SEQ ID NO:94)
U2-2	ISRVEAEDVG	VYYC	IQGTHW	.PTT	FGQGTR LEIK	(SEQ ID NO:95)
U2-3	ISRVEAEDVG	VYYC	MQGTHW	.PIT	FGQGTR LEIK	(SEQ ID NO:96)
U2-4	ISRVEAEDVG	VYYC	MQGTHW	.PIT	FGQGTR LEIK	(SEQ ID NO:96)
U2-5	ISRVEAEDVG	VYYC	MQGIQL	.PCS	FGQGTK LEIK	(SEQ ID NO:97)
U2-6	ISRVEAEDVG	VYYC	MQSIQL	.PLT	FGGGTK VEIK	(SEQ ID NO:98)
U2-7	ISRVEAEDVG	VYYC	MQSIQL	.PLT	FGGGTK VEIK	(SEQ ID NO:98)
U2-8	ISRVEAEDVG	VYYC	MQSIQL	.PIT	FGHGTR LEIK	(SEQ ID NO:99)
U2-9	ISRVEAEDVG	VYYC	MQSIQL	.PIT	FGHGTR LEIK	(SEQ ID NO:99)
U2-11	ISSLQPEDVA	TYYC	QNYNSA	.PFT	FGPGTK VDIK	(SEQ ID NO:100)
U2-12	ISSLQPEDVA	TYYC	QKYNSV	.PLT	FGGGTK VEIK	(SEQ ID NO:101)
U2-13	ISRVEAEDVG	VYYC	MQATQF	.PHT	FGPGTK VDIK	(SEQ ID NO:102)
U2-14	ISRVEAEDVG	VYYC	MQATQF	.PHT	FGPGTK VDIK	(SEQ ID NO:102)
U2-15	ISRVEAEDVG	VYYC	MQATQF	.PHT	FGGGTK VEIK	(SEQ ID NO:103)
U2-16	ISRLEPEDFA	VYYC	QQYGSS	.PRT	FGQGTK VEIK	(SEQ ID NO:104)
U2-17	ISRLEPEDFA	VYYC	QQYGSS	.PRS	FGQGTK LEIK	(SEQ ID NO:105)
U2-18	ISSLQPEDFA	TYYC	LQHNSY	.PPT	FGQGTK VEIK	(SEQ ID NO:106)
U2-19	ISSLQAEDVA	VYYC	QQYYSF	.PWT	FGQGTK VEIK	(SEQ ID NO:107)
U2-20	ISSLQAEDVA	VYYC	QQYYSF	.PWT	FGQGTK VEIK	(SEQ ID NO:107)
U2-21	ISSLQAEDVA	VYYC	QQYYST	.TWT	FGQGTK VEIK	(SEQ ID NO:108)
U2-22	ISSLQAEDVA	VYFC	QQYYGT	.PRT	FGQGTK VEIK	(SEQ ID NO:109)
U2-23	ISSLQAEDVA	VYFC	QQYYGT	.PRT	FGQGTK VEIK	(SEQ ID NO:110)
U2-24	ISSLQAEDVA	VYYC	QQYYSI	.SRT	FGQGTK VEIK	(SEQ ID NO:111)
U2-25	ISSLQAEDVA	VYYC	QQYYSI	.SRT	FGQGTK VEIK	(SEQ ID NO:111)
U2-26	ISSLQADDVA	VYYC	QQYYST	.TWT	FGPGTK VEIK	(SEQ ID NO:112)
U2-27	ISSLQADDVA	VYYC	QQYYST	.TWT	FGPGTK VEIK	(SEQ ID NO:113)
U2-28	ISGLQAEDVA	LYYC	QQYYST	.MFS	FGQGTK LEIK	(SEQ ID NO:114)
U2-29	ISGLQAEDVA	LYYC	QQYYST	.MFS	FGQGTK LEIK	(SEQ ID NO:114)
U2-30	ISSLQAEDVA	VFYC	HQYYST	.PLT	FGGGTK VAIK	(SEQ ID NO:115)
U2-31	ISSLQAEDVA	VFYC	HQYYST	.PLT	FGGGTK VAIK	(SEQ ID NO:115)
U2-32	ISSLQAEDVA	VYFC	QQYFIT	.PLT	FGGGTK VEIK	(SEQ ID NO:116)
U2-33	ISSLQAEDVA	VYFC	QQYFIT	.PLT	FGGGTK VEIK	(SEQ ID NO:116)
U2-34	ISSLQPEDFA	TYYC	QQYNNY	.PFT	FGPGTK VDIK	(SEQ ID NO:117)
U2-35	ISSLQPEDFA	TYYC	QQYNTY	.PFT	FGPGTK MDIK	(SEQ ID NO:118)
U2-36	ISSLQSEDFA	VYYC	QQHNNW	PPWT	FGQGTK VEIK	(SEQ ID NO:119)
U2-37	ISSLQSEDFA	VYYC	QQHNNW	PPWT	FGQGTK VEIK	(SEQ ID NO:119)
U2-38	ISSLQPEDFA	TYYC	QQANSF	.PPT	FGQGTK VEFK	(SEQ ID NO:120)
U2-39	ISSLQPEDFA	AYYC	QQSHSA	.PFT	FGPGTK VDIK	(SEQ ID NO:121)
U2-40	ISSLQPEDFA	TYYC	QQSYST	..LT	FGGGTK VEIK	(SEQ ID NO:122)
U2-41	IRSLQPEDFA	TYYC	QQSYSI	.PLT	FGGGTK VEIK	(SEQ ID NO:123)
U2-42	LSSLQPEDFA	TYYC	QQIYST	.SIT	FGQGTR LEIK	(SEQ ID NO:124)
U2-43	ISSLQPEDFA	TYYC	QQSYIT	.PIT	FGQGTR LEII	(SEQ ID NO:125)
U2-44	ISSLQPENFA	TYYC	QQSYFT	.PIT	FGQGTR LEIK	(SEQ ID NO:126)
U2-45	FSSLQPEDFA	TYYC	QQSYFS	.PIT	FGQGTR LEIK	(SEQ ID NO:127)
U2-46	LSSLQPEDFA	SYYC	QQSFYT	.PIT	FGQGTR LEIK	(SEQ ID NO:128)
U2-47	LSSLQPEDFA	SYYC	QQSFYT	.PIT	FGQGTR LEIK	(SEQ ID NO:128)
U2-48	ISSLQPEDFA	TYYC	QQSYFT	.PIT	FGQGTR LEIK	(SEQ ID NO:129)
U2-49	ISSLQPEDFA	TYYC	QQSYFT	.PIT	FGQGTR LEIK	(SEQ ID NO:129)
U2-50	ISSLQPEDFA	TYYC	QQSYFT	.PIT	FGQGTR LEIK	(SEQ ID NO:129)
U2-51	ISSLQPEDFA	SYYC	QQSFYA	.PIT	FGQGTR LEIK	(SEQ ID NO:130)
U2-52	ISSLQPEDFA	SYYC	QQSFYA	.PIT	FGQGTR LEIK	(SEQ ID NO:130)
U2-53	ISSLQPEDFA	TYYC	QQSYFT	.PIT	FGQGTR LEIK	(SEQ ID NO:131)
U2-54	ISSLQPEDIA	TYYC	QQYDYL	.PFT	FGPGTK VDIK	(SEQ ID NO:132)
U2-55	ISSLQPEDIA	TYYC	QQYDYL	.PFT	FGPGTK VDIK	(SEQ ID NO:132)
U2-56	ISSLQPEDIA	TYYC	QQCDDL	.PLT	FGGGTK VEIK	(SEQ ID NO:133)
U2-57	ISSLQPEDIA	TYYC	QHYDNL	.PLT	FGGGTK VEIK	(SEQ ID NO:134)
U2-58	ISSLQPEDIA	TYYC	QQYDNL	.PLT	FGGGTK VEIK	(SEQ ID NO:135)
U2-59	ISSLQPEDIA	TYYC	QQYDNL	.PLT	FGGGTK VEIK	(SEQ ID NO:135)
U2-60	ISSLQPEDIA	TYYC	QQCDIL	.PLS	FGGGTK VEIK	(SEQ ID NO:136)
U2-61	ISSLQPEDIA	TYYC	QQYDNL	.PLA	FGGGTK VEIR	(SEQ ID NO:137)
U2-62	ISSLQPEDIA	TYYC	QQYDSL	.PIT	FGQGTR LEIK	(SEQ ID NO:138)
U2-63	ISSLQPEDIA	TYYC	QQYDNL	.PIT	FGQGTR LEIK	(SEQ ID NO:139)
U2-64	ISSLQPEDIA	TYYC	QHYDNL	.PIT	FGQGTR LEIK	(SEQ ID NO:140)
U2-65	ISSLQPEDIA	TYYC	QHYDNL	.PIT	FGQGTR LEIK	(SEQ ID NO:141)

CDR3

FIGURE 11A: Heavy Chain Variable Regions

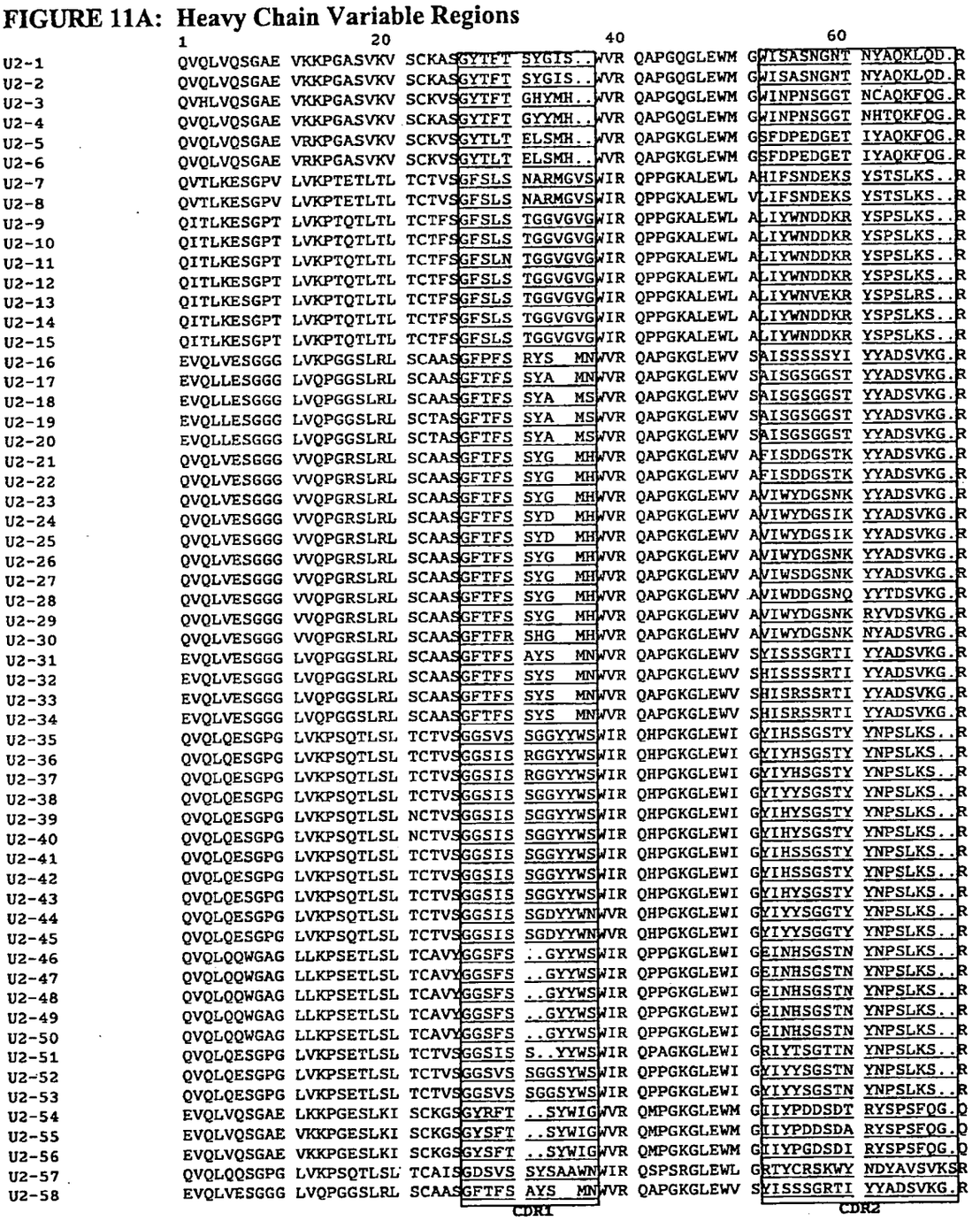

FIGURE 11B

	80	100	CDR3	120	135	
U2-1	VTMTTDTSTS TAYMELRSLR SDDTAVYYCA	REDNW....N	YG.....	FFDYWGQGTL	VTVSS	(SEQ ID NO:142)
U2-2	VTMTTDTSTS TAYMELRSLR SDDTAVYYCA	REDNW....N	YG.....	FFDYWGQGTL	VTVSS	(SEQ ID NO:142)
U2-3	VTMTRDTSIS TAYMELSRLR SDDTAVYYCA	R....SIAV.	.....	ALDYWGQGTL	VTVSS	(SEQ ID NO:143)
U2-4	VTMTRDTSIS TAYMELSRLR SDDTAVYYCA	R....SIAV.	.....	ALDYWGQGTL	VTVSS	(SEQ ID NO:144)
U2-5	VTMLEDTSTD TAYMELSSLR SEDTAVYYCA	TEG.DGG...	.....YYYY	GMDVWGQGTT	VTVSS	(SEQ ID NO:145)
U2-6	VTMLEDTSTD TAYMELSSLR SEDTAVYYCA	TEG.DGG...	.....YYYY	GMDVWGQGTT	VTVSS	(SEQ ID NO:145)
U2-7	LTISKDTSKS QVVLTMTNMD PVDTATYYCA	R.....M	YSSGWYG...	VFDYWGQGTL	VTVSS	(SEQ ID NO:146)
U2-8	LTISKDTSKS QVVLTMTNMD PVDTATYYCA	R.....V	YSSGWS..FY	GMDVWGQGTT	VTVSS	(SEQ ID NO:147)
U2-9	LTITKDTSKN QVVLTMTNMD PVDTATYYCA	H.....R	REL.....	PFDYWGQGTL	VTVSS	(SEQ ID NO:148)
U2-10	LTITKDTSKT QVVLTVTDMD PVDTATYYCA	H.....R	NWT.....	PFDYWGQGTL	VTVSS	(SEQ ID NO:149)
U2-11	LTITKDTSKN QVVLTMTNMD PVDTATYYCA	H.....R	LEL.....	PFDYWGQGTL	VTVSS	(SEQ ID NO:150)
U2-12	LTITKDTSKN QVVLTMTNLD PVDTATYYCA	H.....R	REV.....	PFDYWGQGTL	VTVSS	(SEQ ID NO:151)
U2-13	LTITKATSKN QVVLTMTNMD PVDTATYYCA	H.....R	HTN.....	PFEYWGQGTL	VTVSS	(SEQ ID NO:152)
U2-14	LTITKDTSKN QVVLTMTNMD PVDTATYYCA	H.....R	GEL.....	PFDYWGQGTL	VTVSS	(SEQ ID NO:153)
U2-15	LTITKDTSKN QVVLTMTNMD PVDTATYYCA	H.....R	GEL.....	PFDYWGQGTL	VTVSS	(SEQ ID NO:153)
U2-16	FTISRDNAKN SLYLQMNSLR AEDTAVYYCA	R..DRVGAT.	.....PD	AFDIWGQGTM	VTVSS	(SEQ ID NO:154)
U2-17	FTISRDNSKN TLYLQMNSLR AEDTAVYYCA	KEGIAVAGTA	E....YYYYY	AMDVWGQGTT	VTVSS	(SEQ ID NO:155)
U2-18	FTISRDNSKN TLYLQMNSLR AEDTAVYYCA	KEG..IAARD	.....SYYYY	AMDVWGQGTT	VTVSS	(SEQ ID NO:156)
U2-19	FTISRDNSKN TLYLQMNSLR AEDTAEYYCA	KEG..IAGRD	.....SYYYY	GMDVWGQGTT	VTVSS	(SEQ ID NO:157)
U2-20	FTISRDNSKN TLYLQMNSLR AEDTAEYYCA	KEG..IAGRD	.....SYYYY	GMDVWGQGTT	VTVSS	(SEQ ID NO:157)
U2-21	FTISRDNSMN TLYLQMNSLR AEDTAVYYCA	R.....SYY	DSSGY...YY	GFDYWGQGTL	VTVSS	(SEQ ID NO:158)
U2-22	FTISRDNSMN TLYLQMNSLR AEDTAVYYCA	R.....SYY	DSSGY...YY	GFDYWGQGTL	VTVSS	(SEQ ID NO:158)
U2-23	FTISRDNSKN TLYLQMNSLR AEDTAVYYCA	R.....	..N.....	VIDYWGQGTL	VTVSS	(SEQ ID NO:159)
U2-24	FTISRDNSKN TLYLQMNSLR AEDTAVYYCA	R.....GG	ATG.....AE	YFQHWGQGTL	VTVSS	(SEQ ID NO:160)
U2-25	FTISRDNSKN TLYLQMNSLR AEDTAVYYCA	R.....GG	ATG.....AE	YFQHWGQGTL	VTVSS	(SEQ ID NO:160)
U2-26	FTISRDNSKN TLYLQMNSLR AEDTAVYYCV	L...L....W	FGE.....	TFDYWGQGSL	VTVSP	(SEQ ID NO:161)
U2-27	FTISRDNSKN TLYLQMNSLR AEDTAVYYCA	R.....	.NL.....	PFDYWGQGTL	VTVSS	(SEQ ID NO:162)
U2-28	FTVSRDNSKN TLFLQMNSLR AEDTAVYYCA	R....SHYGG	DYD.....YY	GMDVWGQGTT	VTVSS	(SEQ ID NO:163)
U2-29	FTISRDNSKN TLYLQMNSLR AEDTAVYYCA	R.DGW....Q	QQA.....	PFDYWGQGTL	VTVSS	(SEQ ID NO:164)
U2-30	FTISRDNSKN TLDLQMNSLR AEDTAVYYCA	R...W....G	ISA.....	PFDCWGQGTL	VTVSS	(SEQ ID NO:165)
U2-31	FTISRDNAKN SLFLQMNSLR DEDTAVYYCA	L...W.....	..A.....	PFDYWGQGTL	VTVSS	(SEQ ID NO:166)
U2-32	FTISRDNAKN SVYLQMNSLR DEDTAVYYCA	R..DGYNWNG	GGN.....YY	GMDVWGQGTT	VTVSS	(SEQ ID NO:167)
U2-33	FTISRDNAKN SLYLQMNSLR DEDTAVYYCA	R..DGYNWNN	GGY.....YY	GMDVWGQGTT	VTVSS	(SEQ ID NO:168)
U2-34	FTISRDNAKN SLYLQMNSLR DEDTAVYYCA	R..DGYNWNN	GGY.....YY	GMDVWGQGTT	VTVSS	(SEQ ID NO:168)
U2-35	VTISVDTSKN QFSLNLSSVT AADTAVYYCA	R.....	.GP.....YY	GMDVWGQGTT	VTVSS	(SEQ ID NO:169)
U2-36	VNMSVDTSKN QFSLKLSSVT AADTAVYYCA	R.....ALRG	IVLMVYV.LG	ALDIWGQGTK	VTVSS	(SEQ ID NO:170)
U2-37	VNMSVDTSKN QFSLKLSSVT AADTAVYYCA	R.....ALRG	IVLMVYV.LG	ALDIWGQGTK	VTVSS	(SEQ ID NO:170)
U2-38	VTISVDTSKN QFSLKLSSVT AADTAVYYCA	R..DETVVRG	LIR....YCY	GMDVWGQGTT	VTVSS	(SEQ ID NO:171)
U2-39	ITISADTSKN QFSLKLNSVT AADTAVYYCA	R.....DRGG	GD.....YG	RMDVWGQGTT	VTVSS	(SEQ ID NO:172)
U2-40	ITISADTSKN QFSLKLNSVT AADTAVYYCA	R.....DRGG	GD.....YG	RMDVWGQGTT	VTVSS	(SEQ ID NO:173)
U2-41	ITKSVDTSKN QFSLKLSSVT AADTAVYYCA	R.SN.....N	YG.....	CFALWGRGTL	VTVSS	(SEQ ID NO:174)
U2-42	ITKSVDTSKN QFSLKLSSVT AADTAVYYCA	R.SN.....N	YG.....	CFALWGRGTL	VTVSS	(SEQ ID NO:175)
U2-43	VTISVDTSKN QFSLKLSSVT AADTAVYYCA	SGYNYGLYYY	DSSGYPSYYY	GMDVWGQGTT	VTVSS	(SEQ ID NO:176)
U2-44	VTISVDTSKN QFSLKLFSVT AADTAVYFCA	R.TYYDILTG	YPF.....	YFDYWGQGTL	VTVSS	(SEQ ID NO:177)
U2-45	VTISVDTSKN QFSLKLFSVT AADTAVYFCA	R.TYYDILTG	YPF.....	YFDYWGQGTL	VTVSS	(SEQ ID NO:178)
U2-46	VTISVDTSKN QFSLKLSSVT AADTAVYYCA	R...GGYSSS	WY.....	WFDPWGQGTL	VTVSS	(SEQ ID NO:179)
U2-47	VTISVDTSKN QFSLKLSSVT AADTAVYYCA	R...GGYSSS	WF.....	WFDPWGQGTL	VTVSS	(SEQ ID NO:180)
U2-48	VTISVDTSKN QFSLKLSSVT AADTAVYYCA	R...GGYSSS	WF.....	WFDPWGQGTL	VTVSS	(SEQ ID NO:180)
U2-49	VTISVDTSKN QFSLKLSSVT AADTAVYYCA	R...GGYSSS	WF.....	WFDPWGQGTL	VTVSS	(SEQ ID NO:180)
U2-50	VTISVDTSKN QFSLKLSSVT AADTAVYYCA	R...GGYSSS	WF.....	WFDPWGQGTL	VTVSS	(SEQ ID NO:180)
U2-31	VTMSVDTSKN QFSLKLSSVT AADTAVYYCA	R..DGYSYGH	YYY.....Y	GMDVWGQGTT	VTVSS	(SEQ ID NO:181)
U2-52	VTISIVTSRN QFSLKLSSVT AADTAVYYCA	R....SALRY	FDWLFS...D	VSDIWGQGTM	VTVSS	(SEQ ID NO:182)
U2-53	VTISIVTSRN QFSLKLSSVT AADTAVYYCA	R....SALRY	FDWLFS...D	VSDIWGQGTM	VTVSS	(SEQ ID NO:182)
U2-54	VTISADKSIS TAYLQWSSLK ASDTAMYYCA	RQKSY....G	YS.....	YFDYWGQGTL	VTVSS	(SEQ ID NO:183)
U2-55	VTISADKSIN TAYLQWSSLK ASDTAMYYCA	R...QGYGSG	W.G.....	YFDYWGQGTL	VTVSS	(SEQ ID NO:184)
U2-56	VTISADKSIS TAYLQWSSLK ASDTAMYYCA	R..QGLAVAG	TS...YYYYY	GMDVWGQGTT	VTVSS	(SEQ ID NO:185)
U2-57	ITINPDTSKN QFSLQLNSVT PEDTAVYYCA	R.....DRAV	AGY.....YY	GMDVWGQGTT	VTVSS	(SEQ ID NO:186)
U2-58	FTISRDNAKN SLFLQMNSLR DEDTAVYYCA	L...W.....	..A.....	PFDYWGQGTL	VTVSS	(SEQ ID NO:166)

Cladogram of the Light Chain Variable Regions

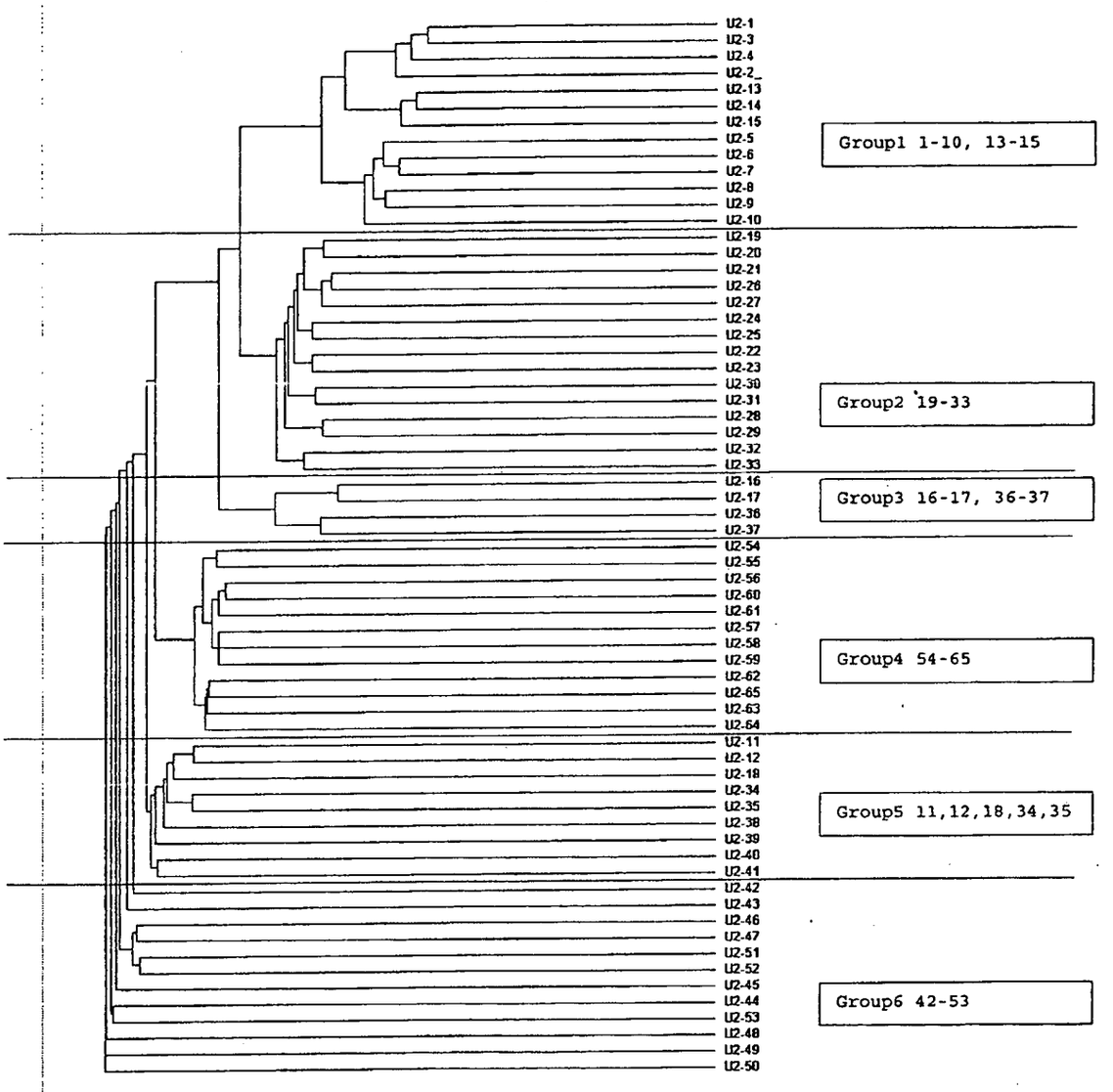

FIG 12A

CDRL3-Cladogram

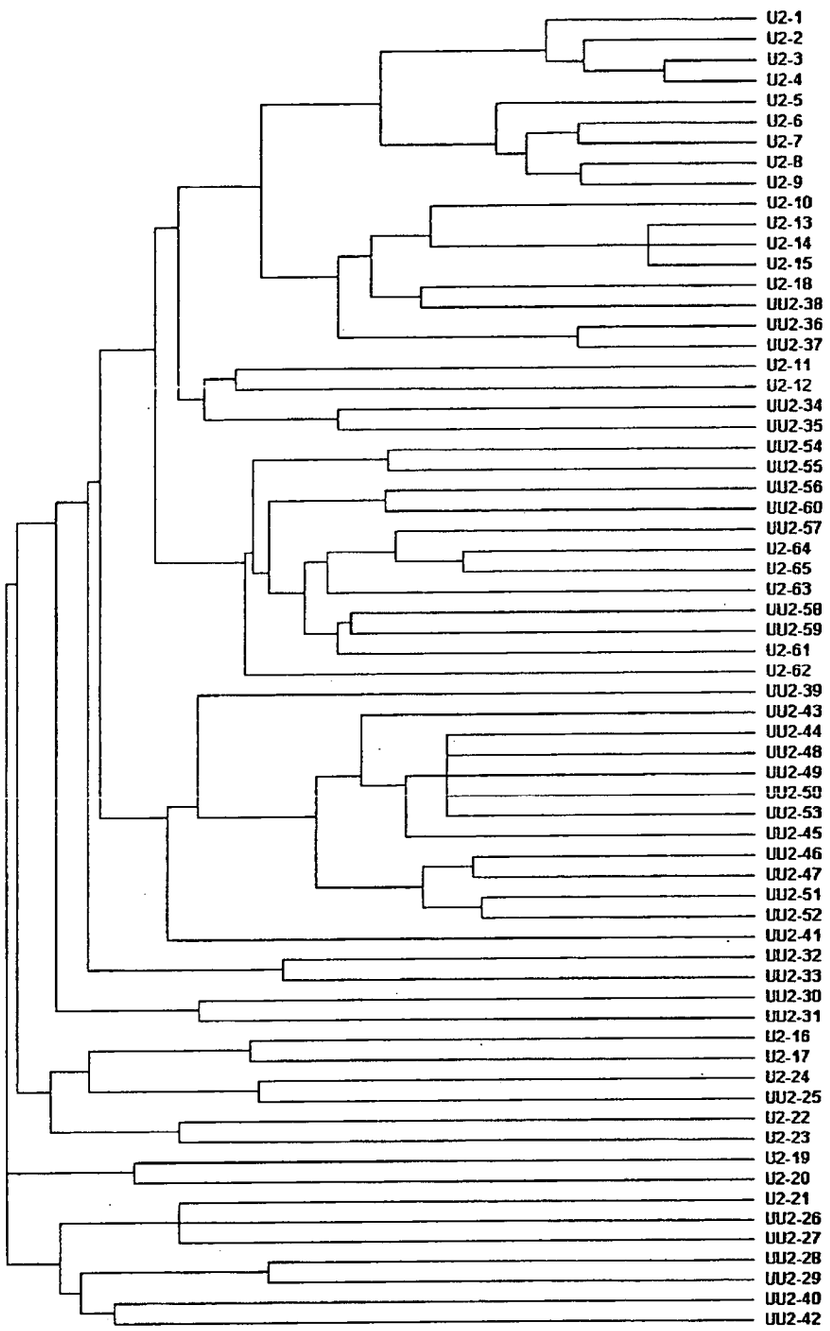

FIG 12B

Cladogram of the Heavy Chain Variable Regions

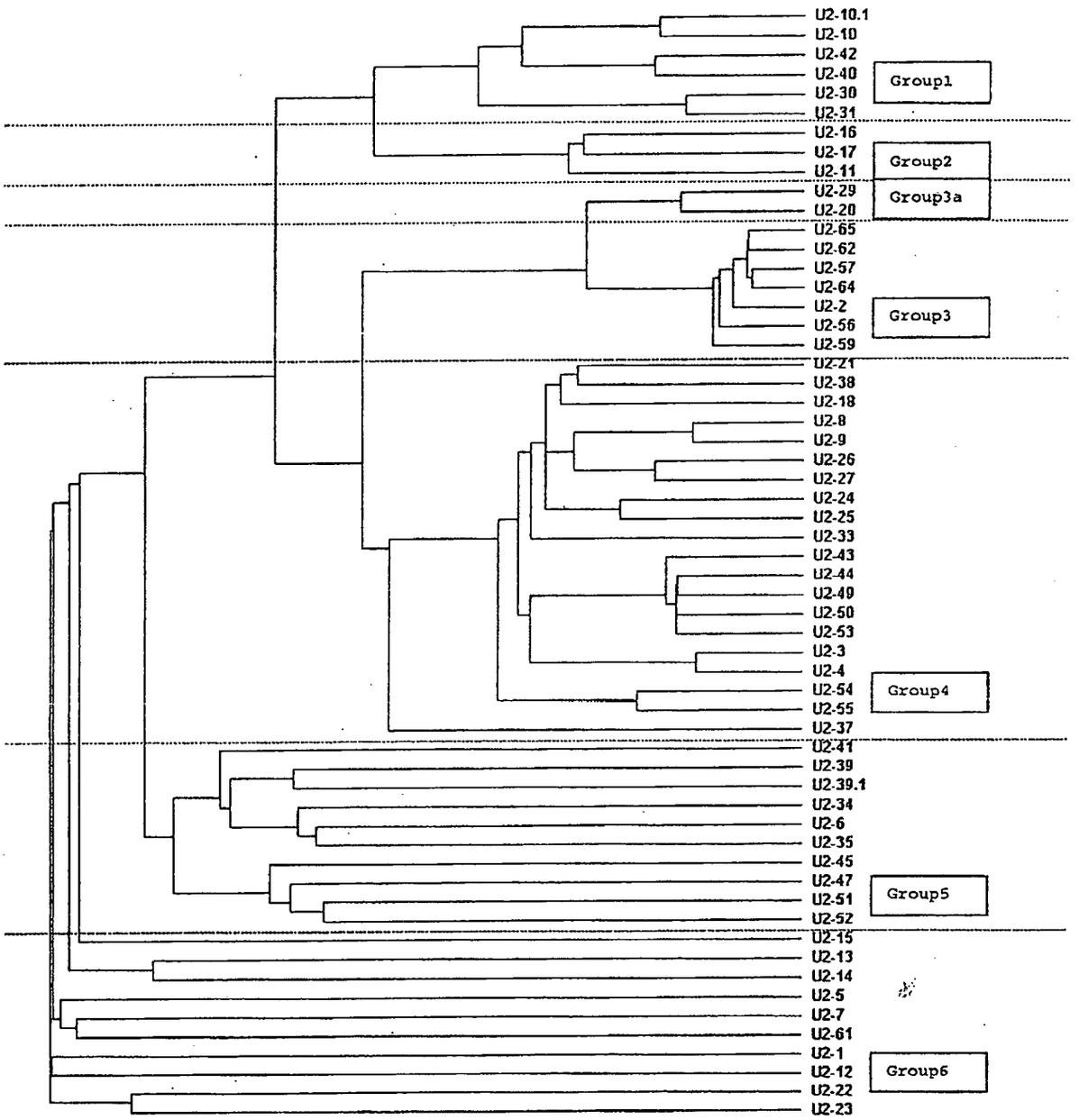

FIGURE 12C

U_L-1 light chain nucleotide sequence (SEQ ID NO:532)

gaygtngtnatgacncarwsnccnmtnwsnmtnccngtnacnmtnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnmtngtntaywsngayggnaayacntaymtnaaytggttycarca
rmgnccnggncarwsnccnmgnmgnmtnathtayaargtnwsnaaytgggaywsnggngtnccn
gaymgnttyaayggnwsnggnwsnggnacngayttyacnmtnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarwsnacncaytggccnathacnttyggncarggnac
nmgnmtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygar
carmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcna
argtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarca
rgaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygar
aarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnt
tyaaymgnggngartgy

U_L-2 light chain nucleotide sequence (SEQ ID NO:533)

gaygtngtnatgacncarwsnccnmtnwsnmtnccngtnacnmtnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnmtngtntaywsngayggnaayacntaymtnaaytggttycarca
rmgnccnggncarwsnccnmgnmgnmtnathtayaargtnwsnaaytgggaywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyathcarggnacncaytggccnacnacnttyggncarggnac
nmgnmtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygar
carmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcna
argtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarca
rgaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygar
aarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnt
tyaaymgnggngartgy

U_L-3 light chain nucleotide sequence (SEQ ID NO:534)

gaygtngtnatgacncarwsnccnmtnwsnmtnccngtnacnmtnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnmtngtntaywsngayggnaayacntaymtnaaytggmtncarca
rmgnccnggncarwsnccnmgnmgnmtnathtayaargtnwsnaaytgggaywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarggnacncaytggccnathacnttyggncarggnac
nmgnmtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygar
carmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcna
argtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarca
rgaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygar
aarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnt
tyaaymgnggngartgy

FIGURE 13A

U_L-4 light chain nucleotide sequence (SEQ ID NO:534)

gaygtngtnatgacncarwsnccnmtnwsnmtnccngtnacnmtnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnmtngtntaywsngayggnaayacntaymtnaaytggmtncarca
rmgnccnggncarwsnccnmgnmgnmtnathtayaargtnwsnaaytgggaywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarggnacncaytggccnathacnttyggncarggnac
nmgnmtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygar
carmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcna
argtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarca
rgaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygar
aarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnt
tyaaymgnggngartgy

U_L-5 light chain nucleotide sequence (SEQ ID NO:535)

gayathgtnatgacncaracnccnmtnwsnmtnwsngtnacnccnggncarccngcnwsnathw
sntgyaarwsnwsncarwsnmtnmtncaywsngayggnaaracntaymtntaytggtaymtnca
raarccnggncarccnccncarmtnmtnathtaygargtnwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarggnathcarmtnccntgywsnttyggncarggnac
naarmtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygar
carmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcna
argtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarca
rgaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygar
aarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnt
tyaaymgnggngartgy

U_L-6 light chain nucleotide sequence (SEQ ID NO:536)

gayathgtnatgacncaracnccnmtnwsnmtnwsngtnacnccnggncarccngcnwsnathw
sntgyaarwsnwsncarwsnmtnmtncaywsngayggnaaracntaymtntaytggtaymtnca
raarccnggncarccnccncarmtnmtnathtaygargtnwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarwsnathcarmtnccnmtnacnttyggnggnggnac
naargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygar
carmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcna
argtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarca
rgaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygar
aarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnt
tyaaymgnggngartgy

FIGURE 13B

U_L-7 light chain nucleotide sequence (SEQ ID NO:536)

gayathgtnatgacncaracnccnmtnwsnmtnwsngtnacnccnggncarccngcnwsnathw
sntgyaarwsnwsncarwsnmtnmtncaywsngayggnaaracntaymtntaytggtaymtnca
raarccnggncarccnccncarmtnmtnathtaygargtnwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarwsnathcarmtnccnmtnacnttyggnggnggnac
naargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygar
carmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcna
argtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarca
rgaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygar
aarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnt
tyaaymgnggngartgy

U_L-8 light chain nucleotide sequence (SEQ ID NO:537)

gayathgtnatgacncaracnccnmtnwsnmtnwsngtnacnccnggncarccngcnwsnathw
sntgyaarwsnwsncarwsnmtnmtncaywsngayggnaaracntaymtntaytggttymtnca
raarccnggncarccnccncarccnmtnathtaygargtnwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarwsnathcarmtnccnathacnttyggncayggnac
nmgnmtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygar
carmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcna
argtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarca
rgaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygar
aarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnt
tyaaymgnggngartgy

U_L-9 light chain nucleotide sequence (SEQ ID NO:537)

gayathgtnatgacncaracnccnmtnwsnmtnwsngtnacnccnggncarccngcnwsnathw
sntgyaarwsnwsncarwsnmtnmtncaywsngayggnaaracntaymtntaytggttymtnca
raarccnggncarccnccncarccnmtnathtaygargtnwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarwsnathcarmtnccnathacnttyggncayggnac
nmgnmtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygar
carmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcna
argtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarca
rgaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygar
aarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnt
tyaaymgnggngartgy

FIGURE 13C

U_L-11 light chain nucleotide sequence (SEQ ID NO:538)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarggnathgcnaaytaymtngcntggtaycarcaraarccnggnaargt
nccnaarmtnmtnathtaygtngcnwsnacnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargaygtngcnacnt
aytaytgycaraaytayaaywsngcnccnttyacnttyggnccnggnacnaargtngayathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-12 light chain nucleotide sequence (SEQ ID NO:539)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
thtgymgngcnwsncarggnathwsnaaygaymtngcntggtaycarcaraarccnggnaargt
nccnaarmtnmtnathtaygcngcnwsnacnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargaygtngcnacnt
aytaytgycaraartayaaywsngtnccnmtnacnttyggnggnggnacnaargtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-13 light chain nucleotide sequence (SEQ ID NO:540)

aayathgtnatgacncaracnccnmtnwsnwsnccngtnacnmtnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnmtngtncaywsngayggnaayacntaymtnwsntggmtncarca
rmgnccnggncarccnccnmgnmtnmtnathtayaarathwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggngcnggnacngayttyacnmtnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcargcnacncarttyccncayacnttyggnccnggnac
naargtngayathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygar
carmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcna
argtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarca
rgaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygar
aarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnt
tyaaymgnggngartgy

FIGURE 13D

U_L-14 light chain nucleotide sequence (SEQ ID NO:540)

aayathgtnatgacncaracnccnmtnwsnwsnccngtnacnmtnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnmtngtncaywsngayggnaayacntaymtnwsntggmtncarca
rmgnccnggncarccnccnmgnmtnmtnathtayaarathwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggngcnggnacngayttyacnmtnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcargcnacncarttyccncayacnttyggnccnggnac
naargtngayathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygar
carmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcna
argtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarca
rgaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygar
aarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnt
tyaaymgnggngartgy

U_L-15 light chain nucleotide sequence (SEQ ID NO:541)

garathgtnatgacncaracnccnmtnwsnwsnccngtnacnmtnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnmtngtncaywsngayggnaayacntaymtnwsntggmtncarca
rmgnccnggncarccnccnmgnmtnmtnathtayaarathwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnacnggngcnggnacngayttyacnmtnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcargcnacncarttyccncayacnttyggnggnggnac
naargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygar
carmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcna
argtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarca
rgaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygar
aarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnt
tyaaymgnggngartgy

U_L-16 light chain nucleotide sequence (SEQ ID NO:542)

garathgtnmtnacncarwsnccnggnacnmtnwsnmtnwsnccnggngarmgngcnacnmtnw
sntgymgngcnwsncaracngtnathwsnwsntaymtngcntggtaycarcaraarccnggnca
rgcnccnmgnmtnmtnathwsnggngcnwsnwsnmgngcnacnggnathccngaymgnttywsn
ggnwsnggnwsnggnacngayttyacnmtnacnathwsnmgnmtngarccngargayttygcng
tntaytaytgycarcartayggnwsnwsnccnmgnacnttyggncarggnacnaargtngarat
haarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsn
ggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartgga
argtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaarga
ywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtn
taygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggng
artgy

FIGURE 13E

U_L-17 light chain nucleotide sequence (SEQ ID NO:543)

garathgtnmtnacncarwsnccnggnacnmtnwsnmtnwsnccnggngarmgngcnacnmtnw
sntgymgngcnwsncarwsngtnwsnmgnmtngcntggtaycarcaraarccnggncargcncc
nmgnmtnmtnathtayggngcnwsnmgnmgngcnacnggnathccngaymgnttywsnggnwsn
ggnwsnggnacngayttyacnmtnacnathwsnmgnmtngarccngargayttygcngtntayt
aytgycarcartayggnwsnwsnccnmgnwsnttyggncarggnacnaarmtngarathaarmg
nacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggnacn
gcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaargtng
ayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargaywsnac
ntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntaygcn
tgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngartgy

U_L-18 light chain nucleotide sequence (SEQ ID NO:544)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarggnathmgnaaygaymtnggntggtaycarcaraarccnggnaargc
nccnaarmgnmtnathtaygcngcnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngarttyacnmtnacnathwsnwsnmtncarccngargayttygcnacnt
aytaytgymtncarcayaaywsntayccnccnacnttyggncarggnacnaargtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-19 light chain nucleotide sequence (SEQ ID NO:545)

gayathgtnatgacncarwsnccngaywsnmtngcngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncarwsngtnmtntaywsnwsnaayaayaaraaytaymtngtntggtayca
rcaraarccnggncarccnccnaarmtnttyathtaytgggcnwsnacnmgngarwsnggngtn
ccngaymgnttyacnggnwsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarg
cngargaygtngcngtntaytaytgycarcartaytaywsnttyccntggacnttyggncargg
nacnaargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

FIGURE 13F

U_L-20 light chain nucleotide sequence (SEQ ID NO:545)

gayathgtnatgacncarwsnccngaywsnmtngcngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncarwsngtnmtntaywsnwsnaayaayaaraaytaymtngtntggtayca
rcaraarccnggncarccnccnaarmtnttyathtaytgggcnwsnacnmgngarwsnggngtn
ccngaymgnttyacnggnwsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarg
cngargaygtngcngtntaytaytgycarcartaytaywsnttyccntggacnttyggncargg
nacnaargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

U_L-21 light chain nucleotide sequence (SEQ ID NO:546)

gayathgtnatgacncarwsnccngaywsnmtngcngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncarwsngtnmtntaywsnwsnaayaayaaraaytaymtngcntggtayca
rcaraarccnggncarccnccnaarmtnmtnathtaytgggcnwsnacnmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarg
cngargaygtngcngtntaytaytgycarcartaytaywsnacnacntggacnttyggncargg
nacnaargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

U_L-22 light chain nucleotide sequence (SEQ ID NO:547)

gayathgtnatgacncarwsnccngaywsnmtngcngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncaraaygtnmtntaywsnwsnaayaayaaraaytaymtngcntggtayca
rcaraarccnggncarccnccnaarmtnmtnathtaytgggcnwsnacnmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarg
cngargaygtngcngtntayttytgycarcartaytayggnacnccnmgnacnttyggncargg
nacnaargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

FIGURE 13G

U_L-23 light chain nucleotide sequence (SEQ ID NO:548)

gayathgtnatgacncarwsnccngaywsnmtngcngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncaraaygtnmtntaywsnwsnaayaayaaraaytaymtngcntggtayca
rcaraarccnggncarccnccnaarmtnmtnathtaytgggcnwsnacnmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarg
cngargaygtngcngtntayttytgycarcartaytayggnacnccnmgnacnttyggncargg
nacnaargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

U_L-24 light chain nucleotide sequence (SEQ ID NO:549)

gayathgtnatgacncarwsnccngaywsnmtnacngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncarwsngtnmtntaywsnwsnaayaayaaraaytaymtngcntggtayca
rcaraarccnggncarccnccnaarmtnmtnathtaytgggcnwsnacnmgngarwsnggngtn
ccngaymgnttyggnggnwsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarg
cngargaygtngcngtntaytaytgycarcartaytaywsnathwsnmgnacnttyggncargg
nacnaargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

U_L-25 light chain nucleotide sequence (SEQ ID NO:549)

gayathgtnatgacncarwsnccngaywsnmtnacngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncarwsngtnmtntaywsnwsnaayaayaaraaytaymtngcntggtayca
rcaraarccnggncarccnccnaarmtnmtnathtaytgggcnwsnacnmgngarwsnggngtn
ccngaymgnttyggnggnwsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarg
cngargaygtngcngtntaytaytgycarcartaytaywsnathwsnmgnacnttyggncargg
nacnaargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

FIGURE 13H

U_L-26 light chain nucleotide sequence (SEQ ID NO:550)

gayathgtnatgacncarwsnccngaywsnmtngcngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncarwsngtnmtntayaaywsnaayaayaaraaytaymtngcntggtayca
rcaraarccnggncarccnccnaarmtnmtnathtaytgggcnwsnacnmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarg
cngaygaygtngcngtntaytaytgycarcartaytaywsnacnacntggacnttyggnccngg
nacnaargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

U_L-27 light chain nucleotide sequence (SEQ ID NO:551)

gayathgtnatgacncarwsnccngaywsnmtngcngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncarwsngtnmtntayaaywsnaayaayaaraaytaymtngcntggtayca
rcaraarccnggncarccnccnaarmtnmtnathtaytgggcnwsnacnmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarg
cngaygaygtngcngtntaytaytgycarcartaytaywsnacnacntggacnttyggnccngg
nacnaargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

U_L-28 light chain nucleotide sequence (SEQ ID NO:552)

gayathgtnatgacncarwsnccngaywsnmtngcngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncarwsngtnmtntaywsnwsnaayaayaaraaytaymtngcntggtayca
rcaraarccnggncarccnccnaargtnmtnathtaytgggcnwsnacnmgnaarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnacnathwsnggnmtncarg
cngargaygtngcnmtntaytaytgycarcartaytaywsnacnatgttywsnttyggncargg
nacnaarmtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

FIGURE 13I

$_L$-29 light chain nucleotide sequence (SEQ ID NO:552)

gayathgtnatgacncarwsnccngaywsnmtngcngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncarwsngtnmtntaywsnwsnaayaayaaraaytaymtngcntggtayca
rcaraarccnggncarccnccnaargtnmtnathtaytgggcnwsnacnmgnaarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnacnathwsnggnmtncarg
cngargaygtngcnmtntaytaytgycarcartaytaywsnacnatgttywsnttyggncargg
nacnaarmtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

U_L-30 light chain nucleotide sequence (SEQ ID NO:553)

gayathgtnatgacncarwsnccngaywsnmtngcngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncarwsngtnmtngaywsnwsnaayaayaaraaytaymtngcntggtayca
rcaraarccnggncarccnccnaarmtnmtnathtaytgggcnwsnacnmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarg
cngargaygtngcngtnttytaytgycaycartaytaywsnacnccnmtnacnttyggnggngg
nacnaargtngcnathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

U_L-31 light chain nucleotide sequence (SEQ ID NO:553)

gayathgtnatgacncarwsnccngaywsnmtngcngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncarwsngtnmtngaywsnwsnaayaayaaraaytaymtngcntggtayca
rcaraarccnggncarccnccnaarmtnmtnathtaytgggcnwsnacnmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarg
cngargaygtngcngtnttytaytgycaycartaytaywsnacnccnmtnacnttyggnggngg
nacnaargtngcnathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

FIGURE 13J

U_L-32 light chain nucleotide sequence (SEQ ID NO:554)

gayathgtnatgacncarwsnccngaywsnmtngcngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncarwsnathmtntaymgnwsnaayaayaaraaytaymtngcntggtayca
rcaraarccnggncarccnccnaarmtnmtnathtaytgggcnwsngcnmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarg
cngargaygtngcngtntayttytgycarcartayttyathacnccnmtnacnttyggnggngg
nacnaargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

U_L-33 light chain nucleotide sequence (SEQ ID NO:554)

gayathgtnatgacncarwsnccngaywsnmtngcngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncarwsnathmtntaymgnwsnaayaayaaraaytaymtngcntggtayca
rcaraarccnggncarccnccnaarmtnmtnathtaytgggcnwsngcnmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarg
cngargaygtngcngtntayttytgycarcartayttyathacnccnmtnacnttyggnggngg
nacnaargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

U_L-34 light chain nucleotide sequence (SEQ ID NO:555)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncargayathwsncaytaymtngcntggttycarcaraarccnggnaargc
nccnaarwsnmtnathtaygcngcnwsnwsnmtncarwsnggngtnccnwsnaarttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargayttygcnacnt
aytaytgycarcartayaayaaytayccnttyacnttyggnccnggnacnaargtngayathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

FIGURE 13K

U_L-35 light chain nucleotide sequence (SEQ ID NO:556)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtngcnatha
cntgymgngcnwsncargayathwsnaaytaymtngcntggmtncarcaraarccnggnaargc
nccnaarwsnmtnathtaygcngcnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargayttygcnacnt
aytaytgycarcartayaayacntayccnttyacnttyggnccnggnacnaaratggayathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-36 light chain nucleotide sequence (SEQ ID NO:557)

garathgtnatgacncarwsnccngcnacnmtnwsngtnwsnccnggngarmgngcnacnmtnw
sntgymgngcnwsncarwsngtnwsnwsnaaymtngcntggtaycarcargayccnggncargc
nccnmgnmtnmtnathtayggngcnwsnmgnmgngcnacnggnathccngcnmgnttywsnggn
wsnggnwsnggnacngarttyacnmtnacnathwsnwsnmtncarwsngargayttygcngtnt
aytaytgycarcarcayaayaaytggccnccntggacnttyggncarggnacnaargtngarat
haarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsn
ggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartgga
argtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaarga
ywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtn
taygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggng
artgy

U_L-37 light chain nucleotide sequence (SEQ ID NO:557)

garathgtnatgacncarwsnccngcnacnmtnwsngtnwsnccnggngarmgngcnacnmtnw
sntgymgngcnwsncarwsngtnwsnwsnaaymtngcntggtaycarcargayccnggncargc
nccnmgnmtnmtnathtayggngcnwsnmgnmgngcnacnggnathccngcnmgnttywsnggn
wsnggnwsnggnacngarttyacnmtnacnathwsnwsnmtncarwsngargayttygcngtnt
aytaytgycarcarcayaayaaytggccnccntggacnttyggncarggnacnaargtngarat
haarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsn
ggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartgga
argtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaarga
ywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtn
taygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggng
artgy

FIGURE 13L

U_L-38 light chain nucleotide sequence (SEQ ID NO:558)

gayathcaratgacncarwsnccnwsnwsngtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncargayathwsnmgntggmtngcntggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtaygcngcnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargayttygcnacnt
aytaytgycarcargcnaaywsnttyccnccnacnttyggncarggnacnaargtngarttyaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-39 light chain nucleotide sequence (SEQ ID NO:559)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarwsnathwsnacntaymtnaaytggtaycarcaraarccnggnaargc
nccnaarttymtnathtaygcngcnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargayttygcngcnt
aytaytgycarcarwsncaywsngcnccnttyacnttyggnccnggnacnaargtngayathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-40 light chain nucleotide sequence (SEQ ID NO:560)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsnmtnggngaymgngtnacnatha
cntgymgngcnwsncaracnathwsnathtaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtaygcngcnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargayttygcnacnt
aytaytgycarcarwsntaywsnacnmtnacnttyggnggnggnacnaargtngarathaarmg
nacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggnacn
gcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaargtng
ayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargaywsnac
ntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntaygcn
tgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngartgy

FIGURE 13M

U_L-41 light chain nucleotide sequence (SEQ ID NO:561)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarwsnathmgnwsntaymtnaaytggtaycarcarmgnccnggnaaygc
nccnaarmtnmtnathtaygcngcnwsnwsnmtncarwsnggngtnccnwsnmgngtnwsnggn
wsnggnwsnggnacngayttyacnmtnacnathmgnwsnmtncarccngargayttygcnacnt
aytaytgycarcarwsntaywsnathccnmtnacnttyggnggnggnacnaargtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-42 light chain nucleotide sequence (SEQ ID NO:562)

gayathcaratgacncarwsnccnwsnwsnmgnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncaracnathwsnmgntaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtaygcngcnwsnacnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnmtnwsnwsnmtncarccngargayttygcnacnt
aytaytgycarcarathtaywsnacnwsnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-43 light chain nucleotide sequence (SEQ ID NO:563)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarmgnathwsnwsntaymtnaaytggtaycarcaraarccnggnaargc
nccnaargtnmtnathtaygcngarwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargayttygcnacnt
aytaytgycarcarwsntayathacnccnathacnttyggncarggnacnmgnmtngarathat
hmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

FIGURE 13N

U_L-44 light chain nucleotide sequence (SEQ ID NO:564)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarwsnathwsnmgntaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtayacngcnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngaraayttygcnacnt
aytaytgycarcarwsntayttyacnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-45 light chain nucleotide sequence (SEQ ID NO:565)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarwsnathwsnwsntaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtayacngcnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnttywsnwsnmtncarccngargayttygcnacnt
aytaytgycarcarwsntayttywsnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-46 light chain nucleotide sequence (SEQ ID NO:566)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarwsnathwsnwsntaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtayacngcnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnmtnwsnwsnmtncarccngargayttygcnwsnt
aytaytgycarcarwsnttytayacnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

FIGURE 13O

U_L-47 light chain nucleotide sequence (SEQ ID NO:566)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarwsnathwsnwsntaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtayacngcnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnmtnwsnwsnmtncarccngargayttygcnwsnt
aytaytgycarcarwsnttytayacnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-48 light chain nucleotide sequence (SEQ ID NO:567)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarwsnathwsnwsntaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtayacngtnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargayttygcnacnt
aytaytgycarcarwsntayttyacnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-49 light chain nucleotide sequence (SEQ ID NO:567)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarwsnathwsnwsntaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtayacngtnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargayttygcnacnt
aytaytgycarcarwsntayttyacnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

FIGURE 13P

U_L-50 light chain nucleotide sequence (SEQ ID NO:567)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarwsnathwsnwsntaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtayacngtnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargayttygcnacnt
aytaytgycarcarwsntayttyacnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargaywsn
acntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-51 light chain nucleotide sequence (SEQ ID NO:568)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarwsnathwsnwsntaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtayacngcnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargayttygcnwsnt
aytaytgycarcarwsnttytaygcnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargaywsn
acntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-52 light chain nucleotide sequence (SEQ ID NO:568)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarwsnathwsnwsntaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtayacngcnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargayttygcnwsnt
aytaytgycarcarwsnttytaygcnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargaywsn
acntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

FIGURE 13Q

U_L-53 light chain nucleotide sequence (SEQ ID NO:569)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarwsnathwsnwsntaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtayacngcnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargayttygcnacnt
aytaytgycarcarwsntayttyacnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-54 light chain nucleotide sequence (SEQ ID NO:570)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgycargcnwsncargayathwsnaaytaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtaygaygcnwsnaaymtngaracnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnttyacnathwsnwsnmtncarccngargayathgcnacnt
aytaytgycarcartaygaytaymtnccnttyacnttyggnccnggnacnaargtngayathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-55 light chain nucleotide sequence (SEQ ID NO:570)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgycargcnwsncargayathwsnaaytaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtaygaygcnwsnaaymtngaracnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnttyacnathwsnwsnmtncarccngargayathgcnacnt
aytaytgycarcartaygaytaymtnccnttyacnttyggnccnggnacnaargtngayathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

FIGURE 13R

U_L-56 light chain nucleotide sequence (SEQ ID NO:571)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgycargcnwsncargayathwsnaaywsnmtnaaytggtaycarcaraarccnggnaargc
nccngarmtnmtnathtaygaygcnwsnaaymtngaracnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnttyacnathwsnwsnmtncarccngargayathgcnacnt
aytaytgycarcartgygaygaymtnccnmtnacnttyggnggnggnacnaargtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-57 light chain nucleotide sequence (SEQ ID NO:572)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgycargcnwsncargayathwsngaytaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtaygaygcnwsnaaymtngaracnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnttyacnathwsnwsnmtncarccngargayathgcnacnt
aytaytgycarcaytaygayaaymtnccnmtnacnttyggnggnggnacnaargtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-58 light chain nucleotide sequence (SEQ ID NO:573)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtngcnatha
cntgycargcnwsncargayathwsnaaytaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtaygaygcnwsnaaymtngaracnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnttyacnathwsnwsnmtncarccngargayathgcnacnt
aytaytgycarcartaygayaaymtnccnmtnacnttyggnggnggnacnaargtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

FIGURE 13S

U_L-59 light chain nucleotide sequence (SEQ ID NO:573)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtngcnatha
cntgycargcnwsncargayathwsnaaytaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtaygaygcnwsnaaymtngaracnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnttyacnathwsnwsnmtncarccngargayathgcnacnt
aytaytgycarcartaygayaaymtnccnmtnacnttyggnggnggnacnaargtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-60 light chain nucleotide sequence (SEQ ID NO:574)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgycargcnwsncargayathwsnaaywsnmtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtaygaygcnwsnathmtngaracnggngtnccnwsnmgnttywsnggn
wsnggnwsngaracngayttyacnttyacnathwsnwsnmtncarccngargayathgcnacnt
aytaytgycarcartgygayathmtnccnmtnwsnttyggnggnggnacnaargtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-61 light chain nucleotide sequence (SEQ ID NO:575)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgycargcnwsncargayathwsnaaywsnmtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtaygaygcnwsnaaymtngaracnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnttyacnathwsnwsnmtncarccngargayathgcnacnt
aytaytgycarcartaygayaaymtnccnmtngcnttyggnggnggnacnaargtngarathmg
nmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

FIGURE 13T

U_L-62 light chain nucleotide sequence (SEQ ID NO:576)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngayggngtnacnatha
cntgycargcnwsncargayathacnaaytaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtaygaygcnwsnaaymtngaracnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnttyacnathwsnwsnmtncarccngargayathgcnacnt
aytaytgycarcartaygaywsnmtnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-63 light chain nucleotide sequence (SEQ ID NO:577)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgycargcnwsncargayathwsnaaytaymtnaaytggtaycarcaraarmtnggnaargc
nccnaarmtnmtnathcaygaygcnwsnaaymtngaracnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnttyacnathwsnwsnmtncarccngargayathgcnacnt
aytaytgycarcartaygayaaymtnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-64 light chain nucleotide sequence (SEQ ID NO:578)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgycargcnwsncargayathwsngaytaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtaygaygcnwsnaaymtngaracnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnttyacnathwsnwsnmtncarccngargayathgcnacnt
aytaytgycarcaytaygayaaymtnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

FIGURE 13U

U_L-65 light chain nucleotide sequence (SEQ ID NO:579)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgycargcnwsncargayathwsnaaywsnmtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtaygaygcnwsnaaymtngaracnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnttyacnathwsnwsnmtncarccngargayathgcnacnt
aytaytgycarcaytaygayaaymtnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

FIGURE 13V

U_H-1 heavy chain nucleotide sequence (SEQ ID NO:580)

cargtncarmtngtncarwsnggngcngargtnaaraarccnggngcnwsngtnaargtnwsnt
gyaargcnwsnggntayacnttyacnwsntayggnathwsntgggtnmgncargcnccnggnca
rggnmtngartggatgggntggathwsngcnwsnaayggnaayacnaaytaygcncaraarmtn
cargaymgngtnacnatgacnacngayacnwsnacnwsnacngcntayatggarmtnmgnwsnm
tnmgnwsngaygayacngcngtntaytaytgygcnmgngargayaaytggaaytayggnttytt
ygaytaytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtn
ttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtna
argaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtnca
yacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccn
wsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaarg
tngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngc
nggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccn
gargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtayg
tngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacntt
ymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgy
aargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarc
cnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnws
nmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggn
carccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtnt
aywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnat
gcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_H-2 heavy chain nucleotide sequence (SEQ ID NO:580)

cargtncarmtngtncarwsnggngcngargtnaaraarccnggngcnwsngtnaargtnwsnt
gyaargcnwsnggntayacnttyacnwsntayggnathwsntgggtnmgncargcnccnggnca
rggnmtngartggatgggntggathwsngcnwsnaayggnaayacnaaytaygcncaraarmtn
cargaymgngtnacnatgacnacngayacnwsnacnwsnacngcntayatggarmtnmgnwsnm
tnmgnwsngaygayacngcngtntaytaytgygcnmgngargayaaytggaaytayggnttytt
ygaytaytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtn
ttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtna
argaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtnca
yacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccn
wsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaarg
tngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngc
nggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccn
gargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtayg
tngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacntt
ymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgy
aargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarc
cnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnws
nmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggn
carccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtnt
aywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnat
gcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURE 14A

U_H-3 heavy chain nucleotide sequence (SEQ ID NO:581)

cargtncaymtngtncarwsnggngcngargtnaaraarccnggngcnwsngtnaargtnwsnt
gyaargtnwsnggntayacnttyacnggncaytayatgcaytgggtnmgncargcnccnggnca
rggnmtngartggatgggntggathaayccnaaywsnggnggnacnaaytgygcncaraartty
carggnmgngtnacnatgacnmgngayacnwsnathwsnacngcntayatggarmtnwsnmgnm
tnmgnwsngaygayacngcngtntaytaytgygcnmgnwsnathgcngtngcnmtngaytaytg
gggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccnmtn
gcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargaytayt
tyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacnttycc
ngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsnaay
ttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngayaara
cngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggnccnws
ngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtnacn
tgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayggng
tngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngtngt
nwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtnwsn
aayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgngarc
cncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnacntg
ymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccngar
aayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsnaarm
tnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcaygargc
nmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_H-4 heavy chain nucleotide sequence (SEQ ID NO:582)

cargtncarmtngtncarwsnggngcngargtnaaraarccnggngcnwsngtnaargtnwsnt
gyaargcnwsnggntayacnttyacnggntaytayatgcaytgggtnmgncargcnccnggnca
rggnmtngartggatgggntggathaayccnaaywsnggnggnacnaaycayacncaraartty
carggnmgngtnacnatgacnmgngayacnwsnathwsnacngcntayatggarmtnwsnmgnm
tnmgnwsngaygayacngcngtntaytaytgygcnmgnwsnathgcngtngcnmtngaytaytg
gggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccnmtn
gcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargaytayt
tyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacnttycc
ngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsnaay
ttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngayaara
cngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggnccnws
ngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtnacn
tgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayggng
tngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngtngt
nwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtnwsn
aayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgngarc
cncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnacntg
ymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccngar
aayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsnaarm
tnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcaygargc
nmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURE 14B

U_B-5 heavy chain nucleotide sequence (SEQ ID NO:583)

cargtncarmtngtncarwsnggngcngargtnmgnaarccnggngcnwsngtnaargtnwsnt
gyaargtnwsnggntayacnmtnacngarmtnwsnatgcaytgggtnmgncargcnccnggnaa
rggnmtngartggatgggnwsnttygayccngargayggngaracnathtaygcncaraartty
carggnmgngtnacnatgmtngargayacnwsnacngayacngcntayatggarmtnwsnwsnm
tnmgnwsngargayacngcngtntaytaytgygcnacngarggngayggnggntaytaytayta
yggnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacnaarggnccn
wsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgym
tngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsngg
ngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacn
gtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaaya
cnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccncc
ngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgn
acnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaayt
ggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaayws
nacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartay
aartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarg
gncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraayca
rgtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsn
aayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyt
tymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgyws
ngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_B-6 heavy chain nucleotide sequence (SEQ ID NO:583)

cargtncarmtngtncarwsnggngcngargtnmgnaarccnggngcnwsngtnaargtnwsnt
gyaargtnwsnggntayacnmtnacngarmtnwsnatgcaytgggtnmgncargcnccnggnaa
rggnmtngartggatgggnwsnttygayccngargayggngaracnathtaygcncaraartty
carggnmgngtnacnatgmtngargayacnwsnacngayacngcntayatggarmtnwsnwsnm
tnmgnwsngargayacngcngtntaytaytgygcnacngarggngayggnggntaytaytayta
yggnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacnaarggnccn
wsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgym
tngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsngg
ngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacn
gtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaaya
cnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccncc
ngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgn
acnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaayt
ggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaayws
nacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartay
aartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarg
gncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraayca
rgtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsn
aayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyt
tymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgyws
ngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURE 14C

U_R-7 heavy chain nucleotide sequence (SEQ ID NO:584)

cargtnacnmtnaargarwsnggnccngtnmtngtnaarccnacngaracnmtnacnmtnacnt
gyacngtnwsnggnttywsnmtnwsnaaygcnmgnatgggngtnwsntggathmgncarccncc
nggnaargcnmtngartggmtngcncayathttywsnaaygaygaraarwsntaywsnacnwsn
mtnaarwsnmgnmtnacnathwsnaargayacnwsnaarwsncargtngtnmtnacnatgacna
ayatggayccngtngayacngcnacntaytaytgygcnmgnatgtaywsnwsnggntggtaygg
ngtnttygaytaytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccn
wsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgym
tngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsngg
ngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacn
gtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaaya
cnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccncc
ngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgn
acnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaayt
ggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaayws
nacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartay
aartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarg
gncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraayca
rgtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsn
aayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyt
tymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgyws
ngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_R-8 heavy chain nucleotide sequence (SEQ ID NO:585)

cargtnacnmtnaargarwsnggnccngtnmtngtnaarccnacngaracnmtnacnmtnacnt
gyacngtnwsnggnttywsnmtnwsnaaygcnmgnatgggngtnwsntggathmgncarccncc
nggnaargcnmtngartggmtngtnmtnathttywsnaaygaygaraarwsntaywsnacnwsn
mtnaarwsnmgnmtnacnathwsnaargayacnwsnaarwsncargtngtnmtnacnatgacna
ayatggayccngtngayacngcnacntaytaytgygcnmgngtntaywsnwsnggntggwsntt
ytayggnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacnaarggn
ccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggnt
gymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnws
nggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtn
acngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsna
ayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcncc
nccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsn
mgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttya
aytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaa
ywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargar
tayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracna
arggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraa
ycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggar
wsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnt
tyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntg
ywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggn
aar

FIGURE 14D

U_B-9 heavy chain nucleotide sequence (SEQ ID NO:586)

carathacnmtnaargarwsnggnccnacnmtngtnaarccnacncaracnmtnacnmtnacnt
gyacnttywsnggnttywsnmtnwsnacnggnggngtnggngtnggntggathmgncarccncc
nggnaargcnmtngartggmtngcnmtnathtaytggaaygaygayaarmgntaywsnccnwsn
mtnaarwsnmgnmtnacnathacnaargayacnwsnaaraaycargtngtnmtnacnatgacna
ayatggayccngtngayacngcnacntaytaytgygcncaymgnmgngarmtnccnttygayta
ytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccn
mtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargayt
ayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacntt
yccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsn
aayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngaya
aracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggncc
nwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtn
acntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayg
gngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngt
ngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtn
wsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgng
arccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnac
ntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccn
garaayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsna
armtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcayga
rgcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_B-10 heavy chain nucleotide sequence (SEQ ID NO:587)

carathacnmtnaargarwsnggnccnacnmtngtnaarccnacncaracnmtnacnmtnacnt
gyacnttywsnggnttywsnmtnwsnacnggnggngtnggngtnggntggathmgncarccncc
nggnaargcnmtngartggmtngcnmtnathtaytggaaygaygayaarmgntaywsnccnwsn
mtnaarwsnmgnmtnacnathacnaargayacnwsnaaracncargtngtnmtnacngtnacng
ayatggayccngtngayacngcnacntaytaytgygcncaymgnaaytggacnccnttygayta
ytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccn
mtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargayt
ayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacntt
yccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsn
aayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngaya
aracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggncc
nwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtn
acntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayg
gngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngt
ngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtn
wsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgng
arccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnac
ntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccn
garaayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsna
armtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcayga
rgcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURE 14E

U_H-11 heavy chain nucleotide sequence (SEQ ID NO:588)

carathacnmtnaargarwsnggnccnacnmtngtnaarccnacncaracnmtnacnmtnacnt
gyacnttywsnggnttywsnmtnaayacnggnggngtnggngtnggntggathmgncarccncc
nggnaargcnmtngartggmtngcnmtnathtaytggaaygaygayaarmgntaywsnccnwsn
mtnaarwsnmgnmtnacnathacnaargayacnwsnaaraaycargtngtnmtnacnatgacna
ayatggayccngtngayacngcnacntaytaytgygcncaymgnmtngarmtnccnttygayta
ytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccn
mtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargayt
ayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacntt
yccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsn
aayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngaya
aracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggncc
nwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtn
acntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayg
gngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngt
ngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtn
wsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgng
arccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnac
ntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccn
garaayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsna
armtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcayga
rgcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_H-12 heavy chain nucleotide sequence (SEQ ID NO:589)

carathacnmtnaargarwsnggnccnacnmtngtnaarccnacncaracnmtnacnmtnacnt
gyacnttywsnggnttywsnmtnwsnacnggnggngtnggngtnggntggathmgncarccncc
nggnaargcnmtngartggmtngcnmtnathtaytggaaygaygayaarmgntaywsnccnwsn
mtnaarwsnmgnmtnacnathacnaargayacnwsnaaraaycargtngtnmtnacnatgacna
aymtngayccngtngayacngcnacntaytaytgygcncaymgnmgngargtnccnttygayta
ytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccn
mtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargayt
ayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacntt
yccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsn
aayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngaya
aracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggncc
nwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtn
acntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayg
gngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngt
ngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtn
wsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgng
arccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnac
ntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccn
garaayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsna
armtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcayga
rgcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURE 14F

U_R-13 heavy chain nucleotide sequence (SEQ ID NO:590)

carathacnmtnaargarwsnggnccnacnmtngtnaarccnacncaracnmtnacnmtnacnt
gyacnttywsnggnttywsnmtnwsnacnggnggngtnggngtnggntggathmgncarccncc
nggnaargcnmtngartggmtngcnmtnathtaytggaaygtngaraarmgntaywsnccnwsn
mtnmgnwsnmgnmtnacnathacnaargcnacnwsnaaraaycargtngtnmtnacnatgacna
ayatggayccngtngayacngcnacntaytaytgygcncaymgncayacnaayccnttygarta
ytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccn
mtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargayt
ayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacntt
yccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsn
aayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngaya
aracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggncc
nwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtn
acntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayg
gngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngt
ngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtn
wsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgng
arccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnac
ntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccn
garaayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsna
armtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcayga
rgcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_R-14 heavy chain nucleotide sequence (SEQ ID NO:591)

carathacnmtnaargarwsnggnccnacnmtngtnaarccnacncaracnmtnacnmtnacnt
gyacnttywsnggnttywsnmtnwsnacnggnggngtnggngtnggntggathmgncarccncc
nggnaargcnmtngartggmtngcnmtnathtaytggaaygaygaygayaarmgntaywsnccnwsn
mtnaarwsnmgnmtnacnathacnaargayacnwsnaaraaycargtngtnmtnacnatgacna
ayatggayccngtngayacngcnacntaytaytgygcncaymgnggngarmtnccnttygayta
ytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccn
mtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargayt
ayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacntt
yccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsn
aayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngaya
aracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggncc
nwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtn
acntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayg
gngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngt
ngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtn
wsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgng
arccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnac
ntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccn
garaayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsna
armtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcayga
rgcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURE 14G

UH-15 heavy chain nucleotide sequence (SEQ ID NO:591)

carathacnmtnaargarwsnggnccnacnmtngtnaarccnacncaracnmtnacnmtnacnt
gyacnttywsnggnttywsnmtnwsnacnggnggngtnggngtnggntggathmgncarccncc
nggnaargcnmtngartggmtngcnmtnathtaytggaaygaygayaarmgntaywsnccnwsn
mtnaarwsnmgnmtnacnathacnaargayacnwsnaaraaycargtngtnmtnacnatgacna
ayatggayccngtngayacngcnacntaytaytgygcncaymgnggngarmtnccnttygayta
ytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccn
mtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargayt
ayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacntt
yccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsn
aayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngaya
aracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggncc
nwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtn
acntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayg
gngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngt
ngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtn
wsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgng
arccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnac
ntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccn
garaayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsna
armtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcayga
rgcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_R-16 heavy chain nucleotide sequence (SEQ ID NO:592)

gargtncarmtngtngarwsnggnggnggnmtngtnaarccnggnggnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyccnttywsnmgntaywsnatgaaytgggtnmgncargcnccnggnaa
rggnmtngartgggtnwsngcnathwsnwsnwsnwsnwsntayathtaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaygcnaaraaywsnmtntaymtncaratgaaywsnm
tnmgngcngargayacngcngtntaytaytgygcnmgngaymgngtnggngcnacnccngaygc
nttygayathtggggncarggnacnatggtnacngtnwsnwsngcnwsnacnaarggnccnwsn
gtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtng
tnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngt
ncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtn
ccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacna
argtngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngt
ngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacn
ccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggt
aygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnac
nttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaar
tgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggnc
arccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargt
nwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaay
ggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttym
tntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngt
natgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURE 14H

U_B-17 heavy chain nucleotide sequence (SEQ ID NO:593)

gargtncarmtnmtngarwsnggnggnggnmtngtncarccnggnggnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntaygcnatgaaytgggtnmgncargcnccnggnaa
rggnmtngartgggtnwsngcnathwsnggnwsnggnggnwsnacntaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaywsnaaraayacnmtntaymtncaratgaaywsnm
tnmgngcngargayacngcngtntaytaytgygcnaargarggnathgcngtngcnggnacngc
ngartaytaytaytaytaygcnatggaygtntggggncarggnacnacngtnacngtnwsnwsn
gcnwsnacnaarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsna
cngcngcnmtnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaayws
nggngcnmtnacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsn
mtnwsnwsngtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtng
aycayaarccnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgycc
nccntgyccngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargay
acnmtnatgathwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayc
cngargtncarttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmg
ngargarcarttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytgg
mtnaayggnaargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraara
cnathwsnaaracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgnga
rgaratgacnaaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayath
gcngtngartgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtng
aywsngayggnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcargg
naaygtnttywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtn
wsnmtnwsnccnggnaar

U_B-18 heavy chain nucleotide sequence (SEQ ID NO:594)

gargtncarmtnmtngarwsnggnggnggnmtngtncarccnggnggnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntaygcnatgwsntgggtnmgncargcnccnggnaa
rggnmtngartgggtnwsngcnathwsnggnwsnggnggnwsnacntaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaywsnaaraayacnmtntaymtncaratgaaywsnm
tnmgngcngargayacngcngtntaytaytgygcnaargarggnathgcngcnmgngaywsnta
ytaytaytaygcnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacn
aarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnm
tnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmt
nacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsn
gtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarc
cnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgycc
ngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatg
athwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtnc
arttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarca
rttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggn
aargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsna
aracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgac
naaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngar
tgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayg
gnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtntt
ywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsn
ccnggnaar

FIGURE 14I

U_B-19 heavy chain nucleotide sequence (SEQ ID NO:595)

gargtncarmtnmtngarwsnggnggnggnmtngtncarccnggnggnwsnmtnmgnmtnwsnt
gyacngcnwsnggnttyacnttywsnwsntaygcnatgwsntgggtnmgncargcnccnggnaa
rggnmtngartgggtnwsngcnathwsnggnwsnggnggnwsnacntaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaywsnaaraayacnmtntaymtncaratgaaywsnm
tnmgngcngargayacngcngartaytaytgygcnaargarggnathgcnggnmgngaywsnta
ytaytaytayggnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacn
aarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnm
tnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmt
nacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsn
gtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarc
cnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgycc
ngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatg
athwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtnc
arttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarca
rttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggn
aargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsna
aracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgac
naaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngar
tgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayg
gnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtntt
ywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsn
ccnggnaar

U_B-20 heavy chain nucleotide sequence (SEQ ID NO:595)

gargtncarmtnmtngarwsnggnggnggnmtngtncarccnggnggnwsnmtnmgnmtnwsnt
gyacngcnwsnggnttyacnttywsnwsntaygcnatgwsntgggtnmgncargcnccnggnaa
rggnmtngartgggtnwsngcnathwsnggnwsnggnggnwsnacntaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaywsnaaraayacnmtntaymtncaratgaaywsnm
tnmgngcngargayacngcngartaytaytgygcnaargarggnathgcnggnmgngaywsnta
ytaytaytayggnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacn
aarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnm
tnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmt
nacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsn
gtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarc
cnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgycc
ngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatg
athwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtnc
arttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarca
rttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggn
aargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsna
aracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgac
naaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngar
tgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayg
gnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtntt
ywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsn
ccnggnaar

FIGURE 14J

U_B-21 heavy chain nucleotide sequence (SEQ ID NO:596)

cargtncarmtngtngarwsnggnggnggngtngtncarccnggnmgnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnmtngartgggtngcnttyathwsngaygayggnwsnacnaartaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaywsnatgaayacnmtntaymtncaratgaaywsnm
tnmgngcngargayacngcngtntaytaytgygcnmgnwsntaytaygaywsnwsnggntayta
ytayggnttygaytaytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggn
ccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggnt
gymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnws
nggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtn
acngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsna
ayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcncc
nccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsn
mgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttya
aytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaa
ywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargar
tayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracna
arggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraa
ycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggar
wsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnt
tyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntg
ywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggn
aar

U_B-22 heavy chain nucleotide sequence (SEQ ID NO:596)

cargtncarmtngtngarwsnggnggnggngtngtncarccnggnmgnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnmtngartgggtngcnttyathwsngaygayggnwsnacnaartaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaywsnatgaayacnmtntaymtncaratgaaywsnm
tnmgngcngargayacngcngtntaytaytgygcnmgnwsntaytaygaywsnwsnggntayta
ytayggnttygaytaytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggn
ccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggnt
gymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnws
nggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtn
acngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsna
ayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcncc
nccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsn
mgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttya
aytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaa
ywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargar
tayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracna
arggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraa
ycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggar
wsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnt
tyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntg
ywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggn
aar

FIGURE 14K

U_B-23 heavy chain nucleotide sequence (SEQ ID NO:597)

cargtncarmtngtngarwsnggnggnggngtngtncarccnggnmgnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnmtngartgggtngcngtnathtggtaygayggnwsnaayaartaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaywsnaaraayacnmtntaymtncaratgaaywsnm
tnmgngcngargayacngcngtntaytaytgygcnmgnaaygtnathgaytaytggggncargg
nacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccnmtngcnccntgy
wsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargaytayttyccngarc
cngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacnttyccngcngtnmt
ncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsnaayttyggnacn
caracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngayaaracngtngarm
gnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggnccnwsngtnttymt
nttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtnacntgygtngtn
gtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayggngtngargtnc
ayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngtngtnwsngtnmt
nacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtnwsnaayaarggn
mtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgngarccncargtnt
ayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnacntgymtngtnaa
rggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccngaraayaaytay
aaracnacnccnccnatgmtngaywsngayggnwsnttytttymtntaywsnaarmtnacngtng
ayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcaygargcnmtncayaa
ycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_B-24 heavy chain nucleotide sequence (SEQ ID NO:598)

cargtncarmtngtngarwsnggnggnggngtngtncarccnggnmgnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntaygayatgcaytgggtnmgncargcnccnggnaa
rggnmtngartgggtngcngtnathtggtaygayggnwsnathaartaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaywsnaaraayacnmtntaymtncaratgaaywsnm
tnmgngcngargayacngcngtntaytaytgygcnmgnggnggngcnacnggngcngartaytt
ycarcaytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtn
ttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtna
argaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtnca
yacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccn
wsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaarg
tngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngc
nggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccn
gargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtayg
tngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacntt
ymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgy
aargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarc
cnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnws
nmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggn
carccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttytttymtnt
aywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnat
gcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURE 14L

U_R-25 heavy chain nucleotide sequence (SEQ ID NO:598)

cargtncarmtngtngarwsnggnggnggngtngtncarccnggnmgnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntaygayatgcaytgggtnmgncargcnccnggnaa
rggnmtngartgggtngcngtnathtggtaygayggnwsnathaartaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaywsnaaraayacnmtntaymtncaratgaaywsnm
tnmgngcngargayacngcngtntaytaytgygcnmgnggnggngcnacnggngcngartaytt
ycarcaytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtn
ttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtna
argaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtnca
yacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccn
wsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaarg
tngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngc
nggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccn
gargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtayg
tngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacntt
ymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgy
aargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarc
cnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnws
nmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggn
carccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtnt
aywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnat
gcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_R-26 heavy chain nucleotide sequence (SEQ ID NO:599)

cargtncarmtngtngarwsnggnggnggngtngtncarccnggnmgnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnmtngartgggtngcngtnathtggtaygayggnwsnaayaartaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaywsnaaraayacnmtntaymtncaratgaaywsnm
tnmgngcngargayacngcngtntaytaytgygtnmtnmtntggttyggngaracnttygayta
ytggggncarggnwsnmtngtnacngtnwsnccngcnwsnacnaarggnccnwsngtnttyccn
mtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargayt
ayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacntt
yccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsn
aayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngaya
aracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggncc
nwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtn
acntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayg
gngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngt
ngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtn
wsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgng
arccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnac
ntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccn
garaayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsna
armtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcayga
rgcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURE 14M

U_H-27 heavy chain nucleotide sequence (SEQ ID NO:600)

cargtncarmtngtngarwsnggnggnggngtngtncarccnggnmgnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnmtngartgggtngcngtnathtggwsngayggnwsnaayaartaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaywsnaaraayacnmtntaymtncaratgaaywsnm
tnmgngcngargayacngcngtntaytaytgygcnmgnaaymtnccnttygaytaytggggnca
rggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccnmtngcnccn
tgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargaytayttyccng
arccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacnttyccngcngt
nmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsnaayttyggn
acncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngayaaracngtng
armgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggnccnwsngtntt
ymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtnacntgygtn
gtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayggngtngarg
tncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngtngtnwsngt
nmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtnwsnaayaar
ggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgngarccncarg
tntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnacntgymtngt
naarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccngaraayaay
tayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsnaarmtnacng
tngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcaygargcnmtnca
yaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_H-28 heavy chain nucleotide sequence (SEQ ID NO:601)

cargtncarmtngtngarwsnggnggnggngtngtncarccnggnmgnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnmtngartgggtngcngtnathtgggaygayggnwsnaaycartaytayacngaywsngtn
aarggnmgnttyacngtnwsnmgngayaaywsnaaraayacnmtnttymtncaratgaaywsnm
tnmgngcngargayacngcngtntaytaytgygcnmgnwsncaytayggnggngaytaygayta
ytayggnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacnaarggn
ccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggnt
gymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnws
nggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtn
acngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsna
ayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcncc
nccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsn
mgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttya
aytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaa
ywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargar
tayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracna
arggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraa
ycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggar
wsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnt
tyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntg
ywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggn
aar

FIGURE 14N

U_B-29 heavy chain nucleotide sequence (SEQ ID NO:602)

cargtncarmtngtngarwsnggnggnggngtngtncarccnggnmgnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnmtngartgggtngcngtnathtggtaygayggnwsnaayaarmgntaygtngaywsngtn
aarggnmgnttyacnathwsnmgngayaaywsnaaraaayacnmtntaymtncaratgaaywsnm
tnmgngcngargayacngcngtntaytaytgygcnmgngayggntggcarcarcargcnccntt
ygaytaytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtn
ttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtna
argaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtnca
yacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccn
wsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaarg
tngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngc
nggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccn
gargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtayg
tngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacntt
ymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgy
aargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarc
cnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnws
nmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggn
carccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtnt
aywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnat
gcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_B-30 heavy chain nucleotide sequence (SEQ ID NO:603)

cargtncarmtngtngarwsnggnggnggngtngtncarccnggnmgnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttymgnwsncayggnatgcaytgggtnmgncargcnccnggnaa
rggnmtngartgggtngcngtnathtggtaygayggnwsnaayaaraaytaygcngaywsngtn
mgnggnmgnttyacnathwsnmgngayaaywsnaaraaayacnmtngaymtncaratgaaywsnm
tnmgngcngargayacngcngtntaytaytgygcnmgntggggnathwsngcnccnttygaytg
ytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccn
mtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargayt
ayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacntt
yccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsn
aayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngaya
aracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggncc
nwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtn
acntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayg
gngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngt
ngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtn
wsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgng
arccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnac
ntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccn
garaayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsna
armtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcayga
rgcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURE 14O

U_R-31 heavy chain nucleotide sequence (SEQ ID NO:604)

gargtncarmtngtngarwsnggnggnggnmtngtncarccnggnggnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsngcntaywsnatgaaytgggtnmgncargcnccnggnaa
rggnmtngartgggtnwsntayathwsnwsnwsnggnmgnacnathtaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaygcnaaraaywsnmtnttymtncaratgaaywsnm
tnmgngaygargayacngcngtntaytaytgygcnmtntgggcnccnttygaytaytggggnca
rggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccnmtngcnccn
tgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargaytayttyccng
arccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacnttyccngcngt
nmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsnaayttyggn
acncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngayaaracngtng
armgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggnccnwsngtntt
ymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtnacntgygtn
gtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayggngtngarg
tncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngtngtnwsngt
nmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtnwsnaayaar
ggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgngarccncarg
tntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnacntgymtngt
naarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccngaraayaay
tayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsnaarmtnacng
tngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcaygargcnmtnca
yaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_R-32 heavy chain nucleotide sequence (SEQ ID NO:605)

gargtncarmtngtngarwsnggnggnggnmtngtncarccnggnggnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntaywsnatgaaytgggtnmgncargcnccnggnaa
rggnmtngartgggtnwsncayathwsnwsnwsnwsnmgnacnathtaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaygcnaaraaywsngtntaymtncaratgaaywsnm
tnmgngaygargayacngcngtntaytaytgygcnmgngayggntayaaytggaayggnggngg
naaytaytayggnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacn
aarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnm
tnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmt
nacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsn
gtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarc
cnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgycc
ngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatg
athwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtnc
arttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarca
rttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggn
aargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsna
aracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgac
naaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngar
tgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayg
gnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtntt
ywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsn
ccnggnaar

FIGURE 14P

U_B-33 heavy chain nucleotide sequence (SEQ ID NO:606)

gargtncarmtngtngarwsnggnggnggnmtngtncarccnggnggnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntaywsnatgaaytgggtnmgncargcnccnggnaa
rggnmtngartgggtnwsncayathwsnmgnwsnwsnmgnacnathtaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaygcnaaraaywsnmtntaymtncaratgaaywsnm
tnmgngaygargayacngcngtntaytaytgygcnmgngayggntayaaytggaayaayggngg
ntaytaytayggnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacn
aarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnm
tnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmt
nacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsn
gtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarc
cnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgycc
ngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatg
athwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtnc
arttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarca
rttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggn
aargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsna
aracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgac
naaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngar
tgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayg
gnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtntt
ywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsn
ccnggnaar

U_B-34 heavy chain nucleotide sequence (SEQ ID NO:606)

gargtncarmtngtngarwsnggnggnggnmtngtncarccnggnggnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntaywsnatgaaytgggtnmgncargcnccnggnaa
rggnmtngartgggtnwsncayathwsnmgnwsnwsnmgnacnathtaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaygcnaaraaywsnmtntaymtncaratgaaywsnm
tnmgngaygargayacngcngtntaytaytgygcnmgngayggntayaaytggaayaayggngg
ntaytaytayggnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacn
aarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnm
tnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmt
nacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsn
gtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarc
cnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgycc
ngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatg
athwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtnc
arttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarca
rttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggn
aargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsna
aracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgac
naaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngar
tgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayg
gnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtntt
ywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsn
ccnggnaar

FIGURE 14Q

U_R-35 heavy chain nucleotide sequence (SEQ ID NO:607)

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsncaracnmtnwsnmtnacnt
gyacngtnwsnggnggnwsngtnwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnmtngartggathggntayathcaywsnwsnggnwsnacntaytayaayccnwsn
mtnaarwsnmgngtnacnathwsngtngayacnwsnaaraaycarttywsnmtnaaymtnwsnw
sngtnacngcngcngayacngcngtntaytaytgygcnmgnggnccntaytayggnatggaygt
ntggggncarggnacnacngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccn
mtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargayt
ayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacntt
yccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsn
aayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngaya
aracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggncc
nwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtn
acntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayg
gngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngt
ngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtn
wsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgng
arccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnac
ntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccn
garaayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsna
armtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcayga
rgcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_R-36 heavy chain nucleotide sequence (SEQ ID NO:608)

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsncaracnmtnwsnmtnacnt
gyacngtnwsnggnggnwsnathwsnmgnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnmtngartggathggntayathtaycaywsnggnwsnacntaytayaayccnwsn
mtnaarwsnmgngtnaayatgwsngtngayacnwsnaaraaycarttywsnmtnaarmtnwsnw
sngtnacngcngcngayacngcngtntaytaytgygcnmgngcnmtnmgnggnathgtnmtnat
ggtntaygtnmtnggngcnmtngayathtggggncarggnacnaargtnacngtnwsnwsngcn
wsnacnaarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacng
cngcnmtnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsngg
ngcnmtnacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtn
wsnwsngtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngayc
ayaarccnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccncc
ntgyccngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacn
mtnatgathwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccng
argtncarttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgnga
rgarcarttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtn
aayggnaargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracna
thwsnaaracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngarga
ratgacnaaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcn
gtngartgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngayw
sngayggnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaa
ygtnttywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsn
mtnwsnccnggnaar

FIGURE 14R

U_B-37 heavy chain nucleotide sequence (SEQ ID NO:608)

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsncaracnmtnwsnmtnacnt
gyacngtnwsnggnggnwsnathwsnmgnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnmtngartggathggntayathtaycaywsnggnwsnacntaytayaayccnwsn
mtnaarwsnmgngtnaayatgwsngtngayacnwsnaaraaycarttywsnmtnaarmtnwsnw
sngtnacngcngcngayacngcngtntaytaytgygcnmgngcnmtnmgnggnathgtnmtnat
ggtntaygtnmtnggngcnmtngayathtggggncarggnacnaargtnacngtnwsnwsngcn
wsnacnaarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacng
cngcnmtnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsngg
ngcnmtnacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtn
wsnwsngtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngayc
ayaarccnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccncc
ntgyccngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacn
mtnatgathwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccng
argtncarttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgnga
rgarcarttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtn
aayggnaargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracna
thwsnaaracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngarga
ratgacnaaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcn
gtngartgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngayw
sngayggnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaa
ygtnttywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsn
mtnwsnccnggnaar

U_B-38 heavy chain nucleotide sequence (SEQ ID NO:609)

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsncaracnmtnwsnmtnacnt
gyacngtnwsnggnggnwsnathwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnmtngartggathggntayathtaytaywsnggnwsnacntaytayaayccnwsn
mtnaarwsnmgngtnacnathwsngtngayacnwsnaaraaycarttywsnmtnaarmtnwsnw
sngtnacngcngcngayacngcngtntaytaytgygcnmgngaygaracngtngtnmgnggnmt
nathmgntaytgytayggnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcn
wsnacnaarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacng
cngcnmtnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsngg
ngcnmtnacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtn
wsnwsngtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngayc
ayaarccnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccncc
ntgyccngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacn
mtnatgathwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccng
argtncarttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgnga
rgarcarttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtn
aayggnaargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracna
thwsnaaracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngarga
ratgacnaaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcn
gtngartgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngayw
sngayggnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaa
ygtnttywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsn
mtnwsnccnggnaar

FIGURE 14S

U_B-39 heavy chain nucleotide sequence (SEQ ID NO:610)

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsncaracnmtnwsnmtnaayt
gyacngtnwsnggnggnwsnathwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnmtngartggathggntayathcaytaywsnggnwsnacntaytayaayccnwsn
mtnaarwsnmgnathacnathwsngcngayacnwsnaaraaycarttywsnmtnaarmtnaayw
sngtnacngcngcngayacngcngtntaytaytgygcnmgngaymgnggnggnggngaytaygg
nmgnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacnaarggnccn
wsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgym
tngtnaargaytaytttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsngg
ngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacn
gtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaaya
cnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccncc
ngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgn
acnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaayt
ggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaayws
nacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartay
aartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarg
gncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraayca
rgtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsn
aayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyt
tymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgyws
ngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_B-40 heavy chain nucleotide sequence (SEQ ID NO:611)

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsncaracnmtnwsnmtnaayt
gyacngtnwsnggnggnwsnathwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnmtngartggathggntayathcaytaywsnggnwsnacntaytayaayccnwsn
mtnaarwsnmgnathacnathwsngcngayacnwsnaaraaycarttywsnmtnaarmtnaayw
sngtnacngcngcngayacngcngtntaytaytgygcnmgngaymgnggnggnggngaytaygg
nmgnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacnaarggnccn
wsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgym
tngtnaargaytaytttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsngg
ngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacn
gtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaaya
cnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccncc
ngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgn
acnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaayt
ggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaayws
nacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartay
aartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarg
gncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraayca
rgtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsn
aayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyt
tymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgyws
ngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURE 14T

U_B-41 heavy chain nucleotide sequence (SEQ ID NO:612)

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsncaracnmtnwsnmtnacnt
gyacngtnwsnggnggnwsnathwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnmtngartggathggntayathcaywsnwsnggnwsnacntaytayaayccnwsn
mtnaarwsnmgnathacnaarwsngtngayacnwsnaaraaycarttywsnmtnaarmtnwsnw
sngtnacngcngcngayacngcngtntaytaytgygcnmgnwsnaayaaytayggntgyttygc
nmtntggggnmgnggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtntty
ccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaarg
aytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayac
nttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsn
wsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtng
ayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcngg
nccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngar
gtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtng
ayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymg
ngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaar
gtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnm
gngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmt
nacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncar
ccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntayw
snaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgca
ygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_B-42 heavy chain nucleotide sequence (SEQ ID NO:613)

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsncaracnmtnwsnmtnacnt
gyacngtnwsnggnggnwsnathwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnmtngartggathggntayathcaywsnwsnggnwsnacntaytayaayccnwsn
mtnaarwsnmgnathacnaarwsngtngayacnwsnaaraaycarttywsnmtnaarmtnwsnw
sngtnacngcngcngayacngcngtntaytaytgygcnmgnwsnaayaaytayggntgyttygc
nmtntggggnmgnggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtntty
ccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaarg
aytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayac
nttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsn
wsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtng
ayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcngg
nccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngar
gtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtng
ayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymg
ngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaar
gtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnm
gngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmt
nacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncar
ccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntayw
snaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgca
ygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURE 14U

U_B-43 heavy chain nucleotide sequence (SEQ ID NO:614)

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsncaracnmtnwsnmtnacnt
gyacngtnwsnggnggnwsnathwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnmtngartggathggntayathcaytaywsnggnwsnacntaytayaayccnwsn
mtnaarwsnmgngtnacnathwsngtngayacnwsnaaraaycarttywsnmtnaarmtnwsnw
sngtnacngcngcngayacngcngtntaytaytgygcnwsnggntayaaytayggnmtntayta
ytaygaywsnwsnggntayccnwsntaytaytayggnatggaygtntggggncarggnacnacn
gtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccnmtngcnccntgywsnmgnw
snacnwsngarwsnacngcngcnmtnggntgymtngtnaargaytayttyccngarccngtnac
ngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacnttyccngcngtnmtncarwsn
wsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsnaayttyggnacncaracnt
ayacntgyaaygtngaycayaarccnwsnaayacnaargtngayaaracngtngarmgnaartg
ytgygtngartgyccnccntgyccngcnccnccngtngcnggnccnwsngtnttymtnttyccn
ccnaarccnaargayacnmtnatgathwsnmgnacnccngargtnacntgygtngtngtngayg
tnwsncaygargayccngargtncarttyaaytggtaygtngayggngtngargtncayaaygc
naaracnaarccnmgngargarcarttyaaywsnacnttymgngtngtnwsngtnmtnacngtn
gtncaycargaytggmtnaayggnaargartayaartgyaargtnwsnaayaarggnmtnccng
cnccnathgaraaracnathwsnaaracnaarggncarccnmgngarccncargtntayacnmt
nccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnacntgymtngtnaarggntty
tayccnwsngayathgcngtngartgggarwsnaayggncarccngaraayaaytayaaracna
cnccnccnatgmtngaywsngayggnwsnttyttymtntaywsnaarmtnacngtngayaarws
nmgntggcarcarggnaaygtnttywsntgywsngtnatgcaygargcnmtncayaaycaytay
acncaraarwsnmtnwsnmtnwsnccnggnaar

U_B-44 heavy chain nucleotide sequence (SEQ ID NO:615)

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsncaracnmtnwsnmtnacnt
gyacngtnwsnggnggnwsnathwsnwsnggngaytaytaytggaaytgggtnmgncarcaycc
nggnaarggnmtngartggathggntayathtaytaywsnggnggnacntaytayaayccnwsn
mtnaarwsnmgngtnacnathwsngtngayacnwsnaaraaycarttywsnmtnaarmtnttyw
sngtnacngcngcngayacngcngtntayttytgygcnmgnacntaytaygayathmtnacngg
ntayccnttytayttygaytaytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacn
aarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnm
tnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmt
nacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsn
gtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarc
cnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgycc
ngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatg
athwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtnc
arttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarca
rttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggn
aargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsna
aracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgac
naaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngar
tgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayg
gnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtntt
ywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsn
ccnggnaar

FIGURE 14V

U_B-45 heavy chain nucleotide sequence (SEQ ID NO:616)

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsncaracnmtnwsnmtnacnt
gyacngtnwsnggnggnwsnathwsnwsnggngaytaytaytggaaytgggtnmgncarcaycc
nggnaarggnmtngartggathggntayathtaytaywsnggnggnacntaytayaayccnwsn
mtnaarwsnmgngtnacnathwsngtngayacnwsnaaraaycarttywsnmtnaarmtnttyw
sngtnacngcngcngayacngcngtntayttytgygcnmgnacntaytaygayathmtnacngg
ntayccnttytayttygaytaytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacn
aarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnm
tnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmt
nacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsn
gtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarc
cnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgycc
ngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatg
athwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtnc
arttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarca
rttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggn
aargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsna
aracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgac
naaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngar
tgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayg
gnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtntt
ywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsn
ccnggnaar

U_B-46 heavy chain nucleotide sequence (SEQ ID NO:617)

cargtncarmtncarcartggggngcnggnmtnmtnaarccnwsngaracnmtnwsnmtnacnt
gygcngtntayggnggnwsnttywsnggntaytaytggwsntggathmgncarccnccnggnaa
rggnmtngartggathggngarathaaycaywsnggnwsnacnaaytayaayccnwsnmtnaar
wsnmgngtnacnathwsngtngayacnwsnaaraaycarttywsnmtnaarmtnwsnwsngtna
cngcngcngayacngcngtntaytaytgygcnmgnggnggntaywsnwsnwsntggtaytggtt
ygayccntggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtn
ttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtna
argaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtnca
yacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccn
wsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaarg
tngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngc
nggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccn
gargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtayg
tngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacntt
ymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgy
aargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarc
cnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnws
nmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggn
carccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtnt
aywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnat
gcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURE 14W

U_B-47 heavy chain nucleotide sequence (SEQ ID NO:618)

cargtncarmtncarcartggggngcnggnmtnmtnaarccnwsngaracnmtnwsnmtnacnt
gygcngtntayggnggnwsnttywsnggntaytaytggwsntggathmgncarccnccnggnaa
rggnmtngartggathggngarathaaycaywsnggnwsnacnaaytayaayccnwsnmtnaar
wsnmgngtnacnathwsngtngayacnwsnaaraaycarttywsnmtnaarmtnwsnwsngtna
cngcngcngayacngcngtntaytaytgygcnmgnggnggntaywsnwsnwsntggttytggtt
ygayccntggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtn
ttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtna
argaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtnca
yacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccn
wsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaarg
tngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngc
nggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccn
gargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtayg
tngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacntt
ymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgy
aargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarc
cnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnws
nmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggn
carccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtnt
aywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnat
gcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_B-48 heavy chain nucleotide sequence (SEQ ID NO:618)

cargtncarmtncarcartggggngcnggnmtnmtnaarccnwsngaracnmtnwsnmtnacnt
gygcngtntayggnggnwsnttywsnggntaytaytggwsntggathmgncarccnccnggnaa
rggnmtngartggathggngarathaaycaywsnggnwsnacnaaytayaayccnwsnmtnaar
wsnmgngtnacnathwsngtngayacnwsnaaraaycarttywsnmtnaarmtnwsnwsngtna
cngcngcngayacngcngtntaytaytgygcnmgnggnggntaywsnwsnwsntggttytggtt
ygayccntggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtn
ttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtna
argaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtnca
yacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccn
wsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaarg
tngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngc
nggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccn
gargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtayg
tngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacntt
ymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgy
aargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarc
cnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnws
nmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggn
carccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtnt
aywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnat
gcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURE 14X

U_B-49 heavy chain nucleotide sequence (SEQ ID NO:618)

cargtncarmtncarcartggggngcnggnmtnmtnaarccnwsngaracnmtnwsnmtnacnt
gygcngtntayggnggnwsnttywsnggntaytaytggwsntggathmgncarccnccnggnaa
rggnmtngartggathggngarathaaycaywsnggnwsnacnaaytayaayccnwsnmtnaar
wsnmgngtnacnathwsngtngayacnwsnaaraaycarttywsnmtnaarmtnwsnwsngtna
cngcngcngayacngcngtntaytaytgygcnmgnggnggntaywsnwsnwsntggttytggtt
ygayccntggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtn
ttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtna
argaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtnca
yacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccn
wsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaarg
tngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngc
nggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccn
gargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtayg
tngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacntt
ymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgy
aargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarc
cnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnws
nmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggn
carccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtnt
aywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnat
gcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_B-50 heavy chain nucleotide sequence (SEQ ID NO:618)

cargtncarmtncarcartggggngcnggnmtnmtnaarccnwsngaracnmtnwsnmtnacnt
gygcngtntayggnggnwsnttywsnggntaytaytggwsntggathmgncarccnccnggnaa
rggnmtngartggathggngarathaaycaywsnggnwsnacnaaytayaayccnwsnmtnaar
wsnmgngtnacnathwsngtngayacnwsnaaraaycarttywsnmtnaarmtnwsnwsngtna
cngcngcngayacngcngtntaytaytgygcnmgnggnggntaywsnwsnwsntggttytggtt
ygayccntggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtn
ttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtna
argaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtnca
yacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccn
wsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaarg
tngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngc
nggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccn
gargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtayg
tngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacntt
ymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgy
aargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarc
cnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnws
nmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggn
carccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtnt
aywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnat
gcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURE 14Y

U_H-51 heavy chain nucleotide sequence (SEQ ID NO:619)

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsngaracnmtnwsnmtnacnt
gyacngtnwsnggnggnwsnathwsnwsntaytaytggwsntggathmgncarccngcnggnaa
rggnmtngartggathggnmgnathtayacnwsnggnacnacnaaytayaayccnwsnmtnaar
wsnmgngtnacnatgwsngtngayacnwsnaaraaycarttywsnmtnaarmtnwsnwsngtna
cngcngcngayacngcngtntaytaytgygcnmgngayggntaywsntayggncaytaytaytа
ytayggnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacnaarggn
ccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggnt
gymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnws
nggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtn
acngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsna
ayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcncc
nccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsn
mgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttya
aytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaa
ywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargar
tayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracna
arggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraa
ycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggar
wsnaaygggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnt
tyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntg
ywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggn
aar

U_H-52 heavy chain nucleotide sequence (SEQ ID NO:620)

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsngaracnmtnwsnmtnacnt
gyacngtnwsnggnggnwsngtnwsnwsnggnggnwsntaytggwsntggathmgncarccncc
nggnaarggnmtngartggathggntayathtaytaywsnggnwsnacnaaytayaayccnwsn
mtnaarwsnmgngtnacnathwsnathgtnacnwsnmgnaaycarttywsnmtnaarmtnwsnw
sngtnacngcngcngayacngcngtntaytaytgygcnmgnwsngcnmtnmgntayttygaytg
gmtnttywsngaygtnwsngayathtggggncarggnacnatggtnacngtnwsnwsngcnwsn
acnaarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcng
cnmtnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngc
nmtnacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsn
wsngtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycaya
arccnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntg
yccngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtn
atgathwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngarg
tncarttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngarga
rcarttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaay
ggnaargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathw
snaaracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargarat
gacnaaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtn
gartgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsng
ayggnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygt
nttywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtn
wsnccnggnaar

FIGURE 14Z

U_H-53 heavy chain nucleotide sequence (SEQ ID NO:620)

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsngaracnmtnwsnmtnacnt
gyacngtnwsnggnggnwsngtnwsnwsnggnggnwsntaytggwsntggathmgncarccncc
nggnaarggnmtngartggathggntayathtaytaywsnggnwsnacnaaytayaayccnwsn
mtnaarwsnmgngtnacnathwsnathgtnacnwsnmgnaaycarttywsnmtnaarmtnwsnw
sngtnacngcngcngayacngcngtntaytaytgygcnmgnwsngcnmtnmgntayttygaytg
gmtnttywsngaygtnwsngayathtggggncarggnacnatggtnacngtnwsnwsngcnwsn
acnaarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcng
cnmtnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngc
nmtnacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsn
wsngtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycaya
arccnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntg
yccngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtn
atgathwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngarg
tncarttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngarga
rcarttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaay
ggnaargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathw
snaaracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargarat
gacnaaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtn
gartgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsng
ayggnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygt
nttywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtn
wsnccnggnaar

U_H-54 heavy chain nucleotide sequence (SEQ ID NO:621)

gargtncarmtngtncarwsnggngcngarmtnaaraarccnggngarwsnmtnaarathwsnt
gyaarggnwsnggntaymgnttyacnwsntaytggathggntgggtnmgncaratgccnggnaa
rggnmtngartggatgggnathathtayccngaygaywsngayacnmgntaywsnccnwsntty
carggncargtnacnathwsngcngayaarwsnathwsnacngcntaymtncartggwsnwsnm
tnaargcnwsngayacngcnatgtaytaytgygcnmgncaraarwsntayggntaywsntaytt
ygaytaytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtn
ttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtna
argaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtnca
yacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccn
wsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaarg
tngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngc
nggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccn
gargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtayg
tngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacntt
ymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgy
aargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarc
cnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnws
nmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggn
carccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtnt
aywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnat
gcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURE 14AA

U_B-55 heavy chain nucleotide sequence (SEQ ID NO:622)

gargtncarmtngtncarwsnggngcngargtnaaraarccnggngarwsnmtnaarathwsnt
gyaarggnwsnggntaywsnttyacnwsntaytggathggntgggtnmgncaratgccnggnaa
rggnmtngartggatgggnathathtayccngaygaywsngaygcnmgntaywsnccnwsntty
carggncargtnacnathwsngcngayaarwsnathaayacngcntaymtncartggwsnwsnm
tnaargcnwsngayacngcnatgtaytaytgygcnmgncarggntayggnwsnggntggggnta
yttygaytaytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsn
gtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtng
tnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngt
ncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtn
ccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacna
argtngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngt
ngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacn
ccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggt
aygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnac
nttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaar
tgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggnc
arccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargt
nwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaay
ggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttym
tntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngt
natgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_B-56 heavy chain nucleotide sequence (SEQ ID NO:623)

gargtncarmtngtncarwsnggngcngargtnaaraarccnggngarwsnmtnaarathwsnt
gyaarggnwsnggntaywsnttyacnwsntaytggathggntgggtnmgncaratgccnggnaa
rggnmtngartggatgggnathathtayccnggngaywsngayathmgntaywsnccnwsntty
carggncargtnacnathwsngcngayaarwsnathwsnacngcntaymtncartggwsnwsnm
tnaargcnwsngayacngcnatgtaytaytgygcnmgncarggnmtngcngtngcnggnacnws
ntaytaytaytaytayggnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcn
wsnacnaarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacng
cngcnmtnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsngg
ngcnmtnacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtn
wsnwsngtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngayc
ayaarccnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccncc
ntgyccngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacn
mtnatgathwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccng
argtncarttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgnga
rgarcarttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtn
aayggnaargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracna
thwsnaaracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngarga
ratgacnaaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcn
gtngartgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngayw
sngayggnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaa
ygtnttywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsn
mtnwsnccnggnaar

FIGURE 14AB

U_H-57 heavy chain nucleotide sequence (SEQ ID NO:624)

cargtncarmtncarcarwsnggnccnggnmtngtnaarccnwsncaracnmtnwsnmtnacnt
gygcnathwsnggngaywsngtnwsnwsntaywsngcngcntggaaytggathmgncarwsncc
nwsnmgnggnmtngartggmtnggnmgnacntaytgymgnwsnaartggtayaaygaytaygcn
gtnwsngtnaarwsnmgnathacnathaayccngayacnwsnaaraaycarttywsnmtncarm
tnaaywsngtnacnccngargayacngcngtntaytaytgygcnmgngaymgngcngtngcngg
ntaytaytayggnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacn
aarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnm
tnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmt
nacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsn
gtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarc
cnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgycc
ngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatg
athwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtnc
arttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarca
rttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggn
aargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsna
aracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgac
naaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngar
tgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayg
gnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtntt
ywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsn
ccnggnaar

U_H-58 heavy chain nucleotide sequence (SEQ ID NO:604)

gargtncarmtngtngarwsnggnggnggnmtngtncarccnggnggnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsngcntaywsnatgaaytgggtnmgncargcnccnggnaa
rggnmtngartgggtnwsntayathwsnwsnwsnggnmgnacnathtaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaygcnaaraaywsnmtnttymtncaratgaaywsnm
tnmgngaygargayacngcngtntaytaytgygcnmtntgggcnccnttygaytaytggggnca
rggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccnmtngcnccn
tgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargaytayttyccng
arccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacnttyccngcngt
nmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsnaayttyggn
acncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngayaaracngtng
armgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggnccnwsngtntt
ymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtnacntgygtn
gtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayggngtngarg
tncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngtngtnwsngt
nmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtnwsnaayaar
ggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgngarccncarg
tntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnacntgymtngt
naarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccngaraayaay
tayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsnaarmtnacng
tngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcaygargcnmtnca
yaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURE 14AC

U-V_L-1 light chain variable region nucleotide sequence (SEQ ID NO:625)

gaygtngtnatgcancarwsnccnytnwsnytnccngtncanytnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnytngtntaywsngayggnaaycantayytnaaytggttycarca
rmgnccnggncarwsnccnmgnmgnytnathtayaargtnwsnaaytgggaywsnggngtnccn
gaymgnttyaayggnwsnggnwsnggncangayttycanytnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarwsncancaytggccnathcanttyggncarggnca
nmgnytngarathaar

U-V_L-2 light chain variable region nucleotide sequence (SEQ ID NO:626)

gaygtngtnatgcancarwsnccnytnwsnytnccngtncanytnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnytngtntaywsngayggnaaycantayytnaaytggttycarca
rmgnccnggncarwsnccnmgnmgnytnathtayaargtnwsnaaytgggaywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggncangayttycanytnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyathcarggncancaytggccncancanttyggncarggnca
nmgnytngarathaar

U-V_L-3 light chain variable region nucleotide sequence (SEQ ID NO:627)

gaygtngtnatgcancarwsnccnytnwsnytnccngtncanytnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnytngtntaywsngayggnaaycantayytnaaytggytncarca
rmgnccnggncarwsnccnmgnmgnytnathtayaargtnwsnaaytgggaywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggncangayttycanytnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarggncancaytggccnathcanttyggncarggnca
nmgnytngarathaar

U-V_L-4 light chain variable region nucleotide sequence (SEQ ID NO:627)

gaygtngtnatgcancarwsnccnytnwsnytnccngtncanytnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnytngtntaywsngayggnaaycantayytnaaytggytncarca
rmgnccnggncarwsnccnmgnmgnytnathtayaargtnwsnaaytgggaywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggncangayttycanytnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarggncancaytggccnathcanttyggncarggnca
nmgnytngarathaar

U-V_L-5 light chain variable region nucleotide sequence (SEQ ID NO:628)

Gayathgtnatgcancarcanccnytnwsnytnwsngtncanccnggncarccngcnwsnathw
sntgyaarwsnwsncarwsnytnytncaywsngayggnaarcantayytntaytggtayytnca
raarccnggncarccnccncarytnytnathtaygargtnwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggncangayttycanytnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarggnathcarytnccntgywsnttyggncarggnca
naarytngarathaar

FIGURE 15A

U-V_L-6 light chain variable region nucleotide sequence (SEQ ID NO:629)

gayathgtnatgcancarcanccnytnwsnytnwsngtncanccnggncarccngcnwsnathw
sntgyaarwsnwsncarwsnytnytncaywsngayggnaarcantayytntaytggtayytnca
raarccnggncarccnccncarytnytnathtaygargtnwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggncangayttycanytnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarwsnathcarytnccnytncanttyggnggnggnca
naargtngarathaar

U-V_L-7 light chain variable region nucleotide sequence (SEQ ID NO:629)

gayathgtnatgcancarcanccnytnwsnytnwsngtncanccnggncarccngcnwsnathw
sntgyaarwsnwsncarwsnytnytncaywsngayggnaarcantayytntaytggtayytnca
raarccnggncarccnccncarytnytnathtaygargtnwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggncangayttycanytnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarwsnathcarytnccnytncanttyggnggnggnca
naargtngarathaar

U-V_L-8 light chain variable region nucleotide sequence (SEQ ID NO:630)

gayathgtnatgcancarcanccnytnwsnytnwsngtncanccnggncarccngcnwsnathw
sntgyaarwsnwsncarwsnytnytncaywsngayggnaarcantayytntaytggttyytnca
raarccnggncarccnccncarccnytnathtaygargtnwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggncangayttycanytnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarwsnathcarytnccnathcanttyggncayggnca
nmgnytngarathaar

U-V_L-9 light chain variable region nucleotide sequence (SEQ ID NO:630)

gayathgtnatgcancarcanccnytnwsnytnwsngtncanccnggncarccngcnwsnathw
sntgyaarwsnwsncarwsnytnytncaywsngayggnaarcantayytntaytggttyytnca
raarccnggncarccnccncarccnytnathtaygargtnwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggncangayttycanytnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarwsnathcarytnccnathcanttyggncayggnca
nmgnytngarathaar

U-V_L-11 light chain variable region nucleotide sequence (SEQ ID NO:631)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarggnathgcnaaytayytngcntggtaycarcaraarccnggnaargt
nccnaarytnytnathtaygtngcnwsncanytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargaygtngcncant
aytaytgycaraaytayaaywsngcnccnttycanttyggnccnggncanaargtngayathaar

FIGURE 15B

U-V_L-12 light chain variable region nucleotide sequence (SEQ ID NO:632)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanatha
thtgymgngcnwsncarggnathwsnaaygayytngcntggtaycarcaraarccnggnaargt
nccnaarytnytnathtaygcngcnwsncanytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargaygtngcncant
aytaytgycaraartayaaywsngtnccnytncanttyggnggnggncanaargtngarathaar

U-V_L-13 light chain variable region nucleotide sequence (SEQ ID NO:633)

aayathgtnatgcancarcanccnytnwsnwsnccngtncanytnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnytngtncaywsngayggnaaycantayytnwsntggytncarca
rmgnccnggncarccnccnmgnytnytnathtayaarathwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggngcnggncangayttycanytnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcargcncancarttyccncaycanttyggnccnggnca
naargtngayathaar

U-V_L-14 light chain variable region nucleotide sequence (SEQ ID NO:633)

aayathgtnatgcancarcanccnytnwsnwsnccngtncanytnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnytngtncaywsngayggnaaycantayytnwsntggytncarca
rmgnccnggncarccnccnmgnytnytnathtayaarathwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggngcnggncangayttycanytnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcargcncancarttyccncaycanttyggnccnggnca
naargtngayathaar

U-V_L-15 light chain variable region nucleotide sequence (SEQ ID NO:634)

garathgtnatgcancarcanccnytnwsnwsnccngtncanytnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnytngtncaywsngayggnaaycantayytnwsntggytncarca
rmgnccnggncarccnccnmgnytnytnathtayaarathwsnaaymgnttywsnggngtnccn
gaymgnttywsnggncanggngcnggncangayttycanytnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcargcncancarttyccncaycanttyggnggnggnca
naargtngarathaar

U-V_L-16 light chain variable region nucleotide sequence (SEQ ID NO:635)

garathgtnytncancarwsnccnggncanytnwsnytnwsnccnggngarmgngcncanytnw
sntgymgngcnwsncarcangtnathwsnwsntayytngcntggtaycarcaraarccnggnca
rgcnccnmgnytnytnathwsnggngcnwsnwsnmgngcncanggnathccngaymgnttywsn
ggnwsnggnwsnggncangayttycanytncanathwsnmgnytngarccngargayttygcng
tntaytaytgycarcartayggnwsnwsnccnmgncanttyggncarggncanaargtngarat
haar

FIGURE 15C

U-V_L-17 light chain variable region nucleotide sequence (SEQ ID NO:636)

garathgtnytncancarwsnccnggncanytnwsnytnwsnccnggngarmgngcncanytnw
snтgymgngcnwsncarwsngtnwsnmgnytngcntggtaycarcaraarccnggncargcncc
nmgnytnytnathtayggngcnwsnmgnmgngcncanggnathccngaymgnttywsnggnwsn
ggnwsnggncangayttycanytncanathwsnmgnytngarccngargayttygcngtntayt
aytgycarcartayggnwsnwsnccnmgnwsnttyggncarggncanaarytngarathaar

U-V_L-18 light chain variable region nucleotide sequence (SEQ ID NO:637)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarggnathmgnaaygayytnggntggtaycarcaraarccnggnaargc
nccnaarmgnytnathtaygcngcnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangarttycanytncanathwsnwsnytncarccngargayttygcncant
aytaytgyytncarcayaaywsntayccnccncanttyggncarggncanaargtngarathaar

U-V_L-19 light chain variable region nucleotide sequence (SEQ ID NO:638)

gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngtntggtayca
rcaraarccnggncarccnccnaarytnttyathtaytgggcnwsncanmgngarwsnggngtn
ccngaymgnttycanggnwsnggnwsnggncangayttycanytncanathwsnwsnytncarg
cngargaygtngcngtntaytaytgycarcartaytaywsnttyccntggcanttyggncargg
ncanaargtngarathaar

U-V_L-20 light chain variable region nucleotide sequence (SEQ ID NO:638)

gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngtntggtayca
rcaraarccnggncarccnccnaarytnttyathtaytgggcnwsncanmgngarwsnggngtn
ccngaymgnttycanggnwsnggnwsnggncangayttycanytncanathwsnwsnytncarg
cngargaygtngcngtntaytaytgycarcartaytaywsnttyccntggcanttyggncargg
ncanaargtngarathaar

U-V_L-21 light chain variable region nucleotide sequence (SEQ ID NO:639)

gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngcntggtayca
rcaraarccnggncarccnccnaarytnytnathtaytgggcnwsncanmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggncangayttycanytncanathwsnwsnytncarg
cngargaygtngcngtntaytaytgycarcartaytaywsncancantggcanttyggncargg
ncanaargtngarathaar

FIGURE 15D

U-V_L-22 light chain variable region nucleotide sequence (SEQ ID NO:640)

gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncaraaygtnytntaywsnwsnaayaayaaraaytayytngcntggtayca
rcaraarccnggncarccnccnaarytnytnathtaytgggcnwsncanmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggncangayttycanytncanathwsnwsnytncarg
cngargaygtngcngtntayttytgycarcartaytayggncanccnmgncanttyggncargg
ncanaargtngarathaar

U-V_L-23 light chain variable region nucleotide sequence (SEQ ID NO:641)

gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncaraaygtnytntaywsnwsnaayaayaaraaytayytngcntggtayca
rcaraarccnggncarccnccnaarytnytnathtaytgggcnwsncanmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggncangayttycanytncanathwsnwsnytncarg
cngargaygtngcngtntayttytgycarcartaytayggncanccnmgncanttyggncargg
ncanaargtngarathaar

U-V_L-24 light chain variable region nucleotide sequence (SEQ ID NO:642)

gayathgtnatgcancarwsnccngaywsnytncangtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngcntggtayca
rcaraarccnggncarccnccnaarytnytnathtaytgggcnwsncanmgngarwsnggngtn
ccngaymgnttyggnggnwsnggnwsnggncangayttycanytncanathwsnwsnytncarg
cngargaygtngcngtntaytaytgycarcartaytaywsnathwsnmgncanttyggncargg
ncanaargtngarathaar

U-V_L-25 light chain variable region nucleotide sequence (SEQ ID NO:642)

gayathgtnatgcancarwsnccngaywsnytncangtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngcntggtayca
rcaraarccnggncarccnccnaarytnytnathtaytgggcnwsncanmgngarwsnggngtn
ccngaymgnttyggnggnwsnggnwsnggncangayttycanytncanathwsnwsnytncarg
cngargaygtngcngtntaytaytgycarcartaytaywsnathwsnmgncanttyggncargg
ncanaargtngarathaar

U-V_L-26 light chain variable region nucleotide sequence (SEQ ID NO:643)

gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncarwsngtnytntayaaywsnaayaayaaraaytayytngcntggtayca
rcaraarccnggncarccnccnaarytnytnathtaytgggcnwsncanmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggncangayttycanytncanathwsnwsnytncarg
cngaygaygtngcngtntaytaytgycarcartaytaywsncancantggcanttyggnccngg
ncanaargtngarathaar

FIGURE 15E

U-V_L-27 light chain variable region nucleotide sequence (SEQ ID NO:644)

gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncarwsngtnytntayaaywsnaayaayaaraaytayytngcntggtayca
rcaraarccnggncarccnccnaarytnytnathtaytgggcnwsncanmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggncangayttycanytncanathwsnwsnytncarg
cngaygaygtngcngtntaytaytgycarcartaytaywsncancantggcanttyggnccngg
ncanaargtngarathaar

U-V_L-28 light chain variable region nucleotide sequence (SEQ ID NO:645)

gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngcntggtayca
rcaraarccnggncarccnccnaargtnytnathtaytgggcnwsncanmgnaarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggncangayttycanytncanathwsnggnytncarg
cngargaygtngcnytntaytaytgycarcartaytaywsncanatgttywsnttyggncargg
ncanaarytngarathaar

U-V_L-29 light chain variable region nucleotide sequence (SEQ ID NO:645)

gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngcntggtayca
rcaraarccnggncarccnccnaargtnytnathtaytgggcnwsncanmgnaarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggncangayttycanytncanathwsnggnytncarg
cngargaygtngcnytntaytaytgycarcartaytaywsncanatgttywsnttyggncargg
ncanaarytngarathaar

U-V_L-30 light chain variable region nucleotide sequence (SEQ ID NO:646)

gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncarwsngtnytngaywsnwsnaayaayaaraaytayytngcntggtayca
rcaraarccnggncarccnccnaarytnytnathtaytgggcnwsncanmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggncangayttycanytncanathwsnwsnytncarg
cngargaygtngcngtnttytaytgycaycartaytaywsncanccnytncanttyggnggngg
ncanaargtngcnathaar

U-V_L-31 light chain variable region nucleotide sequence (SEQ ID NO:646)

gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncarwsngtnytngaywsnwsnaayaayaaraaytayytngcntggtayca
rcaraarccnggncarccnccnaarytnytnathtaytgggcnwsncanmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggncangayttycanytncanathwsnwsnytncarg
cngargaygtngcngtnttytaytgycaycartaytaywsncanccnytncanttyggnggngg
ncanaargtngcnathaar

FIGURE 15F

U-V_L-32 light chain variable region nucleotide sequence (SEQ ID NO:647)

gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncarwsnathytntaymgnwsnaayaayaaraaytayytngcntggtayca
rcaraarccnggncarccnccnaarytnytnathtaytgggcnwsngcnmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggncangayttycanytncanathwsnwsnytncarg
cngargaygtngcngtntayttytgycarcartayttyathcanccnytncanttyggnggngg
ncanaargtngarathaar

U-V_L-33 light chain variable region nucleotide sequence (SEQ ID NO:647)

gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncarwsnathytntaymgnwsnaayaayaaraaytayytngcntggtayca
rcaraarccnggncarccnccnaarytnytnathtaytgggcnwsngcnmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggncangayttycanytncanathwsnwsnytncarg
cngargaygtngcngtntayttytgycarcartayttyathcanccnytncanttyggnggngg
ncanaargtngarathaar

U-V_L-34 light chain variable region nucleotide sequence (SEQ ID NO:648)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncargayathwsncaytayytngcntggttycarcaraarccnggnaargc
nccnaarwsnytnathtaygcngcnwsnwsnytncarwsnggngtnccnwsnaarttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargayttygcncant
aytaytgycarcartayaayaaytayccnttycanttyggnccnggncanaargtngayathaar

U-V_L-35 light chain variable region nucleotide sequence (SEQ ID NO:649)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtngcnathc
antgymgngcnwsncargayathwsnaaytayytngcntggytncarcaraarccnggnaargc
nccnaarwsnytnathtaygcngcnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargayttygcncant
aytaytgycarcartayaaycantayccnttycanttyggnccnggncanaaratggayathaar

U-V_L-36 light chain variable region nucleotide sequence (SEQ ID NO:650)

garathgtnatgcancarwsnccngcncanytnwsngtnwsnccnggngarmgngcncanytnw
sntgymgngcnwsncarwsngtnwsnwsnaayytngcntggtaycarcargayccnggncargc
nccnmgnytnytnathtayggngcnwsnmgnmgngcncanggnathccngcnmgnttywsnggn
wsnggnwsnggncangarttycanytncanathwsnwsnytncarwsngargayttygcngtnt
aytaytgycarcarcayaayaaytggccnccntggcanttyggncarggncanaargtngarat
haar

FIGURE 15G

U-V_L-37 light chain variable region nucleotide sequence (SEQ ID NO:650)

garathgtnatgcancarwsnccngcncanytnwsngtnwsnccnggngarmgngcncanytnw
sntgymgngcnwsncarwsngtnwsnwsnaayytngcntggtaycarcargayccnggncargc
nccnmgnytnytnathtayggngcnwsnmgnmgngcncanggnathccngcnmgnttywsnggn
wsnggnwsnggncangarttycanytncanathwsnwsnytncarwsngargayttygcngtnt
aytaytgycarcarcayaayaaytggccnccntggcanttyggncarggncanaargtngarat
haar

U-V_L-38 light chain variable region nucleotide sequence (SEQ ID NO:651)

Gayathcaratgcancarwsnccnwsnwsngtnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncargayathwsnmgntggytngcntggtaycarcaraarccnggnaargc
nccnaarytnytnathtaygcngcnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargayttygcncant
aytaytgycarcargcnaaywsnttyccnccncanttyggncarggncanaargtngarttyaar

U-V_L-39 light chain variable region nucleotide sequence (SEQ ID NO:652)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarwsnathwsncantayytnaaytggtaycarcaraarccnggnaargc
nccnaarttyytnathtaygcngcnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargayttygcngcnt
aytaytgycarcarwsncaywsngcnccnttycanttyggnccnggncanaargtngayathaar

U-V_L-40 light chain variable region nucleotide sequence (SEQ ID NO:653)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsnytnggngaymgngtncanathc
antgymgngcnwsncarcanathwsnathtayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaygcngcnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargayttygcncant
aytaytgycarcarwsntaywsncanytncanttyggnggnggncanaargtngarathaar

U-V_L-41 light chain variable region nucleotide sequence (SEQ ID NO:654)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarwsnathmgnwsntayytnaaytggtaycarcarmgnccnggnaaygc
nccnaarytnytnathtaygcngcnwsnwsnytncarwsnggngtnccnwsnmgngtnwsnggn
wsnggnwsnggncangayttycanytncanathmgnwsnytncarccngargayttygcncant
aytaytgycarcarwsntaywsnathccnytncanttyggnggnggncanaargtngarathaar

FIGURE 15H

U-V_L-42 light chain variable region nucleotide sequence (SEQ ID NO:655)

gayathcaratgcancarwsnccnwsnwsnmgnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarcanathwsnmgntayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaygcngcnwsncanytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanytnwsnwsnytncarccngargayttygcncant
aytaytgycarcarathtaywsncanwsnathcanttyggncarggncanmgnytngarathaar

U-V_L-43 light chain variable region nucleotide sequence (SEQ ID NO:656)

Gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarmgnathwsnwsntayytnaaytggtaycarcaraarccnggnaargc
nccnaargtnytnathtaygcngarwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargayttygcncant
aytaytgycarcarwsntayathcanccnathcanttyggncarggncanmgnytngarathath

U-V_L-44 light chain variable region nucleotide sequence (SEQ ID NO:657)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarwsnathwsnmgntayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaycangcnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngaraayttygcncant
aytaytgycarcarwsntayttycanccnathcanttyggncarggncanmgnytngarathaar

U-V_L-45 light chain variable region nucleotide sequence (SEQ ID NO:658)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarwsnathwsnwsntayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaycangcnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanttywsnwsnytncarccngargayttygcncant
aytaytgycarcarwsntayttywsnccnathcanttyggncarggncanmgnytngarathaar

U-V_L-46 light chain variable region nucleotide sequence (SEQ ID NO:659)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarwsnathwsnwsntayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaycangcnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanytnwsnwsnytncarccngargayttygcnwsnt
aytaytgycarcarwsnttytaycanccnathcanttyggncarggncanmgnytngarathaar

FIGURE 15I

U-V_L-47 light chain variable region nucleotide sequence (SEQ ID NO:659)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarwsnathwsnwsntayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaycangcnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanytnwsnwsnytncarccngargayttygcnwsnt
aytaytgycarcarwsnttytaycanccnathcanttyggncarggncanmgnytngarathaar

U-V_L-48 light chain variable region nucleotide sequence (SEQ ID NO:660)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarwsnathwsnwsntayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaycangtnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargayttygcncant
aytaytgycarcarwsntayttycanccnathcanttyggncarggncanmgnytngarathaar

U-V_L-49 light chain variable region nucleotide sequence (SEQ ID NO:660)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarwsnathwsnwsntayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaycangtnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargayttygcncant
aytaytgycarcarwsntayttycanccnathcanttyggncarggncanmgnytngarathaar

U-V_L-50 light chain variable region nucleotide sequence (SEQ ID NO:660)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarwsnathwsnwsntayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaycangtnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargayttygcncant
aytaytgycarcarwsntayttycanccnathcanttyggncarggncanmgnytngarathaar

U-V_L-51 light chain variable region nucleotide sequence (SEQ ID NO:661)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarwsnathwsnwsntayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaycangcnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargayttygcnwsnt
aytaytgycarcarwsnttytaygcnccnathcanttyggncarggncanmgnytngarathaar

FIGURE 15J

U-V_L-52 light chain variable region nucleotide sequence (SEQ ID NO:661)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarwsnathwsnwsntayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaycangcnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargayttygcnwsnt
aytaytgycarcarwsnttytaygcnccnathcanttyggncarggncanmgnytngarathaar

U-V_L-53 light chain variable region nucleotide sequence (SEQ ID NO:662)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarwsnathwsnwsntayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaycangcnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargayttygcncant
aytaytgycarcarwsntayttycanccnathcanttyggncarggncanmgnytngarathaar

U-V_L-54 light chain variable region nucleotide sequence (SEQ ID NO:663)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgycargcnwsncargayathwsnaaytayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaygaygcnwsnaayytngarcanggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanttycanathwsnwsnytncarccngargayathgcncant
aytaytgycarcartaygaytayytnccnttycanttyggnccnggncanaargtngayathaar

U-V_L-55 light chain variable region nucleotide sequence (SEQ ID NO:663)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgycargcnwsncargayathwsnaaytayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaygaygcnwsnaayytngarcanggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanttycanathwsnwsnytncarccngargayathgcncant
aytaytgycarcartaygaytayytnccnttycanttyggnccnggncanaargtngayathaar

U-V_L-56 light chain variable region nucleotide sequence (SEQ ID NO:664)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgycargcnwsncargayathwsnaaywsnytnaaytggtaycarcaraarccnggnaargc
nccngarytnytnathtaygaygcnwsnaayytngarcanggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanttycanathwsnwsnytncarccngargayathgcncant
aytaytgycarcartgygaygayytnccnytncanttyggnggnggncanaargtngarathaar

FIGURE 15K

U-V_L-57 light chain variable region nucleotide sequence (SEQ ID NO:665)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgycargcnwsncargayathwsngaytayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaygaygcnwsnaayytngarcanggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanttycanathwsnwsnytncarccngargayathgcncant
aytaytgycarcaytaygayaayytnccnytncanttyggnggnggncanaargtngarathaar

U-V_L-58 light chain variable region nucleotide sequence (SEQ ID NO:666)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtngcnathc
antgycargcnwsncargayathwsnaaytayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaygaygcnwsnaayytngarcanggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanttycanathwsnwsnytncarccngargayathgcncant
aytaytgycarcartaygayaayytnccnytncanttyggnggnggncanaargtngarathaar

U-V_L-59 light chain variable region nucleotide sequence (SEQ ID NO:666)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtngcnathc
antgycargcnwsncargayathwsnaaytayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaygaygcnwsnaayytngarcanggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanttycanathwsnwsnytncarccngargayathgcncant
aytaytgycarcartaygayaayytnccnytncanttyggnggnggncanaargtngarathaar

U-V_L-60 light chain variable region nucleotide sequence (SEQ ID NO:667)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgycargcnwsncargayathwsnaaywsnytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaygaygcnwsnathytngarcanggngtnccnwsnmgnttywsnggn
wsnggnwsngarcangayttycanttycanathwsnwsnytncarccngargayathgcncant
aytaytgycarcartgygayathytnccnytnwsnttyggnggnggncanaargtngarathaar

U-V_L-61 light chain variable region nucleotide sequence (SEQ ID NO:668)

Gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgycargcnwsncargayathwsnaaywsnytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaygaygcnwsnaayytngarcanggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanttycanathwsnwsnytncarccngargayathgcncant
aytaytgycarcartaygayaayytnccnytngcnttyggnggnggncanaargtngarathmgn

FIGURE 15L

U-V_L-62 light chain variable region nucleotide sequence (SEQ ID NO:669)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngayggngtncanathc
antgycargcnwsncargayathcanaaytayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaygaygcnwsnaayytngarcanggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanttycanathwsnwsnytncarccngargayathgcncant
aytaytgycarcartaygaywsnytnccnathcanttyggncarggncanmgnytngarathaar

U-V_L-63 light chain variable region nucleotide sequence (SEQ ID NO:670)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgycargcnwsncargayathwsnaaytayytnaaytggtaycarcaraarytnggnaargc
nccnaarytnytnathcaygaygcnwsnaayytngarcanggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanttycanathwsnwsnytncarccngargayathgcncant
aytaytgycarcartaygayaayytnccnathcanttyggncarggncanmgnytngarathaar

U-V_L-64 light chain variable region nucleotide sequence (SEQ ID NO:671)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgycargcnwsncargayathwsngaytayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaygaygcnwsnaayytngarcanggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanttycanathwsnwsnytncarccngargayathgcncant
aytaytgycarcaytaygayaayytnccnathcanttyggncarggncanmgnytngarathaar

U-V_L-65 light chain variable region nucleotide sequence (SEQ ID NO:672)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgycargcnwsncargayathwsnaaywsnytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaygaygcnwsnaayytngarcanggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanttycanathwsnwsnytncarccngargayathgcncant
aytaytgycarcaytaygayaayytnccnathcanttyggncarggncanmgnytngarathaar

FIGURE 15M

U-V_H-1 heavy chain variable region nucleotide sequence (SEQ ID NO:673)

cargtncarytngtncarwsnggngcngargtnaaraarccnggngcnwsngtnaargtnwsnt
gyaargcnwsnggntaycanttycanwsntayggnathwsntgggtnmgncargcnccnggnca
rggnytngartggatgggntggathwsngcnwsnaayggnaaycanaaytaygcncaraarytn
cargaymgngtncanatgcancangaycanwsncanwsncangcntayatggarytnmgnwsny
tnmgnwsngaygaycangcngtntaytaytgygcnmgngargayaaytggaaytayggnttytt
ygaytaytggggncarggncanytngtncangtnwsnwsn

U-V_H-2 heavy chain variable region nucleotide sequence (SEQ ID NO:673)

cargtncarytngtncarwsnggngcngargtnaaraarccnggngcnwsngtnaargtnwsnt
gyaargcnwsnggntaycanttycanwsntayggnathwsntgggtnmgncargcnccnggnca
rggnytngartggatgggntggathwsngcnwsnaayggnaaycanaaytaygcncaraarytn
cargaymgngtncanatgcancangaycanwsncanwsncangcntayatggarytnmgnwsny
tnmgnwsngaygaycangcngtntaytaytgygcnmgngargayaaytggaaytayggnttytt
ygaytaytggggncarggncanytngtncangtnwsnwsn

U-V_H-3 heavy chain variable region nucleotide sequence (SEQ ID NO:674)

cargtncayytngtncarwsnggngcngargtnaaraarccnggngcnwsngtnaargtnwsnt
gyaargtnwsnggntaycanttycanggncaytayatgcaytgggtnmgncargcnccnggnca
rggnytngartggatgggntggathaayccnaaywsnggnggncanaaytgygcncaraartty
carggnmgngtncanatgcanmgngaycanwsnathwsncangcntayatggarytnwsnmgny
tnmgnwsngaygaycangcngtntaytaytgygcnmgnwsnathgcngtngcnytngaytaytg
gggncarggncanytngtncangtnwsnwsn

U-V_H-4 heavy chain variable region nucleotide sequence (SEQ ID NO:675)

cargtncarytngtncarwsnggngcngargtnaaraarccnggngcnwsngtnaargtnwsnt
gyaargcnwsnggntaycanttycanggntaytayatgcaytgggtnmgncargcnccnggnca
rggnytngartggatgggntggathaayccnaaywsnggnggncanaaycaycancaraartty
carggnmgngtncanatgcanmgngaycanwsnathwsncangcntayatggarytnwsnmgny
tnmgnwsngaygaycangcngtntaytaytgygcnmgnwsnathgcngtngcnytngaytaytg
gggncarggncanytngtncangtnwsnwsn

U-V_H-5 heavy chain variable region nucleotide sequence (SEQ ID NO:676)

cargtncarytngtncarwsnggngcngargtnmgnaarccnggngcnwsngtnaargtnwsnt
gyaargtnwsnggntaycanytncangarytnwsnatgcaytgggtnmgncargcnccnggnaa
rggnytngartggatgggnwsnttygayccngargayggngarcanathtaygcncaraartty
carggnmgngtncanatgytngargaycanwsncangaycangcntayatggarytnwsnwsny
tnmgnwsngargaycangcngtntaytaytgygcncangarggngayggnggntaytaytayta
yggnatggaygtntggggncarggncancangtncangtnwsnwsn

FIGURE 16A

U-V_H-6 heavy chain variable region nucleotide sequence (SEQ ID NO:676)

cargtncarytngtncarwsnggngcngargtnmgnaarccnggngcnwsngtnaargtnwsnt
gyaargtnwsnggntaycanytncangarytnwsnatgcaytgggtnmgncargcnccnggnaa
rggnytngartggatgggnwsnttygayccngargayggngarcanathtaygcncaraartty
carggnmgngtncanatgytngargaycanwsncangaycangcntayatggarytnwsnwsny
tnmgnwsngargaycangcngtntaytaytgygcncangarggngayggnggntaytaytayta
yggnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_H-7 heavy chain variable region nucleotide sequence (SEQ ID NO:677)

cargtncanytnaargarwsnggnccngtnytngtnaarccncangarcanytncanytncant
gycangtnwsnggnttywsnytnwsnaaygcnmgnatgggngtnwsntggathmgncarccncc
nggnaargcnytngartggytngcncayathttywsnaaygaygaraarwsntaywsncanwsn
ytnaarwsnmgnytncanathwsnaargaycanwsnaarwsncargtngtnytncanatgcana
ayatggayccngtngaycangcncantaytaytgygcnmgnatgtaywsnwsnggntggtaygg
ngtnttygaytaytggggncarggncanytngtncangtnwsnwsn

U-V_H-8 heavy chain variable region nucleotide sequence (SEQ ID NO:678)

cargtncanytnaargarwsnggnccngtnytngtnaarccncangarcanytncanytncant
gycangtnwsnggnttywsnytnwsnaaygcnmgnatgggngtnwsntggathmgncarccncc
nggnaargcnytngartggytngtnytnathttywsnaaygaygaraarwsntaywsncanwsn
ytnaarwsnmgnytncanathwsnaargaycanwsnaarwsncargtngtnytncanatgcana
ayatggayccngtngaycangcncantaytaytgygcnmgngtntaywsnwsnggntggwsntt
ytayggnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_H-9 heavy chain variable region nucleotide sequence (SEQ ID NO:679)

carathcanytnaargarwsnggnccncanytngtnaarccncancarcanytncanytncant
gycanttywsnggnttywsnytnwsncanggnggngtnggngtnggntggathmgncarccncc
nggnaargcnytngartggytngcnytnathtaytggaaygaygayaarmgntaywsnccnwsn
ytnaarwsnmgnytncanathcanaargaycanwsnaaraaycargtngtnytncanatgcana
ayatggayccngtngaycangcncantaytaytgygcncaymgnmgngarytnccnttygayta
ytggggncarggncanytngtncangtnwsnwsn

U-V_H-10 heavy chain variable region nucleotide sequence (SEQ ID NO:680)

carathcanytnaargarwsnggnccncanytngtnaarccncancarcanytncanytncant
gycanttywsnggnttywsnytnwsncanggnggngtnggngtnggntggathmgncarccncc
nggnaargcnytngartggytngcnytnathtaytggaaygaygayaarmgntaywsnccnwsn
ytnaarwsnmgnytncanathcanaargaycanwsnaarcancargtngtnytncangtncang
ayatggayccngtngaycangcncantaytaytgygcncaymgnaaytggcanccnttygayta
ytggggncarggncanytngtncangtnwsnwsn

FIGURE 16B

U-V_H-11 heavy chain variable region nucleotide sequence (SEQ ID NO:681)

carathcanytnaargarwsnggnccncanytngtnaarccncancarcanytncanytncant
gycanttywsnggnttywsnytnaaycanggnggngtnggngtnggntggathmgncarccncc
nggnaargcnytngartggytngcnytnathtaytggaaygaygayaarmgntaywsnccnwsn
ytnaarwsnmgnytncanathcanaargaycanwsnaaraaycargtngtnytncanatgcana
ayatggayccngtngaycangcncantaytaytgygcncaymgnytngarytnccnttygayta
ytggggncarggncanytngtncangtnwsnwsn

U-V_H-12 heavy chain variable region nucleotide sequence (SEQ ID NO:682)

carathcanytnaargarwsnggnccncanytngtnaarccncancarcanytncanytncant
gycanttywsnggnttywsnytnwsncanggnggngtnggngtnggntggathmgncarccncc
nggnaargcnytngartggytngcnytnathtaytggaaygaygayaarmgntaywsnccnwsn
ytnaarwsnmgnytncanathcanaargaycanwsnaaraaycargtngtnytncanatgcana
ayytngayccngtngaycangcncantaytaytgygcncaymgnmgngargtnccnttygayta
ytggggncarggncanytngtncangtnwsnwsn

U-V_H-13 heavy chain variable region nucleotide sequence (SEQ ID NO:683)

carathcanytnaargarwsnggnccncanytngtnaarccncancarcanytncanytncant
gycanttywsnggnttywsnytnwsncanggnggngtnggngtnggntggathmgncarccncc
nggnaargcnytngartggytngcnytnathtaytggaaygtngaraarmgntaywsnccnwsn
ytnmgnwsnmgnytncanathcanaargcncanwsnaaraaycargtngtnytncanatgcana
ayatggayccngtngaycangcncantaytaytgygcncaymgncaycanaayccnttygarta
ytggggncarggncanytngtncangtnwsnwsn

U-V_H-14 heavy chain variable region nucleotide sequence (SEQ ID NO:684)

carathcanytnaargarwsnggnccncanytngtnaarccncancarcanytncanytncant
gycanttywsnggnttywsnytnwsncanggnggngtnggngtnggntggathmgncarccncc
nggnaargcnytngartggytngcnytnathtaytggaaygaygayaarmgntaywsnccnwsn
ytnaarwsnmgnytncanathcanaargaycanwsnaaraaycargtngtnytncanatgcana
ayatggayccngtngaycangcncantaytaytgygcncaymgnggngarytnccnttygayta
ytggggncarggncanytngtncangtnwsnwsn

U-V_H-15 heavy chain variable region nucleotide sequence (SEQ ID NO:684)

carathcanytnaargarwsnggnccncanytngtnaarccncancarcanytncanytncant
gycanttywsnggnttywsnytnwsncanggnggngtnggngtnggntggathmgncarccncc
nggnaargcnytngartggytngcnytnathtaytggaaygaygayaarmgntaywsnccnwsn
ytnaarwsnmgnytncanathcanaargaycanwsnaaraaycargtngtnytncanatgcana
ayatggayccngtngaycangcncantaytaytgygcncaymgnggngarytnccnttygayta
ytggggncarggncanytngtncangtnwsnwsn

FIGURE 16C

U-V_H-16 heavy chain variable region nucleotide sequence (SEQ ID NO:685)

gargtncarytngtngarwsnggnggnggnytngtnaarccnggnggnwsnytnmgnytnwsnt
gygcngcnwsnggnttyccnttywsnmgntaywsnatgaaytgggtnmgncargcnccnggnaa
rggnytngartgggtnwsngcnathwsnwsnwsnwsnwsntayathtaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaygcnaaraaywsnytntayytncaratgaaywsny
tnmgngcngargaycangcngtntaytaytgygcnmgngaymgngtnggngcncanccngaygc
nttygayathtggggncarggncanatggtncangtnwsnwsn

U-V_H-17 heavy chain variable region nucleotide sequence (SEQ ID NO:686)

gargtncarytnytngarwsnggnggnggnytngtncarccnggnggnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntaygcnatgaaytgggtnmgncargcnccnggnaa
rggnytngartgggtnwsngcnathwsnggnwsnggnggnwsncantaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaywsnaaraaycanytntayytncaratgaaywsny
tnmgngcngargaycangcngtntaytaytgygcnaargarggnathgcngtngcnggncangc
ngartaytaytaytaytaygcnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_H-18 heavy chain variable region nucleotide sequence (SEQ ID NO:687)

gargtncarytnytngarwsnggnggnggnytngtncarccnggnggnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntaygcnatgwsntgggtnmgncargcnccnggnaa
rggnytngartgggtnwsngcnathwsnggnwsnggnggnwsncantaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaywsnaaraaycanytntayytncaratgaaywsny
tnmgngcngargaycangcngtntaytaytgygcnaargarggnathgcngcnmgngaywsnta
ytaytaytaygcnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_H-19 heavy chain variable region nucleotide sequence (SEQ ID NO:688)

gargtncarytnytngarwsnggnggnggnytngtncarccnggnggnwsnytnmgnytnwsnt
gycangcnwsnggnttycanttywsnwsntaygcnatgwsntgggtnmgncargcnccnggnaa
rggnytngartgggtnwsngcnathwsnggnwsnggnggnwsncantaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaywsnaaraaycanytntayytncaratgaaywsny
tnmgngcngargaycangcngartaytaytgygcnaargarggnathgcnggnmgngaywsnta
ytaytaytayggnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_H-20 heavy chain variable region nucleotide sequence (SEQ ID NO:688)

gargtncarytnytngarwsnggnggnggnytngtncarccnggnggnwsnytnmgnytnwsnt
gycangcnwsnggnttycanttywsnwsntaygcnatgwsntgggtnmgncargcnccnggnaa
rggnytngartgggtnwsngcnathwsnggnwsnggnggnwsncantaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaywsnaaraaycanytntayytncaratgaaywsny
tnmgngcngargaycangcngartaytaytgygcnaargarggnathgcnggnmgngaywsnta
ytaytaytayggnatggaygtntggggncarggncancangtncangtnwsnwsn

FIGURE 16D

U-V_H-21 heavy chain variable region nucleotide sequence (SEQ ID NO:689)

cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnytngartgggtngcnttyathwsngaygayggnwsncanaartaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaywsnatgaaycanytntayytncaratgaaywsny
tnmgngcngargaycangcngtntaytaytgygcnmgnwsntaytaygaywsnwsnggntayta
ytayggnttygaytaytggggncarggncanytngtncangtnwsnwsn

U-V_H-22 heavy chain variable region nucleotide sequence (SEQ ID NO:689)

cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnytngartgggtngcnttyathwsngaygayggnwsncanaartaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaywsnatgaaycanytntayytncaratgaaywsny
tnmgngcngargaycangcngtntaytaytgygcnmgnwsntaytaygaywsnwsnggntayta
ytayggnttygaytaytggggncarggncanytngtncangtnwsnwsn

U-V_H-23 heavy chain variable region nucleotide sequence (SEQ ID NO:690)

cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnytngartgggtngcngtnathtggtaygayggnwsnaayaartaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaywsnaaraaycanytntayytncaratgaaywsny
tnmgngcngargaycangcngtntaytaytgygcnmgnaaygtnathgaytaytggggncargg
ncanytngtncangtnwsnwsn

U-V_H-24 heavy chain variable region nucleotide sequence (SEQ ID NO:691)

cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntaygayatgcaytgggtnmgncargcnccnggnaa
rggnytngartgggtngcngtnathtggtaygayggnwsnathaartaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaywsnaaraaycanytntayytncaratgaaywsny
tnmgngcngargaycangcngtntaytaytgygcnmgnggnggngcncanggngcngartaytt
ycarcaytggggncarggncanytngtncangtnwsnwsn

U-V_H-25 heavy chain variable region nucleotide sequence (SEQ ID NO:691)

cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntaygayatgcaytgggtnmgncargcnccnggnaa
rggnytngartgggtngcngtnathtggtaygayggnwsnathaartaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaywsnaaraaycanytntayytncaratgaaywsny
tnmgngcngargaycangcngtntaytaytgygcnmgnggnggngcncanggngcngartaytt
ycarcaytggggncarggncanytngtncangtnwsnwsn

FIGURE 16E

U-V_H-26 heavy chain variable region nucleotide sequence (SEQ ID NO:692)

Cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnytngartgggtngcngtnathtggtaygayggnwsnaayaartaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaywsnaaraaycanytntayytncaratgaaywsny
tnmgngcngargaycangcngtntaytaytgygtnytnytntggttyggngarcanttygayta
ytggggncarggnwsnytngtncangtnwsnccn

U-V_H-27 heavy chain variable region nucleotide sequence (SEQ ID NO:693)

cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnytngartgggtngcngtnathtggwsngayggnwsnaayaartaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaywsnaaraaycanytntayytncaratgaaywsny
tnmgngcngargaycangcngtntaytaytgygcnmgnaayytnccnttygaytaytggggnca
rggncanytngtncangtnwsnwsn

U-V_H-28 heavy chain variable region nucleotide sequence (SEQ ID NO:694)

cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnytngartgggtngcngtnathtgggaygayggnwsnaaycartaytaycangaywsngtn
aarggnmgnttycangtnwsnmgngayaaywsnaaraaycanytnttyytncaratgaaywsny
tnmgngcngargaycangcngtntaytaytgygcnmgnwsncaytayggnggngaytaygayta
ytayggnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_H-29 heavy chain variable region nucleotide sequence (SEQ ID NO:695)

cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnytngartgggtngcngtnathtggtaygayggnwsnaayaarmgntaygtngaywsngtn
aarggnmgnttycanathwsnmgngayaaywsnaaraaycanytntayytncaratgaaywsny
tnmgngcngargaycangcngtntaytaytgygcnmgngayggntggcarcarcargcnccntt
ygaytaytggggncarggncanytngtncangtnwsnwsn

U-V_H-30 heavy chain variable region nucleotide sequence (SEQ ID NO:696)

cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttymgnwsncayggnatgcaytgggtnmgncargcnccnggnaa
rggnytngartgggtngcngtnathtggtaygayggnwsnaayaaraaytaygcngaywsngtn
mgnggnmgnttycanathwsnmgngayaaywsnaaraaycanytngayytncaratgaaywsny
tnmgngcngargaycangcngtntaytaytgygcnmgntggggnathwsngcnccnttygaytg
ytggggncarggncanytngtncangtnwsnwsn

FIGURE 16F

U-V_H-31 heavy chain variable region nucleotide sequence (SEQ ID NO:697)

gargtncarytngtngarwsnggnggnggnytngtncarccnggnggnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsngcntaywsnatgaaytgggtnmgncargcnccnggnaa
rggnytngartgggtnwsntayathwsnwsnwsnggnmgncanathtaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaygcnaaraaywsnytnttyytncaratgaaywsny
tnmgngaygargaycangcngtntaytaytgygcnytntgggcnccnttygaytaytggggnca
rggncanytngtncangtnwsnwsn

U-V_H-32 heavy chain variable region nucleotide sequence (SEQ ID NO:698)

gargtncarytngtngarwsnggnggnggnytngtncarccnggnggnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntaywsnatgaaytgggtnmgncargcnccnggnaa
rggnytngartgggtnwsncayathwsnwsnwsnwsnmgncanathtaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaygcnaaraaywsngtntayytncaratgaaywsny
tnmgngaygargaycangcngtntaytaytgygcnmgngayggntayaaytggaayggnggngg
naaytaytayggnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_H-33 heavy chain variable region nucleotide sequence (SEQ ID NO:699)

gargtncarytngtngarwsnggnggnggnytngtncarccnggnggnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntaywsnatgaaytgggtnmgncargcnccnggnaa
rggnytngartgggtnwsncayathwsnmgnwsnwsnmgncanathtaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaygcnaaraaywsnytntayytncaratgaaywsny
tnmgngaygargaycangcngtntaytaytgygcnmgngayggntayaaytggaayaayggngg
ntaytaytayggnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_H-34 heavy chain variable region nucleotide sequence (SEQ ID NO:699)

gargtncarytngtngarwsnggnggnggnytngtncarccnggnggnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntaywsnatgaaytgggtnmgncargcnccnggnaa
rggnytngartgggtnwsncayathwsnmgnwsnwsnmgncanathtaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaygcnaaraaywsnytntayytncaratgaaywsny
tnmgngaygargaycangcngtntaytaytgygcnmgngayggntayaaytggaayaayggngg
ntaytaytayggnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_H-35 heavy chain variable region nucleotide sequence (SEQ ID NO:700)

cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncant
gycangtnwsnggnggnwsngtnwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnytngartggathggntayathcaywsnwsnggnwsncantaytayaayccnwsn
ytnaarwsnmgngtncanathwsngtngaycanwsnaaraaycarttywsnytnaayytnwsnw
sngtncangcngcngaycangcngtntaytaytgygcnmgnggnccntaytayggnatggaygt
ntggggncarggncancangtncangtnwsnwsn

FIGURE 16G

U-V_H-36 heavy chain variable region nucleotide sequence (SEQ ID NO:701)

cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncant
gycangtnwsnggnggnwsnathwsnmgnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnytngartggathggntayathtaycaywsnggnwsncantaytayaayccnwsn
ytnaarwsnmgngtnaayatgwsngtngaycanwsnaaraaycarttywsnytnaarytnwsnw
sngtncangcngcngaycangcngtntaytaytgygcnmgngcnytnmgnggnathgtnytnat
ggtntaygtnytnggngcnytngayathtggggncarggncanaargtncangtnwsnwsn

U-V_H-37 heavy chain variable region nucleotide sequence (SEQ ID NO:701)

cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncant
gycangtnwsnggnggnwsnathwsnmgnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnytngartggathggntayathtaycaywsnggnwsncantaytayaayccnwsn
ytnaarwsnmgngtnaayatgwsngtngaycanwsnaaraaycarttywsnytnaarytnwsnw
sngtncangcngcngaycangcngtntaytaytgygcnmgngcnytnmgnggnathgtnytnat
ggtntaygtnytnggngcnytngayathtggggncarggncanaargtncangtnwsnwsn

U-V_H-38 heavy chain variable region nucleotide sequence (SEQ ID NO:702)

cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncant
gycangtnwsnggnggnwsnathwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnytngartggathggntayathtaytaywsnggnwsncantaytayaayccnwsn
ytnaarwsnmgngtncanathwsngtngaycanwsnaaraaycarttywsnytnaarytnwsnw
sngtncangcngcngaycangcngtntaytaytgygcnmgngaygarcangtngtnmgnggnyt
nathmgntaytgytayggnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_H-39 heavy chain variable region nucleotide sequence (SEQ ID NO:703)

cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytnaayt
gycangtnwsnggnggnwsnathwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnytngartggathggntayathcaytaywsnggnwsncantaytayaayccnwsn
ytnaarwsnmgnathcanathwsngcngaycanwsnaaraaycarttywsnytnaarytnaayw
sngtncangcngcngaycangcngtntaytaytgygcnmgngaymgnggnggnggngaytaygg
nmgnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_H-40 heavy chain variable region nucleotide sequence (SEQ ID NO:704)

cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytnaayt
gycangtnwsnggnggnwsnathwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnytngartggathggntayathcaytaywsnggnwsncantaytayaayccnwsn
ytnaarwsnmgnathcanathwsngcngaycanwsnaaraaycarttywsnytnaarytnaayw
sngtncangcngcngaycangcngtntaytaytgygcnmgngaymgnggnggnggngaytaygg
nmgnatggaygtntggggncarggncancangtncangtnwsnwsn

FIGURE 16H

U-V_H-41 heavy chain variable region nucleotide sequence (SEQ ID NO:705)

cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncant
gycangtnwsnggnggnwsnathwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnytngartggathggntayathcaywsnwsnggnwsncantaytayaayccnwsn
ytnaarwsnmgnathcanaarwsngtngaycanwsnaaraaycarttywsnytnaarytnwsnw
sngtncangcngcngaycangcngtntaytaytgygcnmgnwsnaayaaytayggntgyttygc
nytntggggnmgnggncanytngtncangtnwsnwsn

U-V_H-42 heavy chain variable region nucleotide sequence (SEQ ID NO:706)

cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncant
gycangtnwsnggnggnwsnathwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnytngartggathggntayathcaywsnwsnggnwsncantaytayaayccnwsn
ytnaarwsnmgnathcanaarwsngtngaycanwsnaaraaycarttywsnytnaarytnwsnw
sngtncangcngcngaycangcngtntaytaytgygcnmgnwsnaayaaytayggntgyttygc
nytntggggnmgnggncanytngtncangtnwsnwsn

U-V_H-43 heavy chain variable region nucleotide sequence (SEQ ID NO:707)

cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncant
gycangtnwsnggnggnwsnathwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnytngartggathggntayathcaytaywsnggnwsncantaytayaayccnwsn
ytnaarwsnmgngtncanathwsngtngaycanwsnaaraaycarttywsnytnaarytnwsnw
sngtncangcngcngaycangcngtntaytaytgygcnwsnggntayaaytayggnytntayta
ytaygaywsnwsnggntayccnwsntaytaytayggnatggaygtntggggncarggncancan
gtncangtnwsnwsn

U-V_H-44 heavy chain variable region nucleotide sequence (SEQ ID NO:708)

cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncant
gycangtnwsnggnggnwsnathwsnwsnggngaytaytaytggaaytgggtnmgncarcaycc
nggnaarggnytngartggathggntayathtaytaywsnggnggncantaytayaayccnwsn
ytnaarwsnmgngtncanathwsngtngaycanwsnaaraaycarttywsnytnaarytnttyw
sngtncangcngcngaycangcngtntayttytgygcnmgncantaytaygayathytncangg
ntayccnttytayttygaytaytggggncarggncanytngtncangtnwsnwsn

U-V_H-45 heavy chain variable region nucleotide sequence (SEQ ID NO:709)

cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncant
gycangtnwsnggnggnwsnathwsnwsnggngaytaytaytggaaytgggtnmgncarcaycc
nggnaarggnytngartggathggntayathtaytaywsnggnggncantaytayaayccnwsn
ytnaarwsnmgngtncanathwsngtngaycanwsnaaraaycarttywsnytnaarytnttyw
sngtncangcngcngaycangcngtntayttytgygcnmgncantaytaygayathytncangg
ntayccnttytayttygaytaytggggncarggncanytngtncangtnwsnwsn

FIGURE 16I

U-V_H-46 heavy chain variable region nucleotide sequence (SEQ ID NO:710)

cargtncarytncarcartggggngcnggnytnytnaarccnwsngarcanytnwsnytncant
gygcngtntayggnggnwsnttywsnggntaytaytggwsntggathmgncarccnccnggnaa
rggnytngartggathggngarathaaycaywsnggnwsncanaaytayaayccnwsnytnaar
wsnmgngtncanathwsngtngaycanwsnaaraaycarttywsnytnaarytnwsnwsngtnc
angcngcngaycangcngtntaytaytgygcnmgnggnggntaywsnwsnwsntggtaytggtt
ygayccntggggncarggncanytngtncangtnwsnwsn

U-V_H-47 heavy chain variable region nucleotide sequence (SEQ ID NO:711)

cargtncarytncarcartggggngcnggnytnytnaarccnwsngarcanytnwsnytncant
gygcngtntayggnggnwsnttywsnggntaytaytggwsntggathmgncarccnccnggnaa
rggnytngartggathggngarathaaycaywsnggnwsncanaaytayaayccnwsnytnaar
wsnmgngtncanathwsngtngaycanwsnaaraaycarttywsnytnaarytnwsnwsngtnc
angcngcngaycangcngtntaytaytgygcnmgnggnggntaywsnwsnwsntggttytggtt
ygayccntggggncarggncanytngtncangtnwsnwsn

U-V_H-48 heavy chain variable region nucleotide sequence (SEQ ID NO:711)

cargtncarytncarcartggggngcnggnytnytnaarccnwsngarcanytnwsnytncant
gygcngtntayggnggnwsnttywsnggntaytaytggwsntggathmgncarccnccnggnaa
rggnytngartggathggngarathaaycaywsnggnwsncanaaytayaayccnwsnytnaar
wsnmgngtncanathwsngtngaycanwsnaaraaycarttywsnytnaarytnwsnwsngtnc
angcngcngaycangcngtntaytaytgygcnmgnggnggntaywsnwsnwsntggttytggtt
ygayccntggggncarggncanytngtncangtnwsnwsn

U-V_H-49 heavy chain variable region nucleotide sequence (SEQ ID NO:711)

cargtncarytncarcartggggngcnggnytnytnaarccnwsngarcanytnwsnytncant
gygcngtntayggnggnwsnttywsnggntaytaytggwsntggathmgncarccnccnggnaa
rggnytngartggathggngarathaaycaywsnggnwsncanaaytayaayccnwsnytnaar
wsnmgngtncanathwsngtngaycanwsnaaraaycarttywsnytnaarytnwsnwsngtnc
angcngcngaycangcngtntaytaytgygcnmgnggnggntaywsnwsnwsntggttytggtt
ygayccntggggncarggncanytngtncangtnwsnwsn

U-V_H-50 heavy chain variable region nucleotide sequence (SEQ ID NO:711)

cargtncarytncarcartggggngcnggnytnytnaarccnwsngarcanytnwsnytncant
gygcngtntayggnggnwsnttywsnggntaytaytggwsntggathmgncarccnccnggnaa
rggnytngartggathggngarathaaycaywsnggnwsncanaaytayaayccnwsnytnaar
wsnmgngtncanathwsngtngaycanwsnaaraaycarttywsnytnaarytnwsnwsngtnc
angcngcngaycangcngtntaytaytgygcnmgnggnggntaywsnwsnwsntggttytggtt
ygayccntggggncarggncanytngtncangtnwsnwsn

FIGURE 16J

U-V_H-51 heavy chain variable region nucleotide sequence (SEQ ID NO:712)

cargtncarytncargarwsnggnccnggnytngtnaarccnwsngarcanytnwsnytncant
gycangtnwsnggnggnwsnathwsnwsntaytaytggwsntggathmgncarccngcnggnaa
rggnytngartggathggnmgnathtaycanwsnggncancanaaytayaayccnwsnytnaar
wsnmgngtncanatgwsngtngaycanwsnaaraaycarttywsnytnaarytnwsnwsngtnc
angcngcngaycangcngtntaytaytgygcnmgngayggntaywsntayggncaytaytayta
ytayggnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_H-52 heavy chain variable region nucleotide sequence (SEQ ID NO:713)

cargtncarytncargarwsnggnccnggnytngtnaarccnwsngarcanytnwsnytncant
gycangtnwsnggnggnwsngtnwsnwsnggnggnwsntaytggwsntggathmgncarccncc
nggnaarggnytngartggathggntayathtaytaywsnggnwsncanaaytayaayccnwsn
ytnaarwsnmgngtncanathwsnathgtncanwsnmgnaaycarttywsnytnaarytnwsnw
sngtncangcngcngaycangcngtntaytaytgygcnmgnwsngcnytnmgntayttygaytg
gytnttywsngaygtnwsngayathtggggncarggncanatggtncangtnwsnwsn

U-V_H-53 heavy chain variable region nucleotide sequence (SEQ ID NO:713)

cargtncarytncargarwsnggnccnggnytngtnaarccnwsngarcanytnwsnytncant
gycangtnwsnggnggnwsngtnwsnwsnggnggnwsntaytggwsntggathmgncarccncc
nggnaarggnytngartggathggntayathtaytaywsnggnwsncanaaytayaayccnwsn
ytnaarwsnmgngtncanathwsnathgtncanwsnmgnaaycarttywsnytnaarytnwsnw
sngtncangcngcngaycangcngtntaytaytgygcnmgnwsngcnytnmgntayttygaytg
gytnttywsngaygtnwsngayathtggggncarggncanatggtncangtnwsnwsn

U-V_H-54 heavy chain variable region nucleotide sequence (SEQ ID NO:714)

gargtncarytngtncarwsnggngcngarytnaaraarccnggngarwsnytnaarathwsnt
gyaarggnwsnggntaymgnttycanwsntaytggathggntgggtnmgncaratgccnggnaa
rggnytngartggatgggnathathtayccngaygaywsngaycanmgntaywsnccnwsntty
carggncargtncanathwsngcngayaarwsnathwsncangcntayytncartggwsnwsny
tnaargcnwsngaycangcnatgtaytaytgygcnmgncaraarwsntayggntaywsntaytt
ygaytaytggggncarggncanytngtncangtnwsnwsn

U-V_H-55 heavy chain variable region nucleotide sequence (SEQ ID NO:715)

gargtncarytngtncarwsnggngcngargtnaaraarccnggngarwsnytnaarathwsnt
gyaarggnwsnggntaywsnttycanwsntaytggathggntgggtnmgncaratgccnggnaa
rggnytngartggatgggnathathtayccngaygaywsngaygcnmgntaywsnccnwsntty
carggncargtncanathwsngcngayaarwsnathaaycangcntayytncartggwsnwsny
tnaargcnwsngaycangcnatgtaytaytgygcnmgncarggntayggnwsnggntggggnta
yttygaytaytggggncarggncanytngtncangtnwsnwsn

FIGURE 16K

U-V_B-56 heavy chain variable region nucleotide sequence (SEQ ID NO:716)

gargtncarytngtncarwsnggngcngargtnaaraarccnggngarwsnytnaarathwsnt
gyaarggnwsnggntaywsnttycanwsntaytggathggntgggtnmgncaratgccnggnaa
rggnytngartggatgggnathathtayccnggngaywsngayathmgntaywsnccnwsntty
carggncargtncanathwsngcngayaarwsnathwsncangcntayytncartggwsnwsny
tnaargcnwsngaycangcnatgtaytaytgygcnmgncarggnytngcngtngcnggncanws
ntaytaytaytaytayggnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_B-57 heavy chain variable region nucleotide sequence (SEQ ID NO:717)

cargtncarytncarcarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncant
gygcnathwsnggngaywsngtnwsnwsntaywsngcngcntggaaytggathmgncarwsncc
nwsnmgnggnytngartggytnggnmgncantaytgymgnwsnaartggtayaaygaytaygcn
gtnwsngtnaarwsnmgnathcanathaayccngaycanwsnaaraaycarttywsnytncary
tnaaywsngtncanccngargaycangcngtntaytaytgygcnmgngaymgngcngtngcngg
ntaytaytayggnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_B-58 heavy chain variable region nucleotide sequence (SEQ ID NO:697)

gargtncarytngtngarwsnggnggnggnytngtncarccnggnggnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsngcntaywsnatgaaytgggtnmgncargcnccnggnaa
rggnytngartgggtnwsntayathwsnwsnwsnggnmgncanathtaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaygcnaaraaywsnytnttyytncaratgaaywsny
tnmgngaygargaycangcngtntaytaytgygcnytntgggcnccnttygaytaytggggnca
rggncanytngtncangtnwsnwsn

FIGURE 16L

LIGHT CHAIN CONSTANT REGION NUCLEOTIDE SEQUENCE

CGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCTAGCGTTGT
GTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACT
CCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCA
GACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAA
CAGGGGAGAGTGTTAG (SEQ ID NO:718)

FIGURE 17A

HEAVY CHAIN CONSTANT REGION NUCLEOTIDE SEQUENCE

GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCTAGAAGCACCTCCGAGAGCACAGCGGCCCTGGG
CTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCGGCGTGCACA
CCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGC
ACCCAGACCTACACATGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTG
TGTCGAGTGCCCACCGTGCCCAGCACCACCTGTGGCAGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA
CCCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTC
AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGCACGTTCCG
TGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
GCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCC
CCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGC
CGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCT
TCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:719)

FIGURE 17B

LIGHT CHAIN CDR NUCLEOTIDE SEQUENCES

NAME	SEQUENCE	SEQ ID NO
CDRL1-1	mgnwsnwsncarwsnytngtntaywsngayggnaaycantayytnaay	720
CDRL1-2	mgnwsnwsncarwsnytngtntaywsngayggnaaycantayytnaay	720
CDRL1-3	mgnwsnwsncarwsnytngtntaywsngayggnaaycantayytnaay	720
CDRL1-4	mgnwsnwsncarwsnytngtntaywsngayggnaaycantayytnaay	720
CDRL1-5	aarwsnwsncarwsnytnytncaywsngayggnaarcantayytntay	721
CDRL1-6	aarwsnwsncarwsnytnytncaywsngayggnaarcantayytntay	721
CDRL1-7	aarwsnwsncarwsnytnytncaywsngayggnaarcantayytntay	721
CDRL1-8	aarwsnwsncarwsnytnytncaywsngayggnaarcantayytntay	721
CDRL1-9	aarwsnwsncarwsnytnytncaywsngayggnaarcantayytntay	721
CDRL1-11	mgngcnwsncarggnathgcnaaytayytngcn	722
CDRL1-12	mgngcnwsncarggnathwsnaaygayytngcn	723
CDRL1-13	mgnwsnwsncarwsnytngtncaywsngayggnaaycantayytnwsn	724
CDRL1-14	mgnwsnwsncarwsnytngtncaywsngayggnaaycantayytnwsn	724
CDRL1-15	mgnwsnwsncarwsnytngtncaywsngayggnaaycantayytnwsn	724
CDRL1-16	mgngcnwsncarcangtnathwsnwsntayytngcn	725
CDRL1-17	mgngcnwsncarwsngtnwsnmgnytngcn	726
CDRL1-18	mgngcnwsncarggnathmgnaaygayytnggn	727
CDRL1-19	aarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngtn	728
CDRL1-20	aarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngtn	728
CDRL1-21	aarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngcn	729
CDRL1-22	aarwsnwsncaraaygtnytntaywsnwsnaayaayaaraaytayytngcn	730
CDRL1-23	aarwsnwsncaraaygtnytntaywsnwsnaayaayaaraaytayytngcn	730
CDRL1-24	aarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngcn	729
CDRL1-25	aarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngcn	729
CDRL1-26	aarwsnwsncarwsngtnytntayaaywsnaayaayaaraaytayytngcn	731

FIGURE 18A

NAME	SEQUENCE	SEQ ID NO
CDRL1-27	aarwsnwsncarwsngtnytntayaaywsnaayaayaaraaytayytngcn	731
CDRL1-28	aarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngcn	729
CDRL1-29	aarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngcn	729
CDRL1-30	aarwsnwsncarwsngtnytngaywsnwsnaayaayaaraaytayytngcn	732
CDRL1-31	aarwsnwsncarwsngtnytngaywsnwsnaayaayaaraaytayytngcn	732
CDRL1-32	aarwsnwsncarwsnathytntaymgnwsnaayaayaaraaytayytngcn	733
CDRL1-33	aarwsnwsncarwsnathytntaymgnwsnaayaayaaraaytayytngcn	733
CDRL1-34	mgngcnwsncargayathwsncaytayytngcn	734
CDRL1-35	mgngcnwsncargayathwsnaaytayytngcn	735
CDRL1-36	mgngcnwsncarwsngtnwsnwsnaayytngcn	736
CDRL1-37	mgngcnwsncarwsngtnwsnwsnaayytngcn	736
CDRL1-38	mgngcnwsncargayathwsnmgntggytngcn	737
CDRL1-39	mgngcnwsncarwsnathwsncantayytnaay	738
CDRL1-40	mgngcnwsncarcanathwsnathtayytnaay	739
CDRL1-41	mgngcnwsncarwsnathmgnwsntayytnaay	740
CDRL1-42	mgngcnwsncarcanathwsnmgntayytnaay	741
CDRL1-43	mgngcnwsncarmgnathwsnwsntayytnaay	742
CDRL1-44	mgngcnwsncarwsnathwsnmgntayytnaay	743
CDRL1-45	mgngcnwsncarwsnathwsnwsntayytnaay	744
CDRL1-46	mgngcnwsncarwsnathwsnwsntayytnaay	744
CDRL1-47	mgngcnwsncarwsnathwsnwsntayytnaay	744
CDRL1-48	mgngcnwsncarwsnathwsnwsntayytnaay	744
CDRL1-49	mgngcnwsncarwsnathwsnwsntayytnaay	744
CDRL1-50	mgngcnwsncarwsnathwsnwsntayytnaay	744
CDRL1-51	mgngcnwsncarwsnathwsnwsntayytnaay	744
CDRL1-52	mgngcnwsncarwsnathwsnwsntayytnaay	744
CDRL1-53	mgngcnwsncarwsnathwsnwsntayytnaay	744
CDRL1-54	cargcnwsncargayathwsnaaytayytnaay	745
CDRL1-55	cargcnwsncargayathwsnaaytayytnaay	745
CDRL1-56	cargcnwsncargayathwsnaaywsnytnaay	746
CDRL1-57	cargcnwsncargayathwsngaytayytnaay	747

FIGURE 18B

NAME	SEQUENCE	SEQ ID NO
CDRL1-58	cargcnwsncargayathwsnaaytayytnaay	745
CDRL1-59	cargcnwsncargayathwsnaaytayytnaay	745
CDRL1-60	cargcnwsncargayathwsnaaywsnytnaay	746
CDRL1-61	cargcnwsncargayathwsnaaywsnytnaay	746
CDRL1-62	cargcnwsncargayathcanaaytayytnaay	748
CDRL1-63	cargcnwsncargayathwsnaaytayytnaay	745
CDRL1-64	cargcnwsncargayathwsngaytayytnaay	747
CDRL1-65	cargcnwsncargayathwsnaaywsnytnaay	746
CDRL2-1	aargtnwsnaaytgggaywsn	749
CDRL2-2	aargtnwsnaaytgggaywsn	749
CDRL2-3	aargtnwsnaaytgggaywsn	749
CDRL2-4	aargtnwsnaaytgggaywsn	749
CDRL2-5	gargtnwsnaaymgnttywsn	750
CDRL2-6	gargtnwsnaaymgnttywsn	750
CDRL2-7	gargtnwsnaaymgnttywsn	750
CDRL2-8	gargtnwsnaaymgnttywsn	750
CDRL2-9	gargtnwsnaaymgnttywsn	750
CDRL2-11	gtngcnwsncanytncarwsn	751
CDRL2-12	gcngcnwsncanytncarwsn	752
CDRL2-13	aarathwsnaaymgnttywsn	753
CDRL2-14	aarathwsnaaymgnttywsn	753
CDRL2-15	aarathwsnaaymgnttywsn	753
CDRL2-16	ggngcnwsnwsnmgngcncan	754
CDRL2-17	ggngcnwsnmgnmgngcncan	755
CDRL2-18	gcngcnwsnwsnytncarwsn	756
CDRL2-19	tgggcnwsncanmgngarwsn	757
CDRL2-20	tgggcnwsncanmgngarwsn	757
CDRL2-21	tgggcnwsncanmgngarwsn	757
CDRL2-22	tgggcnwsncanmgngarwsn	757
CDRL2-23	tgggcnwsncanmgngarwsn	757
CDRL2-24	tgggcnwsncanmgngarwsn	757
CDRL2-25	tgggcnwsncanmgngarwsn	757
CDRL2-26	tgggcnwsncanmgngarwsn	757
CDRL2-27	tgggcnwsncanmgngarwsn	757
CDRL2-28	tgggcnwsncanmgnaarwsn	758
CDRL2-29	tgggcnwsncanmgnaarwsn	758

FIGURE 18C

NAME	SEQUENCE	SEQ ID NO
CDRL2-30	tgggcnwsncanmgngarwsn	757
CDRL2-31	tgggcnwsncanmgngarwsn	757
CDRL2-32	tgggcnwsngcnmgngarwsn	759
CDRL2-33	tgggcnwsngcnmgngarwsn	759
CDRL2-34	gcngcnwsnwsnytncarwsn	756
CDRL2-35	gcngcnwsnwsnytncarwsn	756
CDRL2-36	ggngcnwsnmgnmgngcncan	755
CDRL2-37	ggngcnwsnmgnmgngcncan	755
CDRL2-38	gcngcnwsnwsnytncarwsn	756
CDRL2-39	gcngcnwsnwsnytncarwsn	756
CDRL2-40	gcngcnwsnwsnytncarwsn	756
CDRL2-41	gcngcnwsnwsnytncarwsn	756
CDRL2-42	gcngcnwsncanytncarwsn	752
CDRL2-43	gcngarwsnwsnytncarwsn	760
CDRL2-44	cangcnwsnwsnytncarwsn	761
CDRL2-45	cangcnwsnwsnytncarwsn	761
CDRL2-46	cangcnwsnwsnytncarwsn	761
CDRL2-47	cangcnwsnwsnytncarwsn	761
CDRL2-48	cangtnwsnwsnytncarwsn	762
CDRL2-49	cangtnwsnwsnytncarwsn	762
CDRL2-50	cangtnwsnwsnytncarwsn	762
CDRL2-51	cangcnwsnwsnytncarwsn	761
CDRL2-52	cangcnwsnwsnytncarwsn	761
CDRL2-53	cangcnwsnwsnytncarwsn	761
CDRL2-54	gaygcnwsnaayytngarcan	763
CDRL2-55	gaygcnwsnaayytngarcan	763
CDRL2-56	gaygcnwsnaayytngarcan	763
CDRL2-57	gaygcnwsnaayytngarcan	763
CDRL2-58	gaygcnwsnaayytngarcan	763
CDRL2-59	gaygcnwsnaayytngarcan	763
CDRL2-60	gaygcnwsnathytngarcan	764
CDRL2-61	gaygcnwsnaayytngarcan	763
CDRL2-62	gaygcnwsnaayytngarcan	763
CDRL2-63	gaygcnwsnaayytngarcan	763
CDRL2-64	gaygcnwsnaayytngarcan	763
CDRL2-65	gaygcnwsnaayytngarcan	763

FIGURE 18D

NAME	SEQUENCE	SEQ ID NO
CDRL3-1	atgcarwsncancaytggccnathcan	765
CDRL3-2	athcarggncancaytggccncancan	766
CDRL3-3	atgcarggncancaytggccnathcan	767
CDRL3-4	atgcarggncancaytggccnathcan	767
CDRL3-5	atgcarggnathcarytnccntgywsn	768
CDRL3-6	atgcarwsnathcarytnccnytncan	769
CDRL3-7	atgcarwsnathcarytnccnytncan	769
CDRL3-8	atgcarwsnathcarytnccnathcan	770
CDRL3-9	atgcarwsnathcarytnccnathcan	770
CDRL3-11	caraaytayaaywsngcnccnttycan	771
CDRL3-12	caraartayaaywsngtnccnytncan	772
CDRL3-13	atgcargcncancarttyccncaycan	773
CDRL3-14	atgcargcncancarttyccncaycan	773
CDRL3-15	atgcargcncancarttyccncaycan	773
CDRL3-16	carcartayggnwsnwsnccnmgncan	774
CDRL3-17	carcartayggnwsnwsnccnmgnwsn	775
CDRL3-18	ytncarcayaaywsntayccnccncan	776
CDRL3-19	carcartaytaywsnttyccntggcan	777
CDRL3-20	carcartaytaywsnttyccntggcan	777
CDRL3-21	carcartaytaywsncancantggcan	778
CDRL3-22	carcartaytayggncanccnmgncan	779
CDRL3-23	carcartaytayggncanccnmgncan	779
CDRL3-24	carcartaytaywsnathwsnmgncan	780
CDRL3-25	carcartaytaywsnathwsnmgncan	780
CDRL3-26	carcartaytaywsncancantggcan	778
CDRL3-27	carcartaytaywsncancantggcan	778
CDRL3-28	carcartaytaywsncanatgttywsn	781
CDRL3-29	carcartaytaywsncanatgttywsn	781
CDRL3-30	caycartaytaywsncanccnytncan	782
CDRL3-31	caycartaytaywsncanccnytncan	782
CDRL3-32	carcartayttyathcanccnytncan	783
CDRL3-33	carcartayttyathcanccnytncan	783
CDRL3-34	carcartayaayaaytayccnttycan	784
CDRL3-35	carcartayaaycantayccnttycan	785
CDRL3-36	carcarcayaayaaytggccnccntggcan	786
CDRL3-37	carcarcayaayaaytggccnccntggcan	786

FIGURE 18E

NAME	SEQUENCE	SEQ ID NO
CDRL3-38	carcargcnaaywsnttyccnccncan	787
CDRL3-39	carcarwsncaywsngcnccnttycan	788
CDRL3-40	carcarwsntaywsncanytncan	789
CDRL3-41	carcarwsntaywsnathccnytncan	790
CDRL3-42	carcarathtaywsncanwsnathcan	791
CDRL3-43	carcarwsntayathcanccnathcan	792
CDRL3-44	carcarwsntayttycanccnathcan	793
CDRL3-45	carcarwsntayttywsnccnathcan	794
CDRL3-46	carcarwsnttytaycanccnathcan	795
CDRL3-47	carcarwsnttytaycanccnathcan	795
CDRL3-48	carcarwsntayttycanccnathcan	793
CDRL3-49	carcarwsntayttycanccnathcan	793
CDRL3-50	carcarwsntayttycanccnathcan	793
CDRL3-51	carcarwsnttytaygcnccnathcan	796
CDRL3-52	carcarwsnttytaygcnccnathcan	796
CDRL3-53	carcarwsntayttycanccnathcan	793
CDRL3-54	carcartaygaytayytnccnttycan	797
CDRL3-55	carcartaygaytayytnccnttycan	797
CDRL3-56	carcartgygaygayytnccnytncan	798
CDRL3-57	carcaytaygayaayytnccnytncan	799
CDRL3-58	carcartaygayaayytnccnytncan	800
CDRL3-59	carcartaygayaayytnccnytncan	800
CDRL3-60	carcartgygayathytnccnytnwsn	801
CDRL3-61	carcartaygayaayytnccnytngcn	802
CDRL3-62	carcartaygaywsnytnccnathcan	803
CDRL3-63	carcartaygayaayytnccnathcan	804
CDRL3-64	carcaytaygayaayytnccnathcan	805
CDRL3-65	carcaytaygayaayytnccnathcan	805

FIGURE 18F

HEAVY CHAIN CDR NUCLEOTIDE SEQUENCES

NAME	NAME	SEQUENCE	SEQ ID NO:
CDRH1-1	CDRH1-10.1	ggntaycanttycanwsntayggnathwsn	806
CDRH1-2	CDRH1-10	ggntaycanttycanwsntayggnathwsn	806
CDRH1-3	CDRH1-42	ggntaycanttycanggncaytayatgcay	807
CDRH1-4	CDRH1-40	ggntaycanttycanggntaytayatgcay	808
CDRH1-5	CDRH1-30	ggntaycanytncangarytnwsnatgcay	809
CDRH1-6	CDRH1-31	ggntaycanytncangarytnwsnatgcay	809
CDRH1-7	CDRH1-29	ggnttywsnytnwsnaaygcnmgnatgggngtnwsn	810
CDRH1-8	CDRH1-20	ggnttywsnytnwsnaaygcnmgnatgggngtnwsn	810
CDRH1-9	CDRH1-65	ggnttywsnytnwsncanggnggngtnggngtnggn	811
CDRH1-10	CDRH1-56	ggnttywsnytnwsncanggnggngtnggngtnggn	811
CDRH1-11	CDRH1-62	ggnttywsnytnaaycanggnggngtnggngtnggn	812
CDRH1-12	CDRH1-2	ggnttywsnytnwsncanggnggngtnggngtnggn	811
CDRH1-13	CDRH1-59	ggnttywsnytnwsncanggnggngtnggngtnggn	811
CDRH1-14	CDRH1-57	ggnttywsnytnwsncanggnggngtnggngtnggn	811
CDRH1-15	CDRH1-64	ggnttywsnytnwsncanggnggngtnggngtnggn	811
CDRH1-16	CDRH1-41	ggnttyccnttywsnmgntaywsnatgaay	813
CDRH1-17	CDRH1-45	ggnttycanttywsnwsntaygcnatgaay	814
CDRH1-18	CDRH1-47	ggnttycanttywsnwsntaygcnatgwsn	815
CDRH1-19	CDRH1-51	ggnttycanttywsnwsntaygcnatgwsn	815
CDRH1-20	CDRH1-52	ggnttycanttywsnwsntaygcnatgwsn	815
CDRH1-21	CDRH1-13	ggnttycanttywsnwsntayggnatgcay	816
CDRH1-22	CDRH1-14	ggnttycanttywsnwsntayggnatgcay	816
CDRH1-23	CDRH1-1	ggnttycanttywsnwsntayggnatgcay	816
CDRH1-24	CDRH1-22	ggnttycanttywsnwsntaygayatgcay	817
CDRH1-25	CDRH1-23	ggnttycanttywsnwsntaygayatgcay	817
CDRH1-26	CDRH1-12	ggnttycanttywsnwsntayggnatgcay	816
CDRH1-27	CDRH1-5	ggnttycanttywsnwsntayggnatgcay	816
CDRH1-28	CDRH1-15	ggnttycanttywsnwsntayggnatgcay	816
CDRH1-29	CDRH1-7	ggnttycanttywsnwsntayggnatgcay	816
CDRH1-30	CDRH1-61	ggnttycanttymgnwsncayggnatgcay	818
CDRH1-31	CDRH1-39	ggnttycanttywsngcntaywsnatgaay	819
CDRH1-32	CDRH1-34	ggnttycanttywsnwsntaywsnatgaay	820
CDRH1-33	CDRH1-6	ggnttycanttywsnwsntaywsnatgaay	820
CDRH1-34	CDRH1-35	ggnttycanttywsnwsntaywsnatgaay	820
CDRH1-35	CDRH1-21	ggnggnwsngtnwsnwsnggnggntaytaytggwsn	821
CDRH1-36	CDRH1-8	ggnggnwsnathwsnmgnggnggntaytaytggwsn	822
CDRH1-37	CDRH1-9	ggnggnwsnathwsnmgnggnggntaytaytggwsn	822
CDRH1-38	CDRH1-18	ggnggnwsnathwsnwsnggnggntaytaytggwsn	823

FIGURE 19A

NAME	NAME	SEQUENCE	SEQ ID NO:
CDRH1-39	CDRH1-24	ggnggnwsnathwsnwsnggnggntaytaytggwsn	823
CDRH1-40	CDRH1-25	ggnggnwsnathwsnwsnggnggntaytaytggwsn	823
CDRH1-41	CDRH1-26	ggnggnwsnathwsnwsnggnggntaytaytggwsn	823
CDRH1-42	CDRH1-27	ggnggnwsnathwsnwsnggnggntaytaytggwsn	823
CDRH1-43	CDRH1-38	ggnggnwsnathwsnwsnggnggntaytaytggwsn	823
CDRH1-44	CDRH1-54	ggnggnwsnathwsnwsnggngaytaytaytggaay	824
CDRH1-45	CDRH1-55	ggnggnwsnathwsnwsnggngaytaytaytggaay	824
CDRH1-46	CDRH1-43	ggnggnwsnttywsnggntaytaytggwsn	825
CDRH1-47	CDRH1-44	ggnggnwsnttywsnggntaytaytggwsn	825
CDRH1-48	CDRH1-49	ggnggnwsnttywsnggntaytaytggwsn	825
CDRH1-49	CDRH1-50	ggnggnwsnttywsnggntaytaytggwsn	825
CDRH1-50	CDRH1-53	ggnggnwsnttywsnggntaytaytggwsn	825
CDRH1-51	CDRH1-33	ggnggnwsnathwsnwsntaytaytggwsn	826
CDRH1-52	CDRH1-3	ggnggnwsngtnwsnwsnggnggnwsntaytggwsn	827
CDRH1-53	CDRH1-4	ggnggnwsngtnwsnwsnggnggnwsntaytggwsn	827
CDRH1-54	CDRH1-16	ggntaymgnttycanwsntaytggathggn	828
CDRH1-55	CDRH1-17	ggntaywsnttycanwsntaytggathggn	829
CDRH1-56	CDRH1-11	ggntaywsnttycanwsntaytggathggn	829
CDRH1-57	CDRH1-37	ggngaywsngtnwsnwsntaywsngcngcntggaay	830
CDRH1-58	CDRH1-39.1	ggnttycanttywsngcntaywsnatgaay	819
CDRH2-1	CDRH2-10.1	tggathwsngcnwsnaayggnaaycanaaytaygcncaraar ytncargay	831
CDRH2-2	CDRH2-10	tggathwsngcnwsnaayggnaaycanaaytaygcncaraar ytncargay	831
CDRH2-3	CDRH2-42	tggathaayccnaaywsnggnggncanaaytgygcncaraar ttycarggn	832
CDRH2-4	CDRH2-40	tggathaayccnaaywsnggnggncanaaycaycancaraar ttycarggn	833
CDRH2-5	CDRH2-30	wsnttygayccngargayggngarcanathtaygcncaraar ttycarggn	834
CDRH2-6	CDRH2-31	wsnttygayccngargayggngarcanathtaygcncaraar ttycarggn	834
CDRH2-7	CDRH2-29	cayathttywsnaaygaygaraarwsntaywsncanwsnytn aarwsn	835
CDRH2-8	CDRH2-20	ytnathttywsnaaygaygaraarwsntaywsncanwsnytn aarwsn	836
CDRH2-9	CDRH2-65	ytnathtaytggaaygaygayaarmgntaywsnccnwsnytn aarwsn	837

FIGURE 19B

NAME	NAME	SEQUENCE	SEQ ID NO:
CDRH2-10	CDRH2-56	ytnathtaytggaaygaygayaarmgntaywsnccnwsnytn aarwsn	837
CDRH2-11	CDRH2-62	ytnathtaytggaaygaygayaarmgntaywsnccnwsnytn aarwsn	837
CDRH2-12	CDRH2-2	ytnathtaytggaaygaygayaarmgntaywsnccnwsnytn aarwsn	837
CDRH2-13	CDRH2-59	ytnathtaytggaaygtngaraarmgntaywsnccnwsnytn mgnwsn	838
CDRH2-14	CDRH2-57	ytnathtaytggaaygaygayaarmgntaywsnccnwsnytn aarwsn	837
CDRH2-15	CDRH2-64	ytnathtaytggaaygaygayaarmgntaywsnccnwsnytn aarwsn	837
CDRH2-16	CDRH2-41	gcnathwsnwsnwsnwsntayathtaytaygcngaywsn gtnaarggn	839
CDRH2-17	CDRH2-45	gcnathwsnggnwsnggnggnwsncantaytaygcngaywsn gtnaarggn	840
CDRH2-18	CDRH2-47	gcnathwsnggnwsnggnggnwsncantaytaygcngaywsn gtnaarggn	840
CDRH2-19	CDRH2-51	gcnathwsnggnwsnggnggnwsncantaytaygcngaywsn gtnaarggn	840
CDRH2-20	CDRH2-52	gcnathwsnggnwsnggnggnwsncantaytaygcngaywsn gtnaarggn	840
CDRH2-21	CDRH2-13	ttyathwsngaygayggnwsncanaartaytaygcngaywsn gtnaarggn	841
CDRH2-22	CDRH2-14	ttyathwsngaygayggnwsncanaartaytaygcngaywsn gtnaarggn	841
CDRH2-23	CDRH2-1	gtnathtggtaygayggnwsnaayaartaytaygcngaywsn gtnaarggn	842
CDRH2-24	CDRH2-22	gtnathtggtaygayggnwsnathaartaytaygcngaywsn gtnaarggn	843
CDRH2-25	CDRH2-23	gtnathtggtaygayggnwsnathaartaytaygcngaywsn gtnaarggn	843
CDRH2-26	CDRH2-12	gtnathtggtaygayggnwsnaayaartaytaygcngaywsn gtnaarggn	842
CDRH2-27	CDRH2-5	gtnathtggwsngayggnwsnaayaartaytaygcngaywsn gtnaarggn	844
CDRH2-28	CDRH2-15	gtnathtgggaygayggnwsnaaycartaytaycangaywsn gtnaarggn	845

FIGURE 19C

NAME	NAME	SEQUENCE	SEQ ID NO:
CDRH2-29	CDRH2-7	gtnathtggtaygayggnwsnaayaarmgntaygtngaywsn gtnaarggn	846
CDRH2-30	CDRH2-61	gtnathtggtaygayggnwsnaayaaraaytaygcngaywsn gtnmgnggn	847
CDRH2-31	CDRH2-39	tayathwsnwsnwsnggnmgncanathtaytaygcngaywsn gtnaarggn	848
CDRH2-32	CDRH2-34	cayathwsnwsnwsnwsnmgncanathtaytaygcngaywsn gtnaarggn	849
CDRH2-33	CDRH2-6	cayathwsnmgnwsnwsnmgncanathtaytaygcngaywsn gtnaarggn	850
CDRH2-34	CDRH2-35	cayathwsnmgnwsnwsnmgncanathtaytaygcngaywsn gtnaarggn	850
CDRH2-35	CDRH2-21	tayathcaywsnwsnggnwsncantaytayaayccnwsnytn aarwsn	851
CDRH2-36	CDRH2-8	tayathtaycaywsnggnwsncantaytayaayccnwsnytn aarwsn	852
CDRH2-37	CDRH2-9	tayathtaycaywsnggnwsncantaytayaayccnwsnytn aarwsn	852
CDRH2-38	CDRH2-18	tayathtaytaywsnggnwsncantaytayaayccnwsnytn aarwsn	853
CDRH2-39	CDRH2-24	tayathcaytaywsnggnwsncantaytayaayccnwsnytn aarwsn	854
CDRH2-40	CDRH2-25	tayathcaytaywsnggnwsncantaytayaayccnwsnytn aarwsn	854
CDRH2-41	CDRH2-26	tayathcaywsnwsnggnwsncantaytayaayccnwsnytn aarwsn	851
CDRH2-42	CDRH2-27	tayathcaywsnwsnggnwsncantaytayaayccnwsnytn aarwsn	851
CDRH2-43	CDRH2-38	tayathcaytaywsnggnwsncantaytayaayccnwsnytn aarwsn	854
CDRH2-44	CDRH2-54	tayathtaytaywsnggnggncantaytayaayccnwsnytn aarwsn	855
CDRH2-45	CDRH2-55	tayathtaytaywsnggnggncantaytayaayccnwsnytn aarwsn	855
CDRH2-46	CDRH2-43	garathaaycaywsnggnwsncanaaytayaayccnwsnytn aarwsn	856
CDRH2-47	CDRH2-44	garathaaycaywsnggnwsncanaaytayaayccnwsnytn aarwsn	856

FIGURE 19D

NAME	NAME	SEQUENCE	SEQ ID NO:
CDRH2-48	CDRH2-49	garathaaycaywsnggnwsncanaaytayaayccnwsnytn aarwsn	856
CDRH2-49	CDRH2-50	garathaaycaywsnggnwsncanaaytayaayccnwsnytn aarwsn	856
CDRH2-50	CDRH2-53	garathaaycaywsnggnwsncanaaytayaayccnwsnytn aarwsn	856
CDRH2-51	CDRH2-33	mgnathtaycanwsnggncancanaaytayaayccnwsnytn aarwsn	857
CDRH2-52	CDRH2-3	tayathtaytaywsnggnwsncanaaytayaayccnwsnytn aarwsn	858
CDRH2-53	CDRH2-4	tayathtaytaywsnggnwsncanaaytayaayccnwsnytn aarwsn	858
CDRH2-54	CDRH2-16	athathtayccngaygaywsngaycanmgntaywsnccnwsn ttycarggn	859
CDRH2-55	CDRH2-17	athathtayccngaygaywsngaygcnmgntaywsnccnwsn ttycarggn	860
CDRH2-56	CDRH2-11	athathtayccnggngaywsngayathmgntaywsnccnwsn ttycarggn	861
CDRH2-57	CDRH2-37	mgncantaytgymgnwsnaartggtayaaygaytaygcngtn wsngtnaarwsn	862
CDRH2-58	CDRH2-39.1	tayathwsnwsnwsnggnmgncanathtaytaygcngaywsn gtnaarggn	848
CDRH3-1	CDRH3-10.1	gargayaaytggaaytayggnttyttygaytay	863
CDRH3-2	CDRH3-10	gargayaaytggaaytayggnttyttygaytay	863
CDRH3-3	CDRH3-42	wsnathgcngtngcnytngaytay	864
CDRH3-4	CDRH3-40	wsnathgcngtngcnytngaytay	864
CDRH3-5	CDRH3-30	garggngayggnggntaytaytaytayggnatggaygtn	865
CDRH3-6	CDRH3-31	garggngayggnggntaytaytaytayggnatggaygtn	865
CDRH3-7	CDRH3-29	atgtaywsnwsnggntggtayggngtnttygaytay	866
CDRH3-8	CDRH3-20	gtntaywsnwsnggntggwsnttytayggnatggaygtn	867
CDRH3-9	CDRH3-65	mgnmgngarytnccnttygaytay	868
CDRH3-10	CDRH3-56	mgnaaytggcanccnttygaytay	869
CDRH3-11	CDRH3-62	mgnytngarytnccnttygaytay	870
CDRH3-12	CDRH3-2	mgnmgngargtnccnttygaytay	871
CDRH3-13	CDRH3-59	mgncaycanaayccnttygartay	872
CDRH3-14	CDRH3-57	mgnggngarytnccnttygaytay	873
CDRH3-15	CDRH3-64	mgnggngarytnccnttygaytay	873
CDRH3-16	CDRH3-41	gaymgngtnggngcncanccngaygcnttygayath	874

FIGURE 19E

NAME	NAME	SEQUENCE	SEQ ID NO:
CDRH3-17	CDRH3-45	garggnathgcngtngcnggncangcngartaytaytaytaytaygcnatggaygtn	875
CDRH3-18	CDRH3-47	garggnathgcngcnmgngaywsntaytaytaytaygcnatggaygtn	876
CDRH3-19	CDRH3-51	garggnathgcnggnmgngaywsntaytaytaytayggnatggaygtn	877
CDRH3-20	CDRH3-52	garggnathgcnggnmgngaywsntaytaytaytayggnatggaygtn	877
CDRH3-21	CDRH3-13	wsntaytaygaywsnwsnggntaytaytayggnttygaytay	878
CDRH3-22	CDRH3-14	wsntaytaygaywsnwsnggntaytaytayggnttygaytay	878
CDRH3-23	CDRH3-1	aaygtnathgaytay	879
CDRH3-24	CDRH3-22	ggnggngcncanggngcngartayttycarcay	880
CDRH3-25	CDRH3-23	ggnggngcncanggngcngartayttycarcay	880
CDRH3-26	CDRH3-12	ytntggttyggngarcanttygaytay	881
CDRH3-27	CDRH3-5	aayytnccnttygaytay	882
CDRH3-28	CDRH3-15	wsncaytayggnggngaytaygaytaytayggnatggaygtn	883
CDRH3-29	CDRH3-7	gayggntggcarcarcargcnccnttygaytay	884
CDRH3-30	CDRH3-61	tggggnathwsngcnccnttygaytgy	885
CDRH3-31	CDRH3-39	tgggcnccnttygaytay	886
CDRH3-32	CDRH3-34	gayggntayaaytggaayggnggnggnaaytaytayggnatggaygtn	887
CDRH3-33	CDRH3-6	gayggntayaaytggaayaayggnggntaytaytayggnatggaygtn	888
CDRH3-34	CDRH3-35	gayggntayaaytggaayaayggnggntaytaytayggnatggaygtn	888
CDRH3-35	CDRH3-21	ggnccntaytayggnatggaygtn	889
CDRH3-36	CDRH3-8	gcnytnmgnggnathgtnytnatggtntaygtnytnggngcnytngayath	890
CDRH3-37	CDRH3-9	gcnytnmgnggnathgtnytnatggtntaygtnytnggngcnytngayath	890
CDRH3-38	CDRH3-18	gaygarcangtngtnmgnggnytnathmgntaytgytayggnatggaygtn	891
CDRH3-39	CDRH3-24	gaymgnggnggnggngaytayggnmgnatggaygtn	892
CDRH3-40	CDRH3-25	gaymgnggnggnggngaytayggnmgnatggaygtn	892
CDRH3-41	CDRH3-26	wsnaayaaytayggntgyttygcnytn	893
CDRH3-42	CDRH3-27	wsnaayaaytayggntgyttygcnytn	893
CDRH3-43	CDRH3-38	ggntayaaytayggnytntaytaytaygaywsnwsnggntayccnwsntaytaytayggnatggaygtn	894
CDRH3-44	CDRH3-54	cantaytaygayathytncanggntayccnttytayttygaytay	895

FIGURE 19F

NAME	NAME	SEQUENCE	SEQ ID NO:
CDRH3-45	CDRH3-55	cantaytaygayathytncanggntayccnttytayttygay tay	895
CDRH3-46	CDRH3-43	ggnggntaywsnwsnwsntggtaytggttygayccn	896
CDRH3-47	CDRH3-44	ggnggntaywsnwsnwsntggttytggttygayccn	897
CDRH3-48	CDRH3-49	ggnggntaywsnwsnwsntggttytggttygayccn	897
CDRH3-49	CDRH3-50	ggnggntaywsnwsnwsntggttytggttygayccn	897
CDRH3-50	CDRH3-53	ggnggntaywsnwsnwsntggttytggttygayccn	897
CDRH3-51	CDRH3-33	gayggntaywsntayggncaytaytaytaytayggnatggay gtn	898
CDRH3-52	CDRH3-3	wsngcnytnmgntayttygaytggytnttywsngaygtnwsn gayath	899
CDRH3-53	CDRH3-4	wsngcnytnmgntayttygaytggytnttywsngaygtnwsn gayath	899
CDRH3-54	CDRH3-16	caraarwsntayggntaywsntayttygaytay	900
CDRH3-55	CDRH3-17	carggntayggnwsnggntggggntayttygaytay	901
CDRH3-56	CDRH3-11	carggnytngcngtngcnggncanwsntaytaytaytaytay ggnatggaygtn	902
CDRH3-57	CDRH3-37	gaymgngcngtngcnggntaytaytayggnatggaygtn	903
CDRH3-58	CDRH3-39.1	tgggcnccnttygaytay	886

FIGURE 19G

LIGHT CHAIN FR NUCLEOTIDE SEQUENCES

NAME	SEQUENCE	SEQ ID NO:
FRL1-1	gaygtngtnatgcancarwsnccnytnwsnytnccngtncanytnggn carccngcnwsnathwsntgy	919
FRL1-2	gaygtngtnatgcancarwsnccnytnwsnytnccngtncanytnggn carccngcnwsnathwsntgy	919
FRL1-3	gaygtngtnatgcancarwsnccnytnwsnytnccngtncanytnggn carccngcnwsnathwsntgy	920
FRL1-4	gaygtngtnatgcancarwsnccnytnwsnytnccngtncanytnggn carccngcnwsnathwsntgy	920
FRL1-5	gayathgtnatgcancarcanccnytnwsnytnwsngtncanccnggn carccngcnwsnathwsntgy	921
FRL1-6	gayathgtnatgcancarcanccnytnwsnytnwsngtncanccnggn carccngcnwsnathwsntgy	921
FRL1-7	gayathgtnatgcancarcanccnytnwsnytnwsngtncanccnggn carccngcnwsnathwsntgy	921
FRL1-8	gayathgtnatgcancarcanccnytnwsnytnwsngtncanccnggn carccngcnwsnathwsntgy	922
FRL1-9	gayathgtnatgcancarcanccnytnwsnytnwsngtncanccnggn carccngcnwsnathwsntgy	922
FRL1-11	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	923
FRL1-12	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathathtgy	923
FRL1-13	aayathgtnatgcancarcanccnytnwsnwsnccngtncanytnggn carccngcnwsnathwsntgy	924
FRL1-14	aayathgtnatgcancarcanccnytnwsnwsnccngtncanytnggn carccngcnwsnathwsntgy	924
FRL1-15	garathgtnatgcancarcanccnytnwsnwsnccngtncanytnggn carccngcnwsnathwsntgy	924
FRL1-16	garathgtnytncancarwsnccnggncanytnwsnytnwsnccnggn garmgngcncanytnwsntgy	925
FRL1-17	garathgtnytncancarwsnccnggncanytnwsnytnwsnccnggn garmgngcncanytnwsntgy	926
FRL1-18	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	927
FRL1-19	gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggn garmgngcncanathaaytgy	928

FIGURE 20A

NAME	SEQUENCE	SEQ ID NO:
FRL1-20	gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggn garmgngcncanathaaytgy	928
FRL1-21	gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggn garmgngcncanathaaytgy	929
FRL1-22	gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggn garmgngcncanathaaytgy	929
FRL1-23	gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggn garmgngcncanathaaytgy	929
FRL1-24	gayathgtnatgcancarwsnccngaywsnytncangtnwsnytnggn garmgngcncanathaaytgy	929
FRL1-25	gayathgtnatgcancarwsnccngaywsnytncangtnwsnytnggn garmgngcncanathaaytgy	929
FRL1-26	gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggn garmgngcncanathaaytgy	929
FRL1-27	gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggn garmgngcncanathaaytgy	929
FRL1-28	gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggn garmgngcncanathaaytgy	930
FRL1-29	gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggn garmgngcncanathaaytgy	930
FRL1-30	gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggn garmgngcncanathaaytgy	929
FRL1-31	gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggn garmgngcncanathaaytgy	929
FRL1-32	gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggn garmgngcncanathaaytgy	929
FRL1-33	gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggn garmgngcncanathaaytgy	929
FRL1-34	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	931
FRL1-35	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtngcnathcantgy	932
FRL1-36	garathgtnatgcancarwsnccngcncanytnwsngtnwsnccnggn garmgngcncanytnwsntgy	933
FRL1-37	garathgtnatgcancarwsnccngcncanytnwsngtnwsnccnggn garmgngcncanytnwsntgy	933
FRL1-38	gayathcaratgcancarwsnccnwsnwsngtnwsngcnwsngtnggn gaymgngtncanathcantgy	934

FIGURE 20B

NAME	SEQUENCE	SEQ ID NO:
FRL1-39	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	935
FRL1-40	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsnytnggn gaymgngtncanathcantgy	934
FRL1-41	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	936
FRL1-42	gayathcaratgcancarwsnccnwsnwsnmgnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-43	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	937
FRL1-44	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-45	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-46	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-47	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-48	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-49	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-50	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-51	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-52	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-53	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-54	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-55	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-56	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	938
FRL1-57	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934

FIGURE 20C

NAME	SEQUENCE	SEQ ID NO:
FRL1-58	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtngcnathcantgy	934
FRL1-59	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtngcnathcantgy	934
FRL1-60	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-61	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-62	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gayggngtncanathcantgy	934
FRL1-63	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	939
FRL1-64	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-65	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL2-1	tggttycarcarmgnccnggncarwsnccnmgnmgnytnathtay	939
FRL2-2	tggttycarcarmgnccnggncarwsnccnmgnmgnytnathtay	939
FRL2-3	tggytncarcarmgnccnggncarwsnccnmgnmgnytnathtay	940
FRL2-4	tggytncarcarmgnccnggncarwsnccnmgnmgnytnathtay	940
FRL2-5	tggtayytncaraarccnggncarccnccncarytnytnathtay	941
FRL2-6	tggtayytncaraarccnggncarccnccncarytnytnathtay	941
FRL2-7	tggtayytncaraarccnggncarccnccncarytnytnathtay	941
FRL2-8	tggttyytncaraarccnggncarccnccncarccnytnathtay	942
FRL2-9	tggttyytncaraarccnggncarccnccncarccnytnathtay	942
FRL2-11	tggtaycarcaraarccnggnaargtnccnaarytnytnathtay	943
FRL2-12	tggtaycarcaraarccnggnaargtnccnaarytnytnathtay	943
FRL2-13	tggytncarcarmgnccnggncarccnccnmgnytnytnathtay	944
FRL2-14	tggytncarcarmgnccnggncarccnccnmgnytnytnathtay	944
FRL2-15	tggytncarcarmgnccnggncarccnccnmgnytnytnathtay	944
FRL2-16	tggtaycarcaraarccnggncargcnccnmgnytnytnathwsn	945
FRL2-17	tggtaycarcaraarccnggncargcnccnmgnytnytnathtay	946
FRL2-18	tggtaycarcaraarccnggnaargcnccnaarmgnytnathtay	947
FRL2-19	tggtaycarcaraarccnggncarccnccnaarytnttyathtay	948
FRL2-20	tggtaycarcaraarccnggncarccnccnaarytnttyathtay	948
FRL2-21	tggtaycarcaraarccnggncarccnccnaarytnytnathtay	949
FRL2-22	tggtaycarcaraarccnggncarccnccnaarytnytnathtay	949
FRL2-23	tggtaycarcaraarccnggncarccnccnaarytnytnathtay	949

FIGURE 20D

NAME	SEQUENCE	SEQ ID NO:
FRL2-24	tggtaycarcaraarccnggncarccnccnaarytnytnathtay	949
FRL2-25	tggtaycarcaraarccnggncarccnccnaarytnytnathtay	949
FRL2-26	tggtaycarcaraarccnggncarccnccnaarytnytnathtay	949
FRL2-27	tggtaycarcaraarccnggncarccnccnaarytnytnathtay	949
FRL2-28	tggtaycarcaraarccnggncarccnccnaargtnytnathtay	950
FRL2-29	tggtaycarcaraarccnggncarccnccnaargtnytnathtay	950
FRL2-30	tggtaycarcaraarccnggncarccnccnaarytnytnathtay	949
FRL2-31	tggtaycarcaraarccnggncarccnccnaarytnytnathtay	949
FRL2-32	tggtaycarcaraarccnggncarccnccnaarytnytnathtay	949
FRL2-33	tggtaycarcaraarccnggncarccnccnaarytnytnathtay	949
FRL2-34	tggttycarcaraarccnggnaargcnccnaarwsnytnathtay	951
FRL2-35	tggytncarcaraarccnggnaargcnccnaarwsnytnathtay	952
FRL2-36	tggtaycarcargayccnggncargcnccnmgnytnytnathtay	953
FRL2-37	tggtaycarcargayccnggncargcnccnmgnytnytnathtay	953
FRL2-38	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-39	tggtaycarcaraarccnggnaargcnccnaarttyytnathtay	955
FRL2-40	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-41	tggtaycarcarmgnccnggnaaygcnccnaarytnytnathtay	956
FRL2-42	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-43	tggtaycarcaraarccnggnaargcnccnaargtnytnathtay	957
FRL2-44	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-45	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-46	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-47	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-48	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-49	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-50	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-51	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-52	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-53	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-54	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-55	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-56	tggtaycarcaraarccnggnaargcnccngarytnytnathtay	958
FRL2-57	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-58	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-59	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954

FIGURE 20E

NAME	SEQUENCE	SEQ ID NO:
FRL2-60	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-61	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-62	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-63	tggtaycarcaraarytnggnaargcnccnaarytnytnathcay	959
FRL2-64	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-65	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL3-1	ggngtnccngaymgnttyaayggnwsnggnwsnggncangayttycan ytnaarathwsnmgngtngargcngargaygtnggngtntaytaytgy	960
FRL3-2	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytnaarathwsnmgngtngargcngargaygtnggngtntaytaytgy	961
FRL3-3	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytnaarathwsnmgngtngargcngargaygtnggngtntaytaytgy	961
FRL3-4	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytnaarathwsnmgngtngargcngargaygtnggngtntaytaytgy	961
FRL3-5	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytnaarathwsnmgngtngargcngargaygtnggngtntaytaytgy	961
FRL3-6	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytnaarathwsnmgngtngargcngargaygtnggngtntaytaytgy	961
FRL3-7	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytnaarathwsnmgngtngargcngargaygtnggngtntaytaytgy	961
FRL3-8	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytnaarathwsnmgngtngargcngargaygtnggngtntaytaytgy	961
FRL3-9	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytnaarathwsnmgngtngargcngargaygtnggngtntaytaytgy	961
FRL3-11	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargaygtngcncantaytaytgy	962
FRL3-12	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargaygtngcncantaytaytgy	962
FRL3-13	ggngtnccngaymgnttywsnggnwsnggngcnggncangayttycan ytnaarathwsnmgngtngargcngargaygtnggngtntaytaytgy	963
FRL3-14	ggngtnccngaymgnttywsnggnwsnggngcnggncangayttycan ytnaarathwsnmgngtngargcngargaygtnggngtntaytaytgy	963
FRL3-15	ggngtnccngaymgnttywsnggncanggngcnggncangayttycan ytnaarathwsnmgngtngargcngargaygtnggngtntaytaytgy	964
FRL3-16	ggnathccngaymgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnmgnytngarccngargayttygcngtntaytaytgy	965
FRL3-17	ggnathccngaymgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnmgnytngarccngargayttygcngtntaytaytgy	965

FIGURE 20F

NAME	SEQUENCE	SEQ ID NO:
FRL3-18	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangarttycan ytncanathwsnwsnytncarccngargayttygcncantaytaytgy	966
FRL3-19	ggngtnccngaymgnttycanggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncargcngargaygtngcngtntaytaytgy	967
FRL3-20	ggngtnccngaymgnttycanggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncargcngargaygtngcngtntaytaytgy	967
FRL3-21	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncargcngargaygtngcngtntaytaytgy	968
FRL3-22	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncargcngargaygtngcngtntayttytgy	969
FRL3-23	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncargcngargaygtngcngtntayttytgy	969
FRL3-24	ggngtnccngaymgnttyggnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncargcngargaygtngcngtntaytaytgy	970
FRL3-25	ggngtnccngaymgnttyggnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncargcngargaygtngcngtntaytaytgy	970
FRL3-26	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncargcngaygaygtngcngtntaytaytgy	971
FRL3-27	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncargcngaygaygtngcngtntaytaytgy	971
FRL3-28	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnggnytncargcngargaygtngcnytntaytaytgy	972
FRL3-29	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnggnytncargcngargaygtngcnytntaytaytgy	972
FRL3-30	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncargcngargaygtngcngtnttytaytgy	973
FRL3-31	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncargcngargaygtngcngtnttytaytgy	973
FRL3-32	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncargcngargaygtngcngtntayttytgy	969
FRL3-33	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncargcngargaygtngcngtntayttytgy	969
FRL3-34	ggngtnccnwsnaarttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargayttygcncantaytaytgy	974
FRL3-35	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargayttygcncantaytaytgy	975
FRL3-36	ggnathccngcnmgnttywsnggnwsnggnwsnggncangarttycan ytncanathwsnwsnytncarwsngargayttygcngtntaytaytgy	976

FIGURE 20G

NAME	SEQUENCE	SEQ ID NO:
FRL3-37	ggnathccngcnmgnttywsnggnwsnggnwsnggncangarttycan ytncanathwsnwsnytncarwsngargayttygcngtntaytaytgy	976
FRL3-38	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargayttygcncantaytaytgy	975
FRL3-39	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargayttygcngcntaytaytgy	977
FRL3-40	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargayttygcncantaytaytgy	975
FRL3-41	ggngtnccnwsnmgngtnwsnggnwsnggnwsnggncangayttycan ytncanathmgnwsnytncarccngargayttygcncantaytaytgy	978
FRL3-42	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanytnwsnwsnytncarccngargayttygcncantaytaytgy	979
FRL3-43	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargayttygcncantaytaytgy	975
FRL3-44	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngaraayttygcncantaytaytgy	980
FRL3-45	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanttywsnwsnytncarccngargayttygcncantaytaytgy	981
FRL3-46	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanytnwsnwsnytncarccngargayttygcnwsntaytaytgy	982
FRL3-47	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanytnwsnwsnytncarccngargayttygcnwsntaytaytgy	982
FRL3-48	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargayttygcncantaytaytgy	975
FRL3-49	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargayttygcncantaytaytgy	975
FRL3-50	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargayttygcncantaytaytgy	975
FRL3-51	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargayttygcnwsntaytaytgy	983
FRL3-52	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargayttygcnwsntaytaytgy	983
FRL3-53	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargayttygcncantaytaytgy	975
FRL3-54	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ttycanathwsnwsnytncarccngargayathgcncantaytaytgy	984
FRL3-55	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ttycanathwsnwsnytncarccngargayathgcncantaytaytgy	984

FIGURE 20H

NAME	SEQUENCE	SEQ ID NO:
FRL3-56	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ttycanathwsnwsnytncarccngargayathgcncantaytaytgy	984
FRL3-57	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ttycanathwsnwsnytncarccngargayathgcncantaytaytgy	984
FRL3-58	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ttycanathwsnwsnytncarccngargayathgcncantaytaytgy	984
FRL3-59	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ttycanathwsnwsnytncarccngargayathgcncantaytaytgy	984
FRL3-60	ggngtnccnwsnmgnttywsnggnwsnggnwsngarcangayttycan ttycanathwsnwsnytncarccngargayathgcncantaytaytgy	985
FRL3-61	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ttycanathwsnwsnytncarccngargayathgcncantaytaytgy	984
FRL3-62	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ttycanathwsnwsnytncarccngargayathgcncantaytaytgy	984
FRL3-63	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ttycanathwsnwsnytncarccngargayathgcncantaytaytgy	984
FRL3-64	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ttycanathwsnwsnytncarccngargayathgcncantaytaytgy	984
FRL3-65	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ttycanathwsnwsnytncarccngargayathgcncantaytaytgy	984
FRL4-1	ttyggncarggncanmgnytngarathaar	986
FRL4-2	ttyggncarggncanmgnytngarathaar	986
FRL4-3	ttyggncarggncanmgnytngarathaar	986
FRL4-4	ttyggncarggncanmgnytngarathaar	986
FRL4-5	ttyggncarggncanaarytngarathaar	988
FRL4-6	ttyggnggnggncanaargtngarathaar	989
FRL4-7	ttyggnggnggncanaargtngarathaar	989
FRL4-8	ttyggncayggncanmgnytngarathaar	990
FRL4-9	ttyggncayggncanmgnytngarathaar	990
FRL4-11	ttyggnccnggncanaargtngayathaar	991
FRL4-12	ttyggnggnggncanaargtngarathaar	989
FRL4-13	ttyggnccnggncanaargtngayathaar	991
FRL4-14	ttyggnccnggncanaargtngayathaar	991
FRL4-15	ttyggnggnggncanaargtngarathaar	989
FRL4-16	ttyggncarggncanaargtngarathaar	992
FRL4-17	ttyggncarggncanaarytngarathaar	988
FRL4-18	ttyggncarggncanaargtngarathaar	992
FRL4-19	ttyggncarggncanaargtngarathaar	992
FRL4-20	ttyggncarggncanaargtngarathaar	992

FIGURE 20I

NAME	SEQUENCE	SEQ ID NO:
FRL4-21	ttyggncarggncanaargtngarathaar	992
FRL4-22	ttyggncarggncanaargtngarathaar	992
FRL4-23	ttyggncarggncanaargtngarathaar	992
FRL4-24	ttyggncarggncanaargtngarathaar	992
FRL4-25	ttyggncarggncanaargtngarathaar	992
FRL4-26	ttyggnccnggncanaargtngarathaar	993
FRL4-27	ttyggnccnggncanaargtngarathaar	993
FRL4-28	ttyggncarggncanaarytngarathaar	988
FRL4-29	ttyggncarggncanaarytngarathaar	988
FRL4-30	ttyggnggnggncanaargtngcnathaar	994
FRL4-31	ttyggnggnggncanaargtngcnathaar	994
FRL4-32	ttyggnggnggncanaargtngarathaar	989
FRL4-33	ttyggnggnggncanaargtngarathaar	989
FRL4-34	ttyggnccnggncanaargtngayathaar	991
FRL4-35	ttyggnccnggncanaaratggayathaar	995
FRL4-36	ttyggncarggncanaargtngarathaar	992
FRL4-37	ttyggncarggncanaargtngarathaar	992
FRL4-38	ttyggncarggncanaargtngarttyaar	996
FRL4-39	ttyggnccnggncanaargtngayathaar	991
FRL4-40	ttyggnggnggncanaargtngarathaar	989
FRL4-41	ttyggnggnggncanaargtngarathaar	989
FRL4-42	ttyggncarggncanmgnytngarathaar	986
FRL4-43	ttyggncarggncanmgnytngarathath	987
FRL4-44	ttyggncarggncanmgnytngarathaar	986
FRL4-45	ttyggncarggncanmgnytngarathaar	986
FRL4-46	ttyggncarggncanmgnytngarathaar	986
FRL4-47	ttyggncarggncanmgnytngarathaar	986
FRL4-48	ttyggncarggncanmgnytngarathaar	986
FRL4-49	ttyggncarggncanmgnytngarathaar	986
FRL4-50	ttyggncarggncanmgnytngarathaar	986
FRL4-51	ttyggncarggncanmgnytngarathaar	986
FRL4-52	ttyggncarggncanmgnytngarathaar	986
FRL4-53	ttyggncarggncanmgnytngarathaar	986
FRL4-54	ttyggnccnggncanaargtngayathaar	991
FRL4-55	ttyggnccnggncanaargtngayathaar	991
FRL4-56	ttyggnggnggncanaargtngarathaar	989

FIGURE 20J

NAME	SEQUENCE	SEQ ID NO:
FRL4-57	ttyggnggnggncanaargtngarathaar	989
FRL4-58	ttyggnggnggncanaargtngarathaar	989
FRL4-59	ttyggnggnggncanaargtngarathaar	989
FRL4-60	ttyggnggnggncanaargtngarathaar	989
FRL4-61	ttyggnggnggncanaargtngarathmgn	997
FRL4-62	ttyggncarggncanmgnytngarathaar	986
FRL4-63	ttyggncarggncanmgnytngarathaar	986
FRL4-64	ttyggncarggncanmgnytngarathaar	986
FRL4-65	ttyggncarggncanmgnytngarathaar	986

FIGURE 20K

HEAVY CHAIN FR NUCLEOTIDE SEQUENCES

NAME	NAME	SEQUENCE	SEQ ID NO:
FRH1-1	FRH1-1	cargtncarytngtncarwsnggngcngargtnaaraarccngg ngcnwsngtnaargtnwsntgyaargcnwsn	998
FRH1-2	FRH1-2	cargtncarytngtncarwsnggngcngargtnaaraarccngg ngcnwsngtnaargtnwsntgyaargcnwsn	998
FRH1-3	FRH1-3	cargtncayytngtncarwsnggngcngargtnaaraarccngg ngcnwsngtnaargtnwsntgyaargtnwsn	999
FRH1-4	FRH1-4	cargtncarytngtncarwsnggngcngargtnaaraarccngg ngcnwsngtnaargtnwsntgyaargcnwsn	998
FRH1-5	FRH1-5	cargtncarytngtncarwsnggngcngargtnmgnaarccngg ngcnwsngtnaargtnwsntgyaargtnwsn	1000
FRH1-6	FRH1-6	cargtncarytngtncarwsnggngcngargtnmgnaarccngg ngcnwsngtnaargtnwsntgyaargtnwsn	1000
FRH1-7	FRH1-7	cargtncanytnaargarwsnggnccngtnytngtnaarccnca ngarcanytncanytncantgycangtnwsn	1001
FRH1-8	FRH1-8	cargtncanytnaargarwsnggnccngtnytngtnaarccnca ngarcanytncanytncantgycangtnwsn	1001
FRH1-9	FRH1-9	carathcanytnaargarwsnggnccncanytngtnaarccnca ncarcanytncanytncantgycanttywsn	1002
FRH1-10	FRH1-10	carathcanytnaargarwsnggnccncanytngtnaarccnca ncarcanytncanytncantgycanttywsn	1002
FRH1-11	FRH1-11	carathcanytnaargarwsnggnccncanytngtnaarccnca ncarcanytncanytncantgycanttywsn	1002
FRH1-12	FRH1-12	carathcanytnaargarwsnggnccncanytngtnaarccnca ncarcanytncanytncantgycanttywsn	1002
FRH1-13	FRH1-13	carathcanytnaargarwsnggnccncanytngtnaarccnca ncarcanytncanytncantgycanttywsn	1002
FRH1-14	FRH1-14	carathcanytnaargarwsnggnccncanytngtnaarccnca ncarcanytncanytncantgycanttywsn	1002
FRH1-15	FRH1-15	carathcanytnaargarwsnggnccncanytngtnaarccnca ncarcanytncanytncantgycanttywsn	1002
FRH1-16	FRH1-16	gargtncarytngtngarwsnggnggnggnytngtnaarccngg nggnwsnytnmgnytnwsntgygcngcnwsn	1003
FRH1-17	FRH1-17	gargtncarytnytngarwsnggnggnggnytngtncarccngg nggnwsnytnmgnytnwsntgygcngcnwsn	1004
FRH1-18	FRH1-18	gargtncarytnytngarwsnggnggnggnytngtncarccngg nggnwsnytnmgnytnwsntgygcngcnwsn	1004

FIGURE 21A

NAME	NAME	SEQUENCE	SEQ ID NO:
FRH1-19	FRH1-19	gargtncarytnytngarwsnggnggnggnytngtncarccnggnggnwsnytnmgnytnwsntgycangcnwsn	1005
FRH1-20	FRH1-20	gargtncarytnytngarwsnggnggnggnytngtncarccnggnggnwsnytnmgnytnwsntgycangcnwsn	1005
FRH1-21	FRH1-21	cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsntgygcngcnwsn	1006
FRH1-22	FRH1-22	cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsntgygcngcnwsn	1006
FRH1-23	FRH1-23	cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsntgygcngcnwsn	1006
FRH1-24	FRH1-24	cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsntgygcngcnwsn	1006
FRH1-25	FRH1-25	cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsntgygcngcnwsn	1006
FRH1-26	FRH1-26	cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsntgygcngcnwsn	1006
FRH1-27	FRH1-27	cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsntgygcngcnwsn	1006
FRH1-28	FRH1-28	cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsntgygcngcnwsn	1006
FRH1-29	FRH1-29	cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsntgygcngcnwsn	1006
FRH1-30	FRH1-30	cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsntgygcngcnwsn	1006
FRH1-31	FRH1-31	gargtncarytngtngarwsnggnggnggnytngtncarccnggnggnwsnytnmgnytnwsntgygcngcnwsn	1007
FRH1-32	FRH1-32	gargtncarytngtngarwsnggnggnggnytngtncarccnggnggnwsnytnmgnytnwsntgygcngcnwsn	1007
FRH1-33	FRH1-33	gargtncarytngtngarwsnggnggnggnytngtncarccnggnggnwsnytnmgnytnwsntgygcngcnwsn	1007
FRH1-34	FRH1-34	gargtncarytngtngarwsnggnggnggnytngtncarccnggnggnwsnytnmgnytnwsntgygcngcnwsn	1007
FRH1-35	FRH1-35	cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncantgycangtnwsn	1008
FRH1-36	FRH1-36	cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncantgycangtnwsn	1008
FRH1-37	FRH1-37	cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncantgycangtnwsn	1008

FIGURE 21B

NAME	NAME	SEQUENCE	SEQ ID NO:
FRH1-38	FRH1-38	Cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncantgycangtnwsn	1008
FRH1-39	FRH1-39	cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytnaaytgycangtnwsn	1009
FRH1-40	FRH1-40	cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytnaaytgycangtnwsn	1009
FRH1-41	FRH1-41	cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncantgycangtnwsn	1008
FRH1-42	FRH1-42	cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncantgycangtnwsn	1008
FRH1-43	FRH1-43	cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncantgycangtnwsn	1008
FRH1-44	FRH1-44	cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncantgycangtnwsn	1008
FRH1-45	FRH1-45	cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncantgycangtnwsn	1008
FRH1-46	FRH1-46	cargtncarytncarcartggggngcnggnytnytnaarccnwsngarcanytnwsnytncantgygcngtntay	1010
FRH1-47	FRH1-47	cargtncarytncarcartggggngcnggnytnytnaarccnwsngarcanytnwsnytncantgygcngtntay	1010
FRH1-48	FRH1-48	gargtncarytncarcartggggngcnggnytnytnaarccnwsngarcanytnwsnytncantgygcngtntay	1010
FRH1-49	FRH1-49	cargtncarytncarcartggggngcnggnytnytnaarccnwsngarcanytnwsnytncantgygcngtntay	1010
FRH1-50	FRH1-50	cargtncarytncarcartggggngcnggnytnytnaarccnwsngarcanytnwsnytncantgygcngtntay	1010
FRH1-51	FRH1-51	cargtncarytncargarwsnggnccnggnytngtnaarccnwsngarcanytnwsnytncantgycangtnwsn	1011
FRH1-52	FRH1-52	cargtncarytncargarwsnggnccnggnytngtnaarccnwsngarcanytnwsnytncantgycangtnwsn	1011
FRH1-53	FRH1-53	cargtncarytncargarwsnggnccnggnytngtnaarccnwsngarcanytnwsnytncantgycangtnwsn	1011
FRH1-54	FRH1-54	gargtncarytngtncarwsnggngcngarytnaaraarccnggngarwsnytnaarathwsntgyaarggnwsn	1012
FRH1-55	FRH1-55	gargtncarytngtncarwsnggngcngargtnaaraarccnggngarwsnytnaarathwsntgyaarggnwsn	1013
FRH1-56	FRH1-56	gargtncarytngtncarwsnggngcngargtnaaraarccnggngarwsnytnaarathwsntgyaarggnwsn	1013
FRH1-57	FRH1-57	cargtncarytncarcarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncantgygcnathwsn	1014
FRH1-58	FRH1-58	gargtncarytngtngarwsnggnggnggnytngtncarccngg	1007

FIGURE 21C

NAME	NAME	SEQUENCE	SEQ ID NO:
FRH2-1	FRH2-1	tgggtnmgncargcnccnggncarggnytngartggatgggn	1015
FRH2-2	FRH2-2	tgggtnmgncargcnccngggncarggnytngartggatgggn	1015
FRH2-3	FRH2-3	tgggtnmgncargcnccngggncarggnytngartggatgggn	1015
FRH2-4	FRH2-4	tgggtnmgncargcnccngggncarggnytngartggatgggn	1015
FRH2-5	FRH2-5	tgggtnmgncargcnccngggnaarggnytngartggatgggn	1016
FRH2-6	FRH2-6	tgggtnmgncargcnccngggnaarggnytngartggatgggn	1016
FRH2-7	FRH2-7	tggathmgncarccnccngggnaargcnytngartggytngcn	1017
FRH2-8	FRH2-20	tggathmgncarccnccngggnaargcnytngartggytngtn	1018
FRH2-9	FRH2-65	tggathmgncarccnccngggnaargcnytngartggytngcn	1017
FRH2-10	FRH2-56	tggathmgncarccnccngggnaargcnytngartggytngcn	1017
FRH2-11	FRH2-62	tggathmgncarccnccngggnaargcnytngartggytngcn	1017
FRH2-12	FRH2-2	tggathmgncarccnccngggnaargcnytngartggytngcn	1017
FRH2-13	FRH2-59	tggathmgncarccnccngggnaargcnytngartggytngcn	1017
FRH2-14	FRH2-57	tggathmgncarccnccngggnaargcnytngartggytngcn	1017
FRH2-15	FRH2-64	tggathmgncarccnccngggnaargcnytngartggytngcn	1017
FRH2-16	FRH2-41	Tgggtnmgncargcnccngggnaarggnytngartgggtnwsn	1019
FRH2-17	FRH2-45	tgggtnmgncargcnccngggnaarggnytngartgggtnwsn	1019
FRH2-18	FRH2-47	tgggtnmgncargcnccngggnaarggnytngartgggtnwsn	1019
FRH2-19	FRH2-51	tgggtnmgncargcnccngggnaarggnytngartgggtnwsn	1019
FRH2-20	FRH2-52	tgggtnmgncargcnccngggnaarggnytngartgggtnwsn	1019
FRH2-21	FRH2-13	tgggtnmgncargcnccngggnaarggnytngartgggtngcn	1020
FRH2-22	FRH2-14	tgggtnmgncargcnccngggnaarggnytngartgggtngcn	1020
FRH2-23	FRH2-1	tgggtnmgncargcnccngggnaarggnytngartgggtngcn	1020
FRH2-24	FRH2-22	tgggtnmgncargcnccngggnaarggnytngartgggtngcn	1020
FRH2-25	FRH2-23	tgggtnmgncargcnccngggnaarggnytngartgggtngcn	1020
FRH2-26	FRH2-12	tgggtnmgncargcnccngggnaarggnytngartgggtngcn	1020
FRH2-27	FRH2-5	tgggtnmgncargcnccngggnaarggnytngartgggtngcn	1020
FRH2-28	FRH2-15	tgggtnmgncargcnccngggnaarggnytngartgggtngcn	1020
FRH2-29	FRH2-7	tgggtnmgncargcnccngggnaarggnytngartgggtngcn	1020
FRH2-30	FRH2-61	tgggtnmgncargcnccngggnaarggnytngartgggtngcn	1020
FRH2-31	FRH2-39	tgggtnmgncargcnccngggnaarggnytngartgggtnwsn	1019
FRH2-32	FRH2-34	tgggtnmgncargcnccngggnaarggnytngartgggtnwsn	1019
FRH2-33	FRH2-6	tgggtnmgncargcnccngggnaarggnytngartgggtnwsn	1019
FRH2-34	FRH2-35	tgggtnmgncargcnccngggnaarggnytngartgggtnwsn	1019
FRH2-35	FRH2-21	tggathmgncarcayccnggnaarggnytngartggathggn	1021
FRH2-36	FRH2-8	tggathmgncarcayccnggnaarggnytngartggathggn	1021
FRH2-37	FRH2-9	tggathmgncarcayccnggnaarggnytngartggathggn	1021
FRH2-38	FRH2-18	tggathmgncarcayccnggnaarggnytngartggathggn	1021
FRH2-39	FRH2-24	tggathmgncarcayccnggnaarggnytngartggathggn	1021

FIGURE 21D

NAME	NAME	SEQUENCE	SEQ ID NO:
FRH2-40	FRH2-25	tggathmgncarcayccnggnaarggnytngartggathggn	1021
FRH2-41	FRH2-26	tggathmgncarcayccnggnaarggnytngartggathggn	1021
FRH2-42	FRH2-27	tggathmgncarcayccnggnaarggnytngartggathggn	1021
FRH2-43	FRH2-38	tggathmgncarcayccnggnaarggnytngartggathggn	1021
FRH2-44	FRH2-54	tgggtnmgncarcayccnggnaarggnytngartggathggn	1022
FRH2-45	FRH2-55	tgggtnmgncarcayccnggnaarggnytngartggathggn	1022
FRH2-46	FRH2-43	tggathmgncarccnccnggnaarggnytngartggathggn	1023
FRH2-47	FRH2-44	tggathmgncarccnccnggnaarggnytngartggathggn	1023
FRH2-48	FRH2-49	tggathmgncarccnccnggnaarggnytngartggathggn	1023
FRH2-49	FRH2-50	tggathmgncarccnccnggnaarggnytngartggathggn	1023
FRH2-50	FRH2-53	tggathmgncarccnccnggnaarggnytngartggathggn	1023
FRH2-51	FRH2-33	tggathmgncarccngcnggnaarggnytngartggathggn	1024
FRH2-52	FRH2-3	tggathmgncarccnccnggnaarggnytngartggathggn	1023
FRH2-53	FRH2-4	tggathmgncarccnccnggnaarggnytngartggathggn	1023
FRH2-54	FRH2-16	tgggtnmgncaratgccnggnaarggnytngartggatgggn	1025
FRH2-55	FRH2-17	tgggtnmgncaratgccnggnaarggnytngartggatgggn	1025
FRH2-56	FRH2-11	tgggtnmgncaratgccnggnaarggnytngartggatgggn	1025
FRH2-57	FRH2-37	tggathmgncarwsnccnwsnmgnggnytngartggytnggn	1026
FRH2-58	FRH2-39.1	tgggtnmgncargcnccnggnaarggnytngartgggtnwsn	1019
FRH3-1	FRH3-10.1	mgngtncanatgcancangaycanwsncanwsncangcntayat ggarytnmgnwsnytnmgnwsngaygaycangcngtntaytayt gygcnmgn	1027
FRH3-2	FRH3-10	mgngtncanatgcancangaycanwsncanwsncangcntayat ggarytnmgnwsnytnmgnwsngaygaycangcngtntaytayt gygcnmgn	1027
FRH3-3	FRH3-42	mgngtncanatgcanmgngaycanwsnathwsncangcntayat ggarytnwsnmgnytnmgnwsngaygaycangcngtntaytayt gygcnmgn	1028
FRH3-4	FRH3-40	mgngtncanatgcanmgngaycanwsnathwsncangcntayat ggarytnwsnmgnytnmgnwsngaygaycangcngtntaytayt gygcnmgn	1028
FRH3-5	FRH3-30	mgngtncanatgytngargaycanwsncangaycangcntayat ggarytnwsnwsnytnmgnwsngargaycangcngtntaytayt gygcncan	1029

FIGURE 21E

NAME	NAME	SEQUENCE	SEQ ID NO:
FRH3-6	FRH3-31	mgngtncanatgytngargaycanwsncangaycangcntayatggarytnwsnwsnytnmgnwsngargaycangcngtntaytaytgygcncan	1029
FRH3-7	FRH3-29	mgnytncanathwsnaargaycanwsnaarwsncargtngtnytncanatgcanaayatggayccngtngaycangcncantaytaytgygcnmgn	1030
FRH3-8	FRH3-20	mgnytncanathwsnaargaycanwsnaarwsncargtngtnytncanatgcanaayatggayccngtngaycangcncantaytaytgygcnmgn	1030
FRH3-9	FRH3-65	mgnytncanathcanaargaycanwsnaaraaycargtngtnytncanatgcanaayatggayccngtngaycangcncantaytaytgygcncay	1031
FRH3-10	FRH3-56	mgnytncanathcanaargaycanwsnaarcancargtngtnytncangtncangayatggayccngtngaycangcncantaytaytgygcncay	1032
FRH3-11	FRH3-62	mgnytncanathcanaargaycanwsnaaraaycargtngtnytncanatgcanaayatggayccngtngaycangcncantaytaytgygcncay	1031
FRH3-12	FRH3-2	mgnytncanathcanaargaycanwsnaaraaycargtngtnytncanatgcanaayytngayccngtngaycangcncantaytaytgygcncay	1033
FRH3-13	FRH3-59	mgnytncanathcanaargcncanwsnaaraaycargtngtnytncanatgcanaayatggayccngtngaycangcncantaytaytgygcncay	1034
FRH3-14	FRH3-57	mgnytncanathcanaargaycanwsnaaraaycargtngtnytncanatgcanaayatggayccngtngaycangcncantaytaytgygcncay	1031
FRH3-15	FRH3-64	mgnytncanathcanaargaycanwsnaaraaycargtngtnytncanatgcanaayatggayccngtngaycangcncantaytaytgygcncay	1031
FRH3-16	FRH3-41	mgnttycanathwsnmgngayaaygcnaaraaywsnytntayytncaratgaaywsnytnmgngcngargaycangcngtntaytaytgygcnmgn	1035
FRH3-17	FRH3-45	mgnttycanathwsnmgngayaaywsnaaraaycanytntayytncaratgaaywsnytnmgngcngargaycangcngtntaytaytgygcnaar	1036

FIGURE 21F

NAME	NAME	SEQUENCE	SEQ ID NO:
FRH3-18	FRH3-47	mgnttycanathwsnmgngayaaywsnaaraaycanytntayyt ncaratgaaywsnytnmgngcngargaycangcngtntaytayt gygcnaar	1036
FRH3-19	FRH3-51	mgnttycanathwsnmgngayaaywsnaaraaycanytntayyt ncaratgaaywsnytnmgngcngargaycangcngartaytayt gygcnaar	1037
FRH3-20	FRH3-52	mgnttycanathwsnmgngayaaywsnaaraaycanytntayyt ncaratgaaywsnytnmgngcngargaycangcngartaytayt gygcnaar	1037
FRH3-21	FRH3-13	mgnttycanathwsnmgngayaaywsnatgaaycanytntayyt ncaratgaaywsnytnmgngcngargaycangcngtntaytayt gygcnmgn	1038
FRH3-22	FRH3-14	mgnttycanathwsnmgngayaaywsnatgaaycanytntayyt ncaratgaaywsnytnmgngcngargaycangcngtntaytayt gygcnmgn	1038
FRH3-23	FRH3-1	mgnttycanathwsnmgngayaaywsnaaraaycanytntayyt ncaratgaaywsnytnmgngcngargaycangcngtntaytayt gygcnmgn	1039
FRH3-24	FRH3-22	mgnttycanathwsnmgngayaaywsnaaraaycanytntayyt ncaratgaaywsnytnmgngcngargaycangcngtntaytayt gygcnmgn	1039
FRH3-25	FRH3-23	mgnttycanathwsnmgngayaaywsnaaraaycanytntayyt ncaratgaaywsnytnmgngcngargaycangcngtntaytayt gygcnmgn	1039
FRH3-26	FRH3-12	mgnttycanathwsnmgngayaaywsnaaraaycanytntayyt ncaratgaaywsnytnmgngcngargaycangcngtntaytayt gygtnytn	1040
FRH3-27	FRH3-5	mgnttycanathwsnmgngayaaywsnaaraaycanytntayyt ncaratgaaywsnytnmgngcngargaycangcngtntaytayt gygcnmgn	1039
FRH3-28	FRH3-15	mgnttycangtnwsnmgngayaaywsnaaraaycanytnttyyt ncaratgaaywsnytnmgngcngargaycangcngtntaytayt gygcnmgn	1041
FRH3-29	FRH3-7	mgnttycanathwsnmgngayaaywsnaaraaycanytntayyt ncaratgaaywsnytnmgngcngargaycangcngtntaytayt gygcnmgn	1039

FIGURE 21G

NAME	NAME	SEQUENCE	SEQ ID NO:
FRH3-30	FRH3-61	mgnttycanathwsnmgngayaaywsnaaraaycanytngayyt ncaratgaaywsnytnmgngcngargaycangcngtntaytayt gygcnmgn	1041
FRH3-31	FRH3-39	mgnttycanathwsnmgngayaaygcnaaraaywsnytnttyyt ncaratgaaywsnytnmgngaygargaycangcngtntaytayt gygcnytn	1042
FRH3-32	FRH3-34	mgnttycanathwsnmgngayaaygcnaaraaywsngtntayyt ncaratgaaywsnytnmgngaygargaycangcngtntaytayt gygcnmgn	1043
FRH3-33	FRH3-6	mgnttycanathwsnmgngayaaygcnaaraaywsnytntayyt ncaratgaaywsnytnmgngaygargaycangcngtntaytayt gygcnmgn	1044
FRH3-34	FRH3-35	mgnttycanathwsnmgngayaaygcnaaraaywsnytntayyt ncaratgaaywsnytnmgngaygargaycangcngtntaytayt gygcnmgn	1044
FRH3-35	FRH3-21	mgngtncanathwsngtngaycanwsnaaraaycarttywsnyt naayytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1045
FRH3-36	FRH3-8	mgngtnaayatgwsngtngaycanwsnaaraaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1046
FRH3-37	FRH3-9	mgngtnaayatgwsngtngaycanwsnaaraaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1046
FRH3-38	FRH3-18	mgngtncanathwsngtngaycanwsnaaraaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1047
FRH3-39	FRH3-24	mgnathcanathwsngcngaycanwsnaaraaycarttywsnyt naarytnaaywsngtncangcngcngaycangcngtntaytayt gygcnmgn	1048
FRH3-40	FRH3-25	mgnathcanathwsngcngaycanwsnaaraaycarttywsnyt naarytnaaywsngtncangcngcngaycangcngtntaytayt gygcnmgn	1048
FRH3-41	FRH3-26	mgnathcanaarwsngtngaycanwsnaaraaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1049

FIGURE 21H

NAME	NAME	SEQUENCE	SEQ ID NO:
FRH3-42	FRH3-27	mgnathcanaarwsngtngaycanwsnaaraaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1049
FRH3-43	FRH3-38	mgngtncanathwsngtngaycanwsnaaraaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnwsn	1050
FRH3-44	FRH3-54	mgngtncanathwsngtngaycanwsnaaraaycarttywsnyt naarytnttywsngtncangcngcngaycangcngtntayttyt gygcnmgn	1051
FRH3-45	FRH3-55	mgngtncanathwsngtngaycanwsnaaraaycarttywsnyt naarytnttywsngtncangcngcngaycangcngtntayttyt gygcnmgn	1051
FRH3-46	FRH3-43	mgngtncanathwsngtngaycanwsnaaraaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1047
FRH3-47	FRH3-44	mgngtncanathwsngtngaycanwsnaaraaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1047
FRH3-48	FRH3-49	mgngtncanathwsngtngaycanwsnaaraaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1047
FRH3-49	FRH3-50	mgngtncanathwsngtngaycanwsnaaraaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1047
FRH3-50	FRH3-53	mgngtncanathwsngtngaycanwsnaaraaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1047
FRH3-51	FRH3-33	mgngtncanatgwsngtngaycanwsnaaraaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1052
FRH3-52	FRH3-3	mgngtncanathwsnathgtncanwsnmgnaaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1053
FRH3-53	FRH3-4	mgngtncanathwsnathgtncanwsnmgnaaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1053

FIGURE 21I

NAME	NAME	SEQUENCE	SEQ ID NO:
FRH3-54	FRH3-16	cargtncanathwsngcngayaarwsnathwsncangcntayyt ncartggwsnwsnytnaargcnwsngaycangcnatgtaytayt gygcnmgn	1054
FRH3-55	FRH3-17	cargtncanathwsngcngayaarwsnathaaycangcntayyt ncartggwsnwsnytnaargcnwsngaycangcnatgtaytayt gygcnmgn	1055
FRH3-56	FRH3-11	cargtncanathwsngcngayaarwsnathwsncangcntayyt ncartggwsnwsnytnaargcnwsngaycangcnatgtaytayt gygcnmgn	1054
FRH3-57	FRH3-37	mgnathcanathaayccngaycanwsnaaraaycarttywsnyt ncarytnaaywsngtncanccngargaycangcngtntaytayt gygcnmgn	1056
FRH3-58	FRH3-39.1	mgnttycanathwsnmgngayaaygcnaaraaywsnytnttyyt ncaratgaaywsnytnmgngaygargaycangcngtntaytayt gygcnytn	1042
FRH4-1	FRH4-10.1	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-2	FRH4-10	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-3	FRH4-42	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-4	FRH4-40	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-5	FRH4-30	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-6	FRH4-31	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-7	FRH4-29	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-8	FRH4-20	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-9	FRH4-65	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-10	FRH4-56	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-11	FRH4-62	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-12	FRH4-2	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-13	FRH4-59	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-14	FRH4-57	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-15	FRH4-64	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-16	FRH4-41	tggggncarggncanatggtncangtnwsnwsn	1059
FRH4-17	FRH4-45	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-18	FRH4-47	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-19	FRH4-51	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-20	FRH4-52	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-21	FRH4-13	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-22	FRH4-14	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-23	FRH4-1	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-24	FRH4-22	tggggncarggncanytngtncangtnwsnwsn	1057

FIGURE 21J

NAME	NAME	SEQUENCE	SEQ ID NO:
FRH4-25	FRH4-23	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-26	FRH4-12	tggggncarggnwsnytngtncangtnwsnccn	1060
FRH4-27	FRH4-5	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-28	FRH4-15	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-29	FRH4-7	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-30	FRH4-61	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-31	FRH4-39	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-32	FRH4-34	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-33	FRH4-6	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-34	FRH4-35	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-35	FRH4-21	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-36	FRH4-8	tggggncarggncanaargtncangtnwsnwsn	1061
FRH4-37	FRH4-9	tggggncarggncanaargtncangtnwsnwsn	1061
FRH4-38	FRH4-18	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-39	FRH4-24	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-40	FRH4-25	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-41	FRH4-26	tggggnmgnggncanytngtncangtnwsnwsn	1062
FRH4-42	FRH4-27	tggggnmgnggncanytngtncangtnwsnwsn	1062
FRH4-43	FRH4-38	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-44	FRH4-54	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-45	FRH4-55	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-46	FRH4-43	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-47	FRH4-44	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-48	FRH4-49	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-49	FRH4-50	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-50	FRH4-53	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-51	FRH4-33	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-52	FRH4-3	tggggncarggncanatggtncangtnwsnwsn	1059
FRH4-53	FRH4-4	tggggncarggncanatggtncangtnwsnwsn	1059
FRH4-54	FRH4-16	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-55	FRH4-17	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-56	FRH4-11	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-57	FRH4-37	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-58	FRH4-39.1	tggggncarggncanytngtncangtnwsnwsn	1057

FIGURE 21K

Inhibition of HBEGF-induced EGFR tyrosine phosphorylation

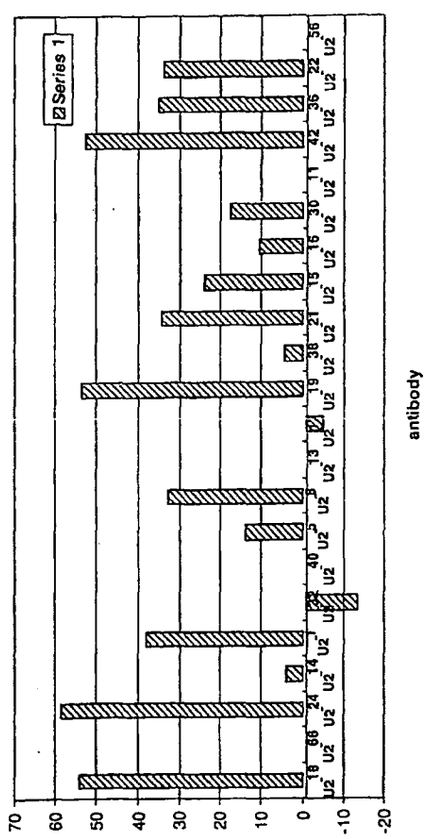

Fig 22a

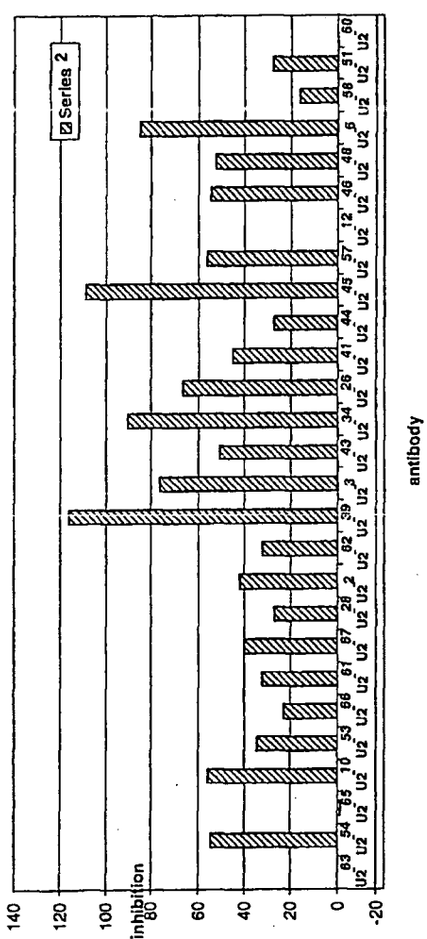

Fig 22b

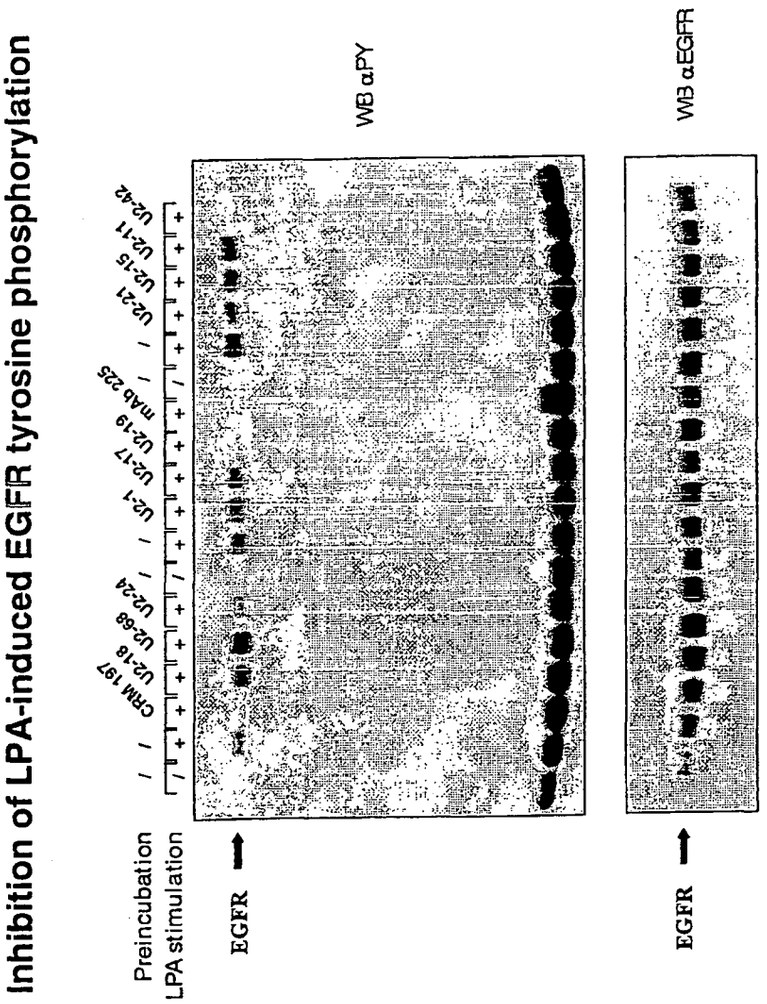
Inhibition of LPA-induced EGFR tyrosine phosphorylation
Preincubation
LPA stimulation
CRM 197
UC-18
UC-68
UC-24
UC-1
UC-17
UC-19
mAb 225
UC-21
UC-15
UC-11
UC-42
WB αPY
WB αEGFR
EGFR
EGFR

Fig 23

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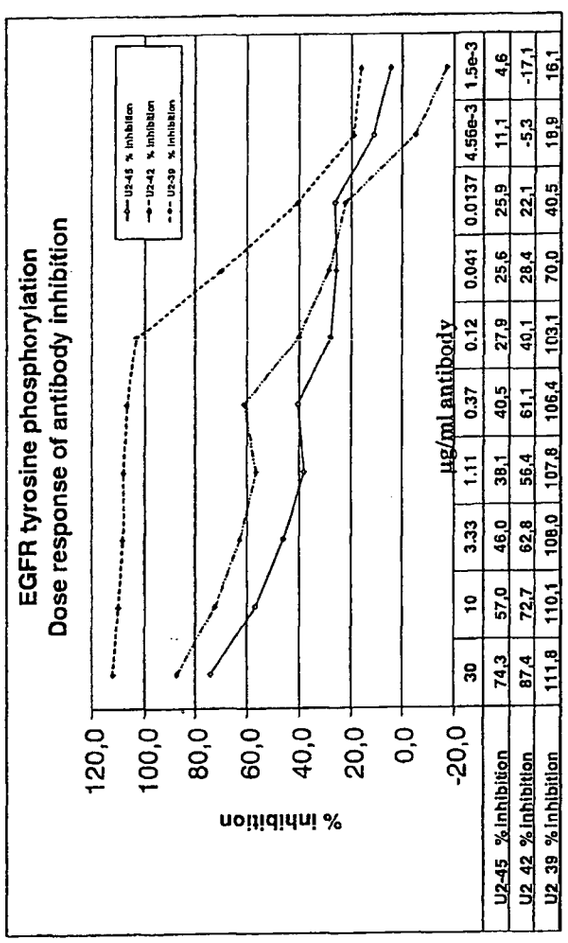
Inhibition of HBEGF-induced EGFR tyrosine phosphorylation - Dose response



µg/ml antibody	30	10	3.33	1.11	0.37	0.12	0.041	0.0137	4.56e-3	1.5e-3
U2-45 %Inhibition	74,3	57,0	46,0	38,1	40,5	27,9	25,6	25,9	11,1	4,6
U2 42 %Inhibition	87,4	72,7	62,8	56,4	61,1	40,1	28,4	22,1	-5,3	-17,1
U2 39 %Inhibition	111,8	110,1	108,0	107,8	106,4	103,1	70,0	40,5	18,9	16,1

Fig 24

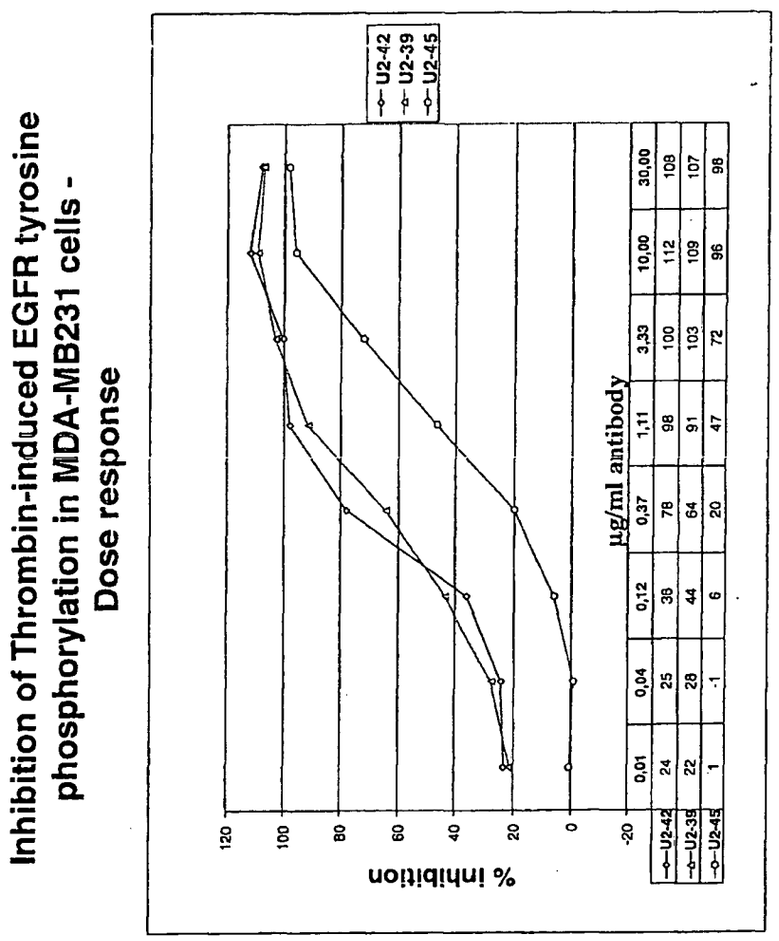

Inhibition of Thrombin-induced EGFR tyrosine phosphorylation in MDA-MB231 cells - Dose response
U2-42
U2-39
U2-45
% inhibition
µg/ml antibody
120
100
80
60
40
20
0
-20
0,01 0,04 0,12 0,37 1,11 3,33 10,00 30,00
U2-42 24 25 36 78 98 100 112 108
U2-39 22 28 44 64 91 103 109 107
U2-45 1 -1 6 20 47 72 96 98

Fig 25

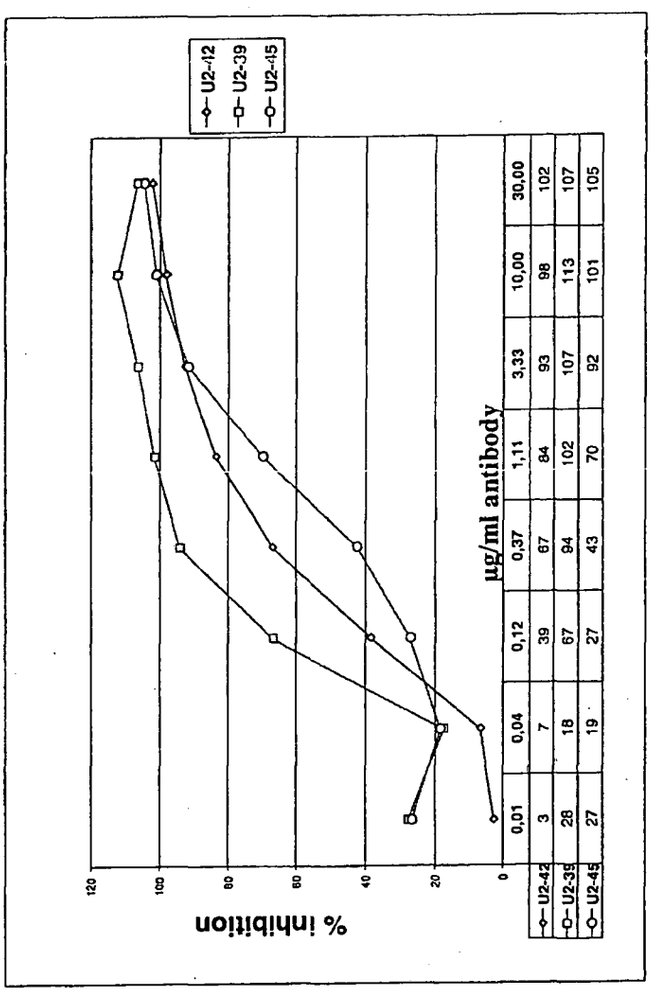

Inhibition of LPA-induced EGFR tyrosine phosphorylation in PPC-1 cells - Dose response
U2-42
U2-39
U2-45
% inhibition
µg/ml antibody
0,01 0,04 0,12 0,37 1,11 3,33 10,00 30,00
U2-42 3 7 39 67 84 93 98 102
U2-39 28 18 67 94 102 107 113 107
U2-45 27 19 27 43 70 92 101 105

Fig 26

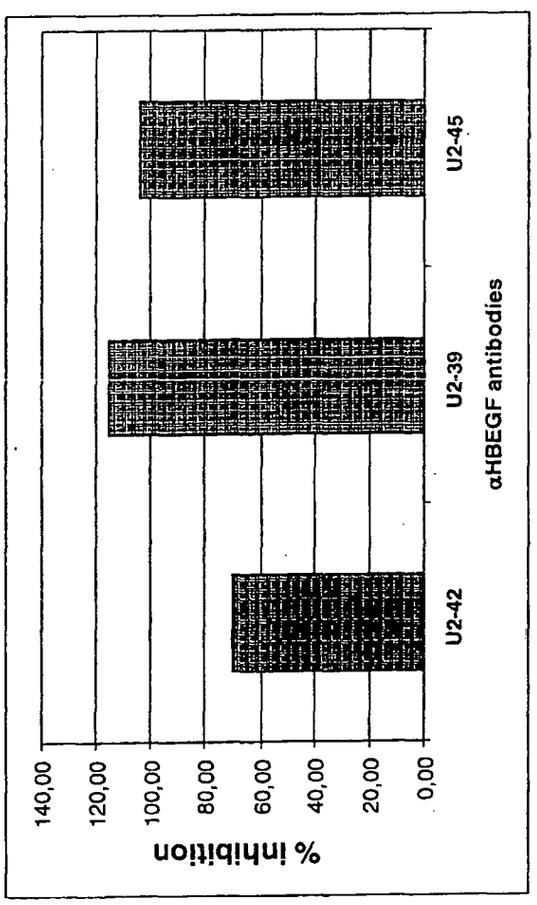

Inhibition of Sphingosine-1-phosphate-induced migration of MDA-MB231 cells
% inhibition
140,00
120,00
100,00
80,00
60,00
40,00
20,00
0,00
U2-42
U2-39
U2-45
αHBEGF antibodies

Fig 27

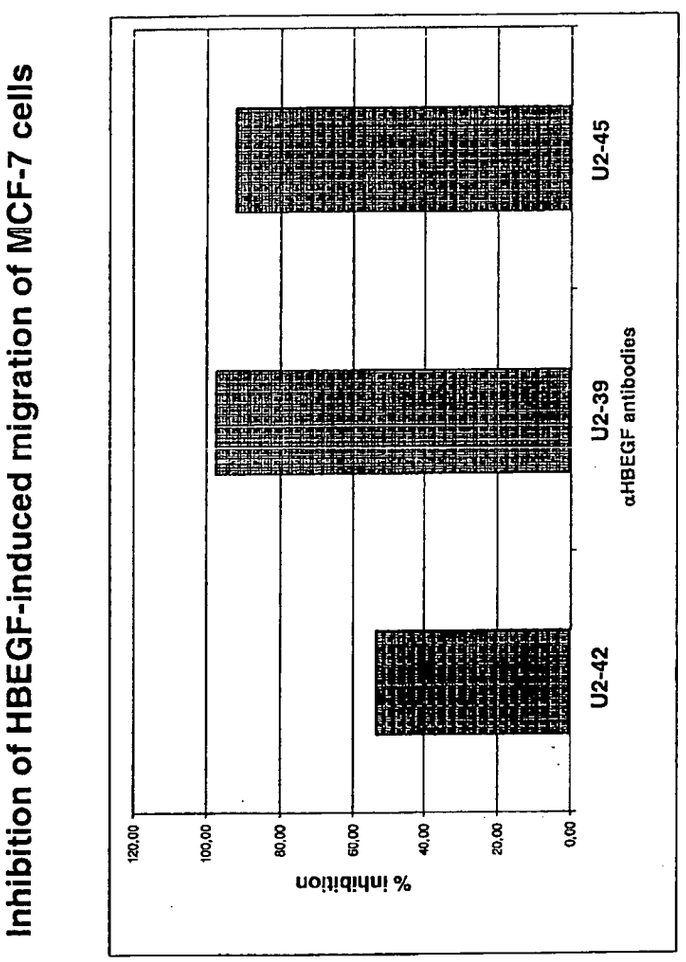

Inhibition of HBEGF-induced migration of MCF-7 cells
% inhibition
120,00
100,00
80,00
60,00
40,00
20,00
0,00
U2-42
U2-39
U2-45
αHBEGF antibodies

Fig 28

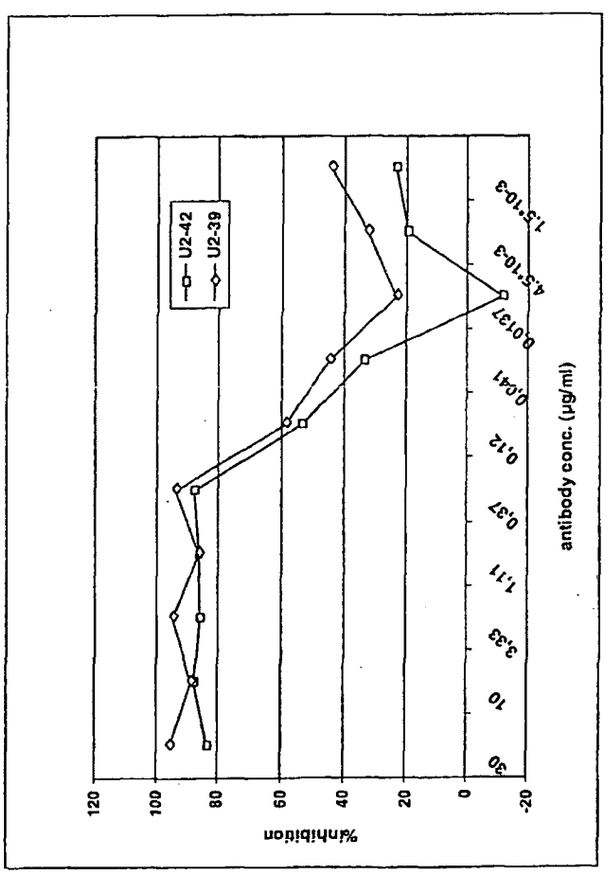
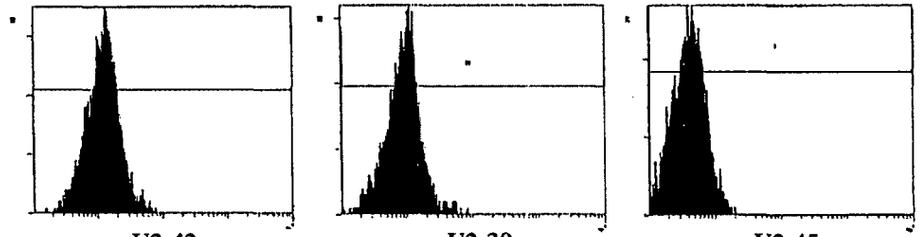

Inhibition of HBEGF-induced HER4 tyrosine phosphorylation - Dose response
U2-42
U2-39
%inhibition
120
100
80
60
40
20
0
-20
30
10
3,33
1,11
0,37
0,12
0,041
0,0137
4,5*10-3
1,5*10-3
antibody conc. (µg/ml)

Fig 29

Cyno and mouse cross reactivity of HBEGF antibodies

HEK 293 cells transiently transfected with pcDNA (empty vector)



HEK 293 cells transiently transfected with pcDNA-cyno HBEGF

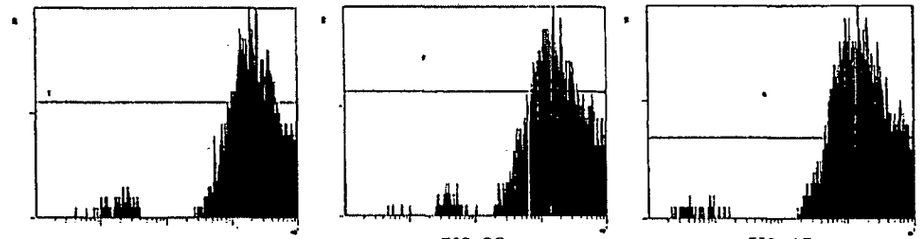


Fig 30 A

HEK 293 cells transiently transfected with pcDNA-mouse HBEGF

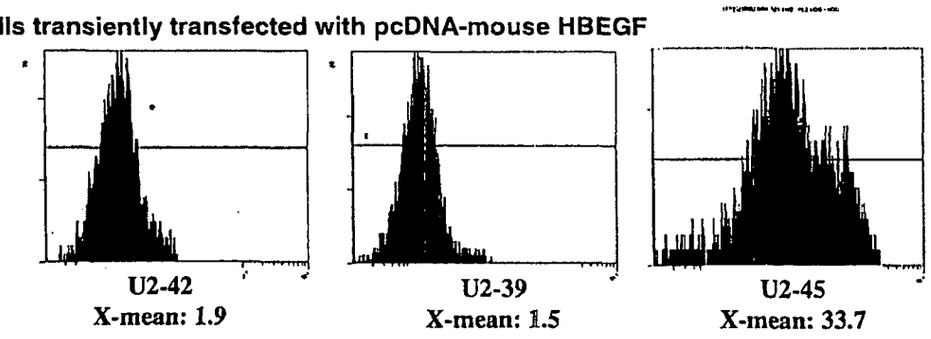
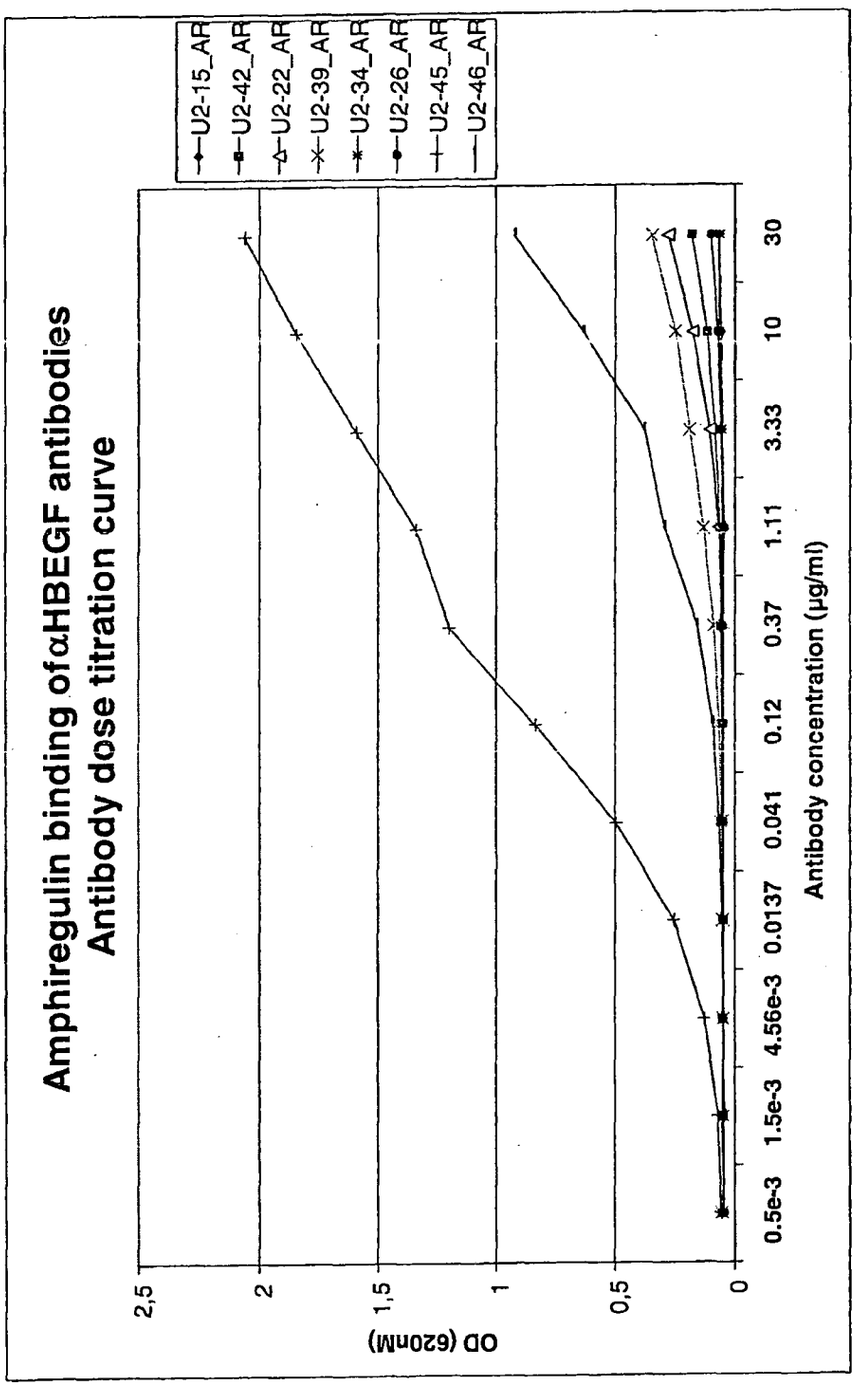
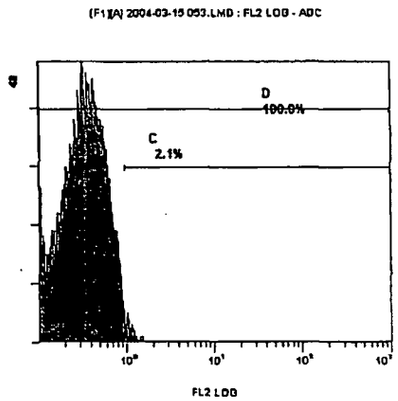


Fig 30 B

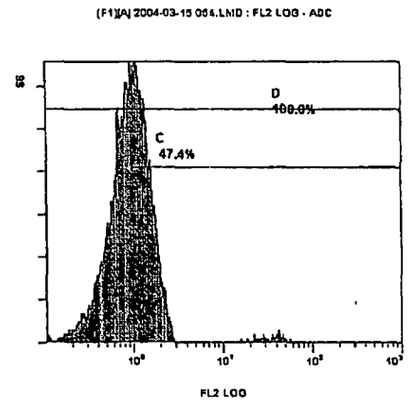
Fig 30 C


Amphiregulin cross reactivity of HBEGF antibodies
Amphiregulin binding ofαHBEGF antibodies
Antibody dose titration curve
U2-15_AR
U2-42_AR
U2-22_AR
U2-39_AR
U2-34_AR
U2-26_AR
U2-45_AR
U2-46_AR
OD (620nM)
2,5
2
1,5
1
0,5
0
0.5e-3
1.5e-3
4.56e-3
0.0137
0.041
0.12
0.37
1.11
3.33
10
30
Antibody concentration (µg/ml)

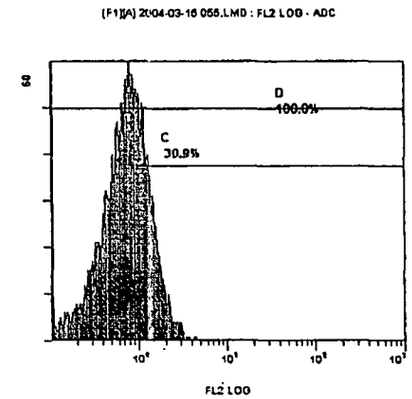
HBEGF expression on HUVECs



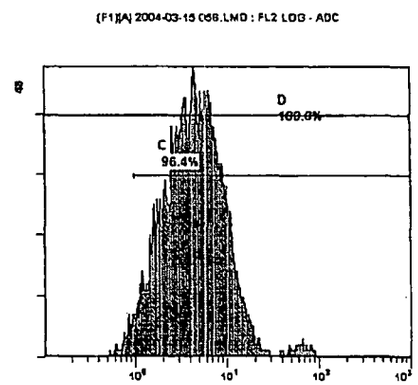
HUVEC
0.3



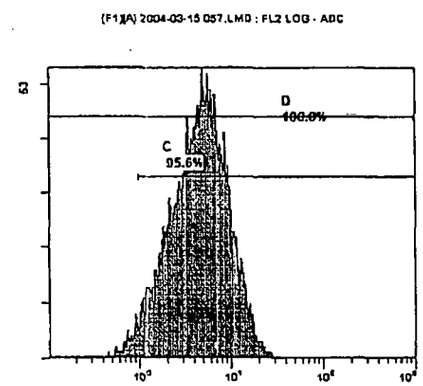
HUVEC
α-goat-PE
2.4



HUVEC
α-mouse-PE
0.8



HUVEC
HBEGF
7.2



HUVEC
EGFR
5.5

Fig 31

380

Effect of HBEGF and HBEGF antibodies on HUVEC proliferation

Fig 32 A

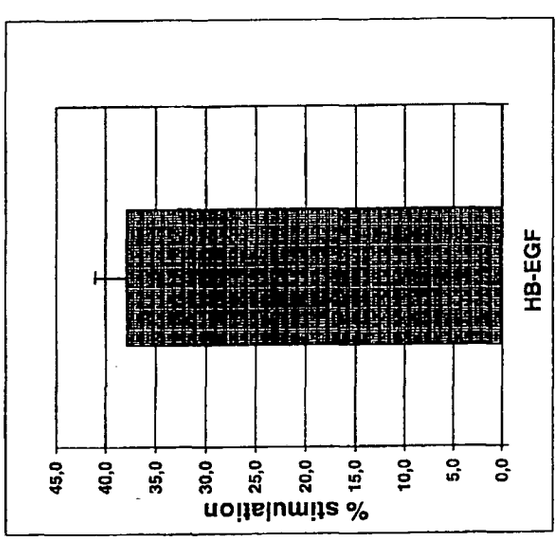
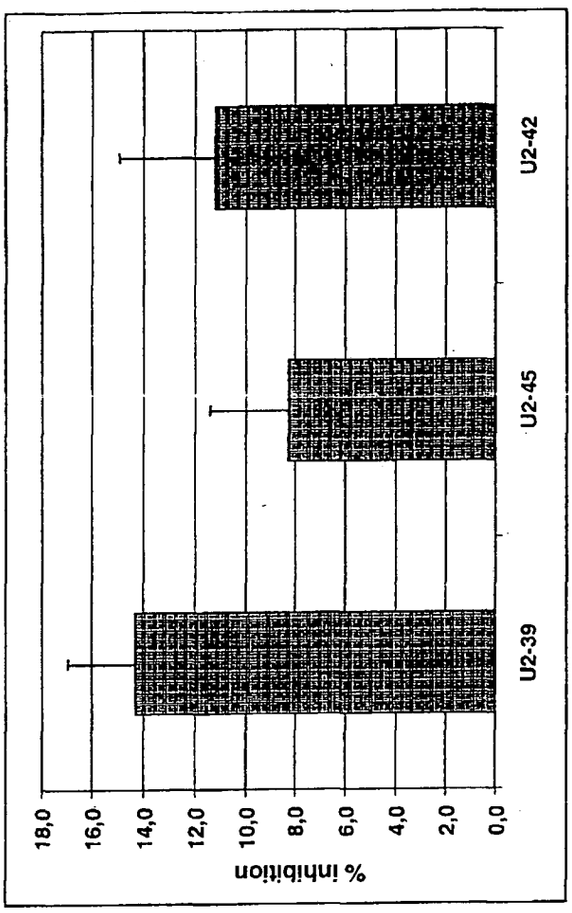
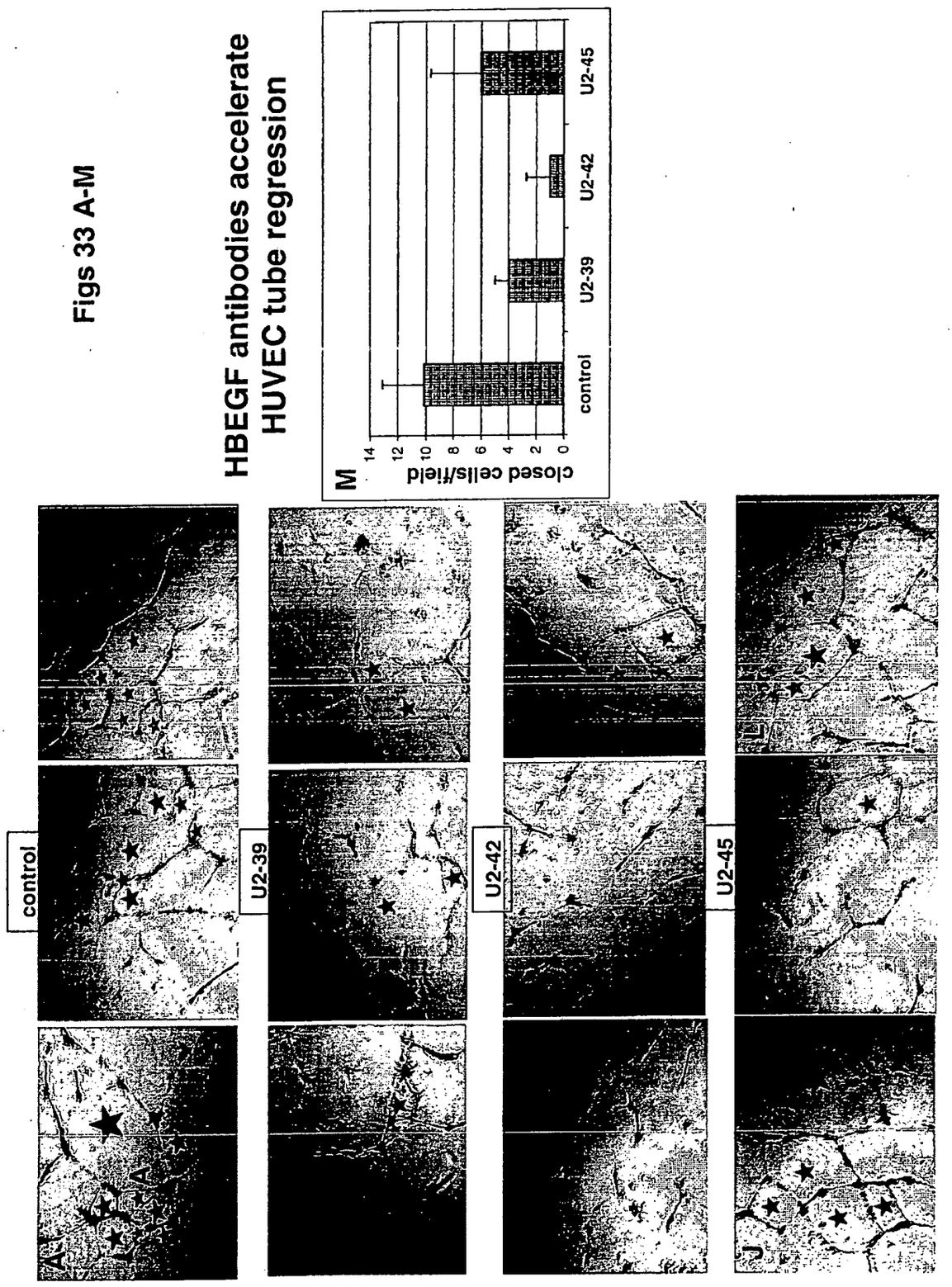


Fig 32 B



Figs 33 A-M


HBEGF antibodies accelerate
HUVEC tube regression
control
U2-39
U2-42
U2-45
A
M
closed cells/field
0
2
4
6
8
10
12
14
control
U2-39
U2-42
U2-45

Soft agar – Inhibition of HBEGF stimulated colony formation

Fig 34 A

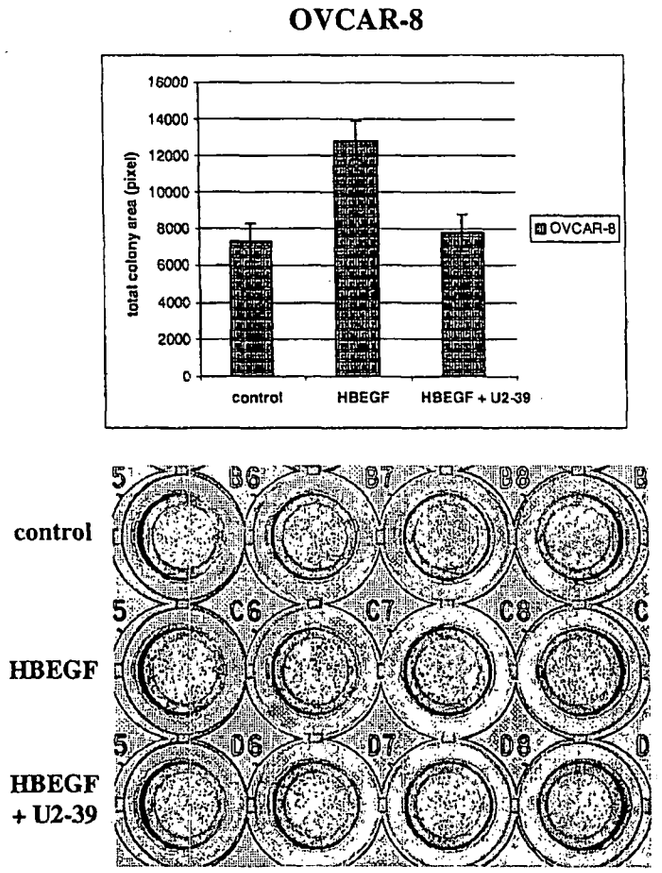
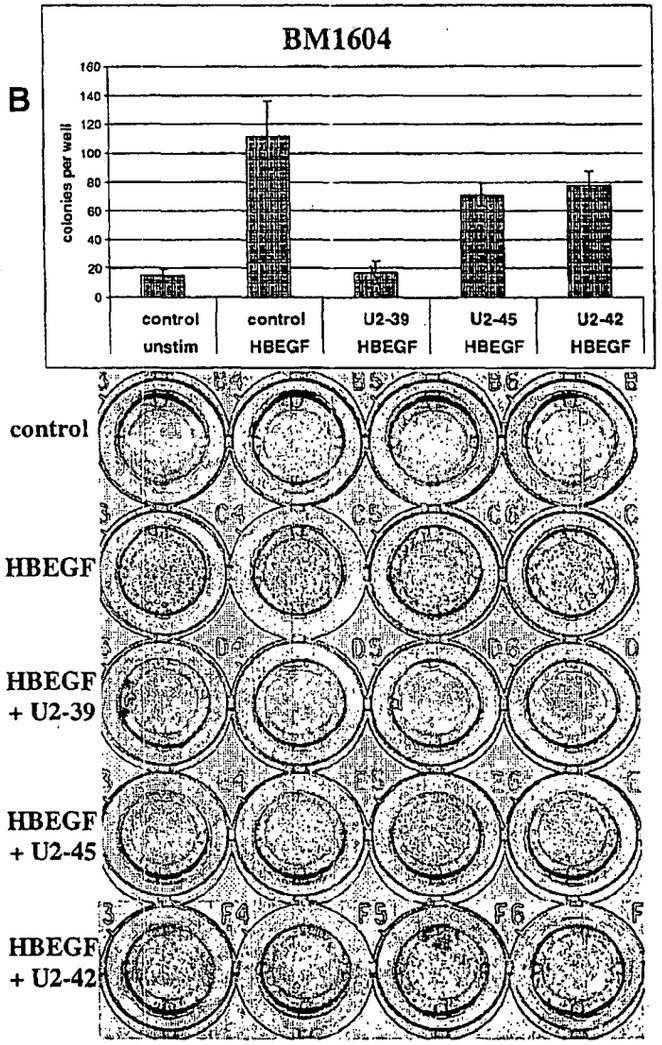


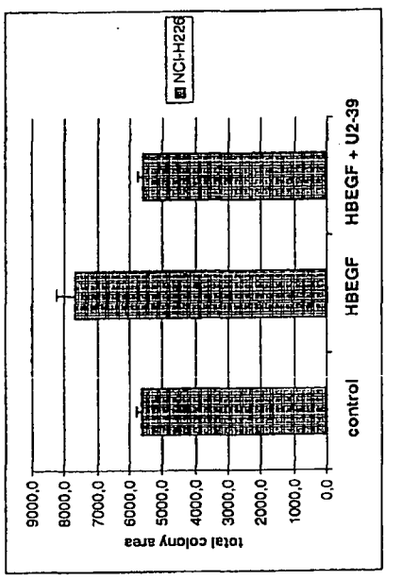
Fig 34 B

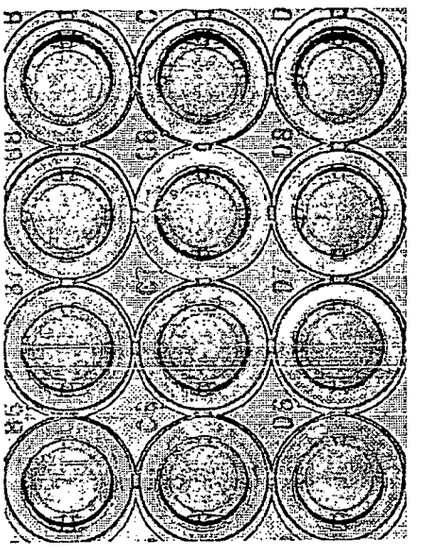


Soft agar – Inhibition of HBEGF stimulated colony formation

Fig 34 C

NCI-H226





control

HBEGF

HBEGF + U2-39

SkOV-3 HBEGF clones - Inhibition of basal colony formation

Fig 34 D

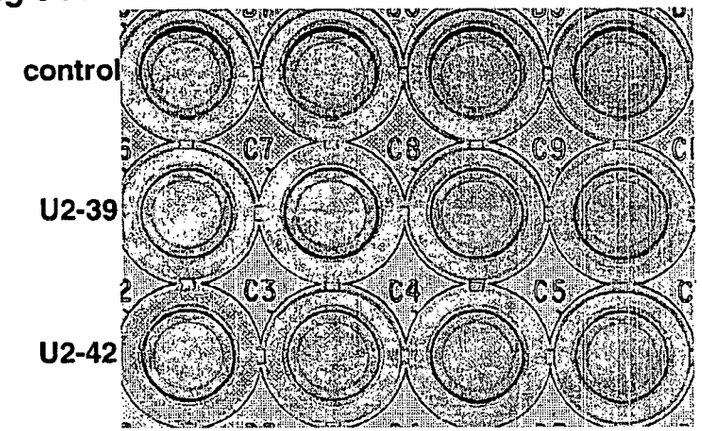
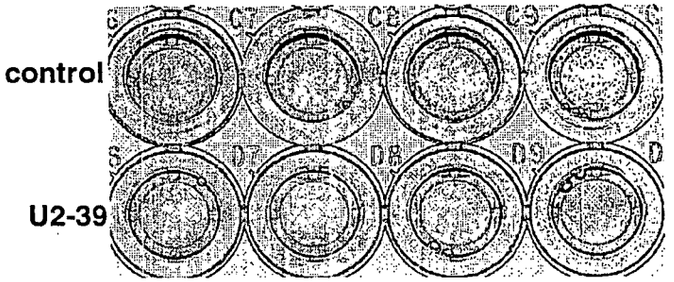
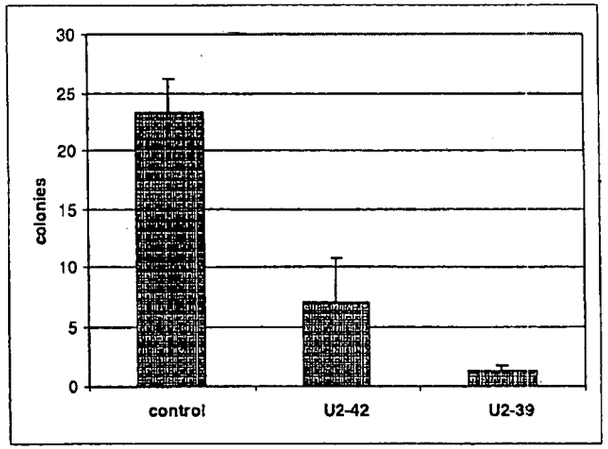


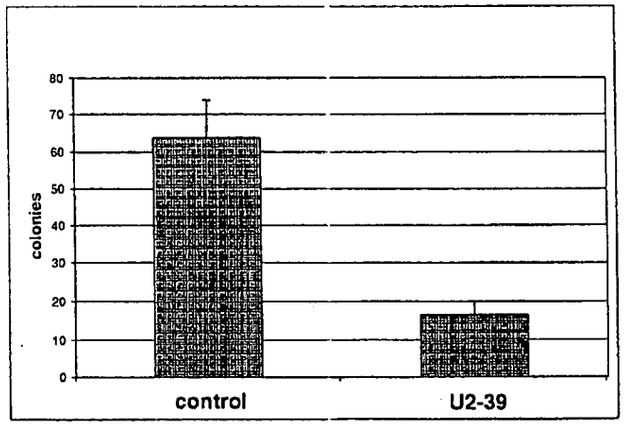
Fig 34 E



SkOV-3 clone 71

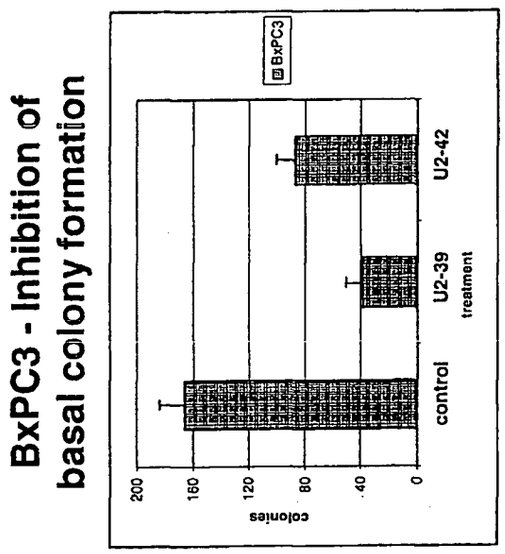


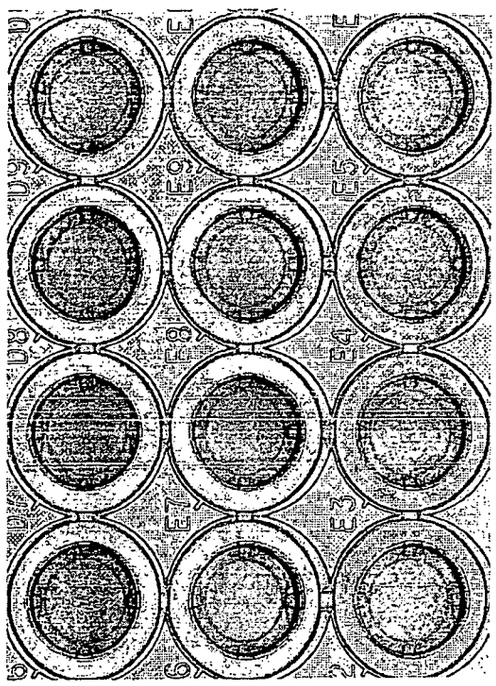
SkOV-3 clone 74



381

Fig 34 F





control

U2-39

U2-42

387

Inhibition of basal colony formation with HBEGF antibodies - synergistic effects in combination with Erbitux

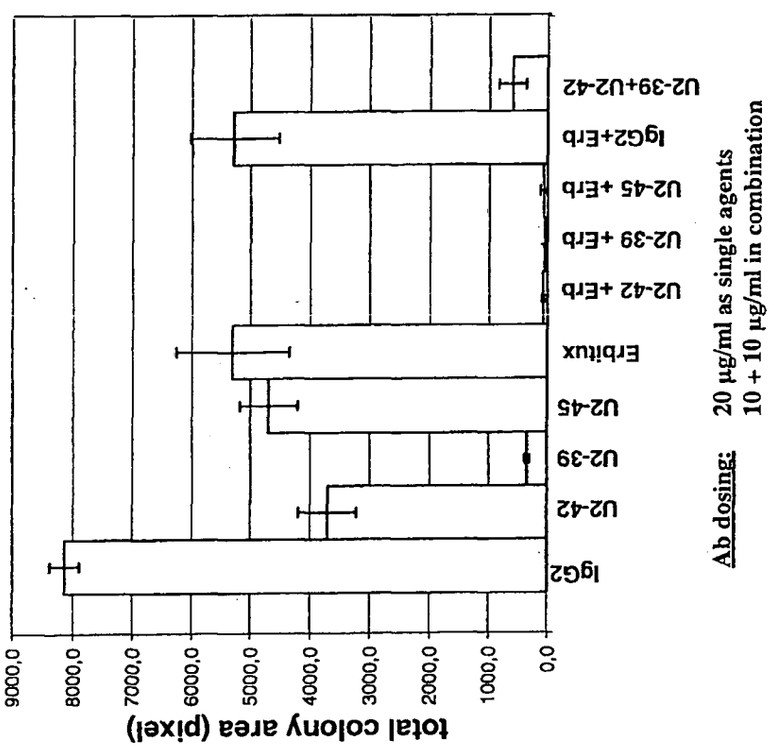
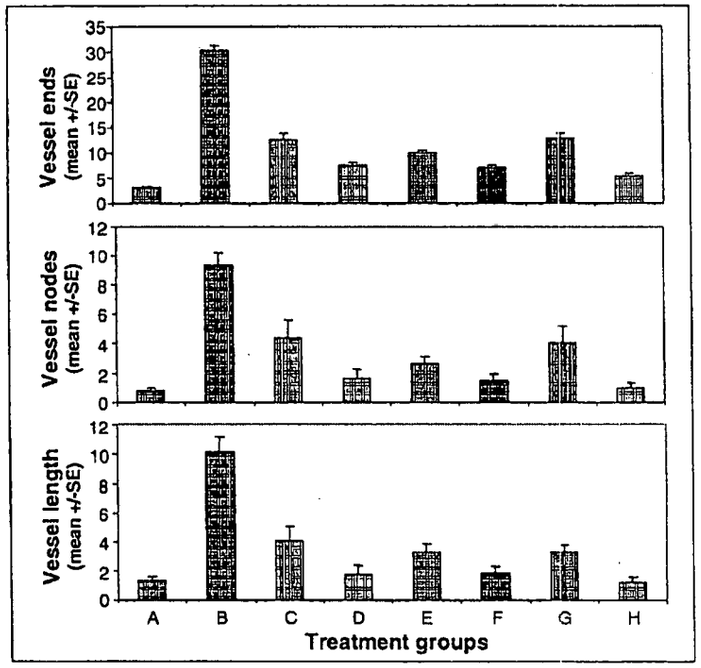


Fig 35

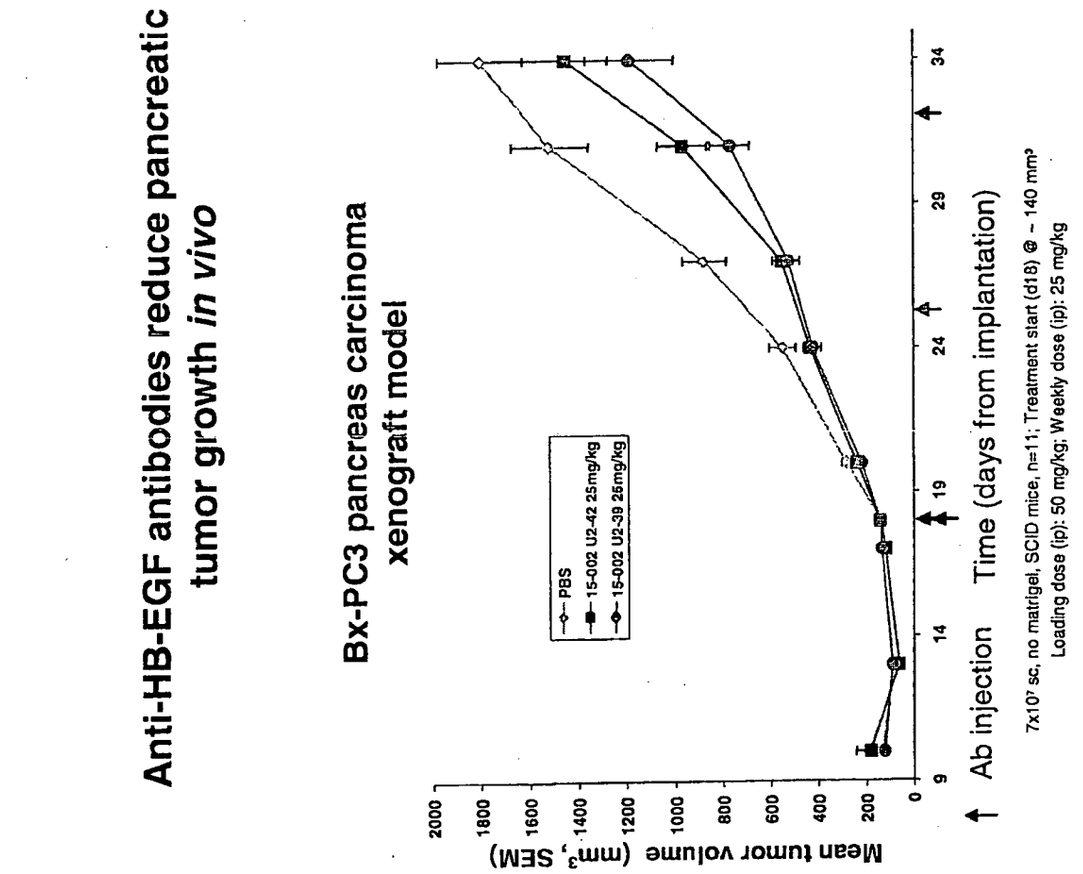
In vivo anti-angiogenic properties of anti-HB-EGF antibodies in the mouse matrigel plug assay

Fig 36



389

Fig 37


Anti-HB-EGF antibodies reduce pancreatic tumor growth *in vivo*
Bx-PC3 pancreas carcinoma xenograft model
PBS
15-002 U2-42 25mg/kg
15-002 U2-39 25mg/kg
Mean tumor volume (mm³, SEM)
2000
1800
1600
1400
1200
1000
800
600
400
200
0
9
14
19
24
29
34
Ab injection
Time (days from implantation)
7x10⁷ sc, no matrigel, SCID mice, n=11; Treatment start (d18) @ ~ 140 mm³
Loading dose (ip): 50 mg/kg; Weekly dose (ip): 25 mg/kg

390

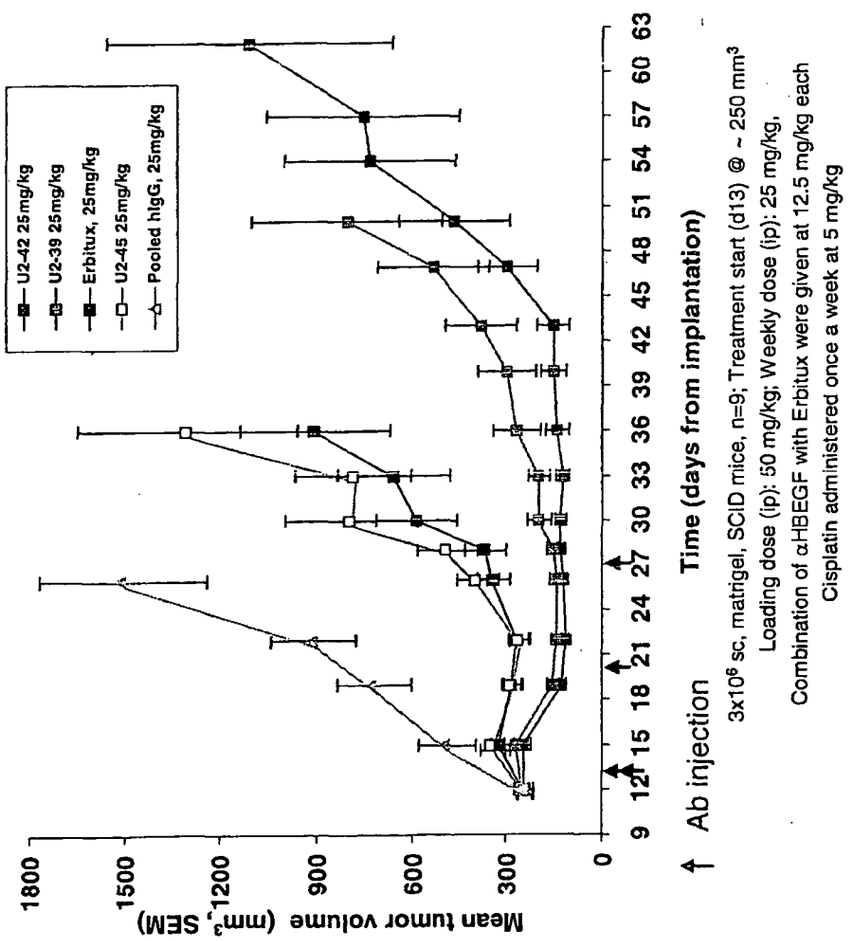

Anti-HB-EGF antibodies reduce ovarian cancer tumor growth *in vivo*
U2-42 25mg/kg
U2-39 25mg/kg
Erbitux, 25mg/kg
U2-45 25mg/kg
Pooled hIgG, 25mg/kg
Mean tumor volume (mm³, SEM)
1800
1500
1200
900
600
300
0
9 12 15 18 21 24 27 30 33 36 39 42 45 48 51 54 57 60 63
Ab injection
Time (days from implantation)
3x10⁶ sc, matrigel, SCID mice, n=9; Treatment start (d13) @ ~ 250 mm³
Loading dose (ip): 50 mg/kg; Weekly dose (ip): 25 mg/kg,
Combination of αHBEGF with Erbitux were given at 12.5 mg/kg each
Cisplatin administered once a week at 5 mg/kg

Fig 38A

Anti-HB-EGF antibodies reduce ovarian cancer tumor growth *in vivo* – dose titration of antibodies

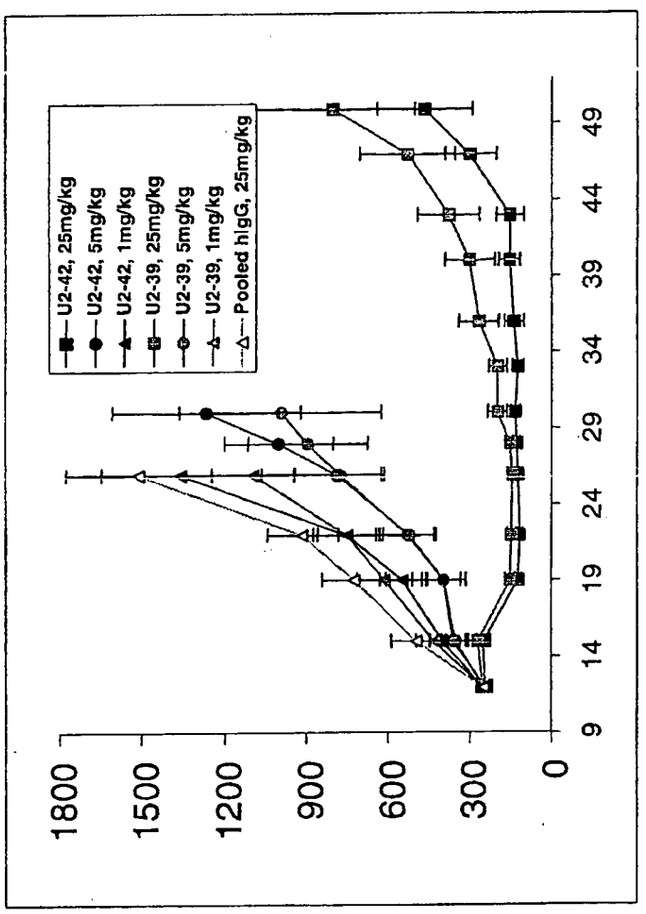


Fig 38 B

392

Anti-HB-EGF antibodies synergize in combination with anti-EGFR therapy in the treatment of ovarian cancer tumor growth *in vivo*

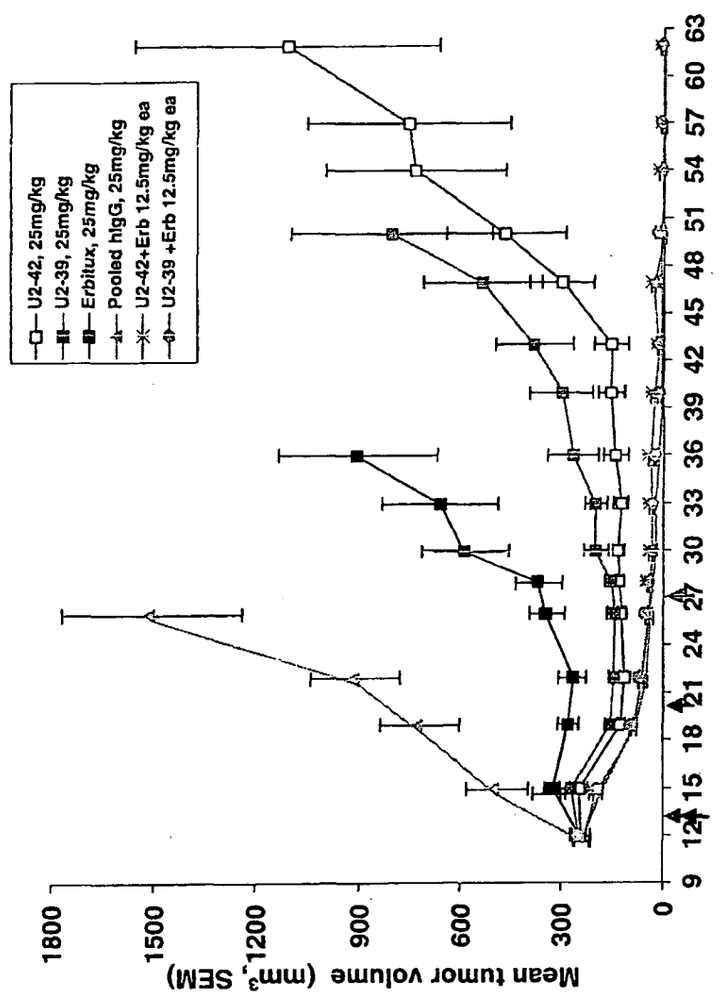


Fig 38C

3x10⁶ sc, matrigel, SCID mice, n=9; Treatment start (d13) @ ~ 250 mm³
Loading dose (ip): 50 mg/kg; Weekly dose (ip): 25 mg/kg,
Combination of αHBEGF with Erbitux were given at 12.5 mg/kg each
Cisplatin administered once a week at 5 mg/kg

Immunohistochemistry of human tissue with human anti HB-EGF antibodies

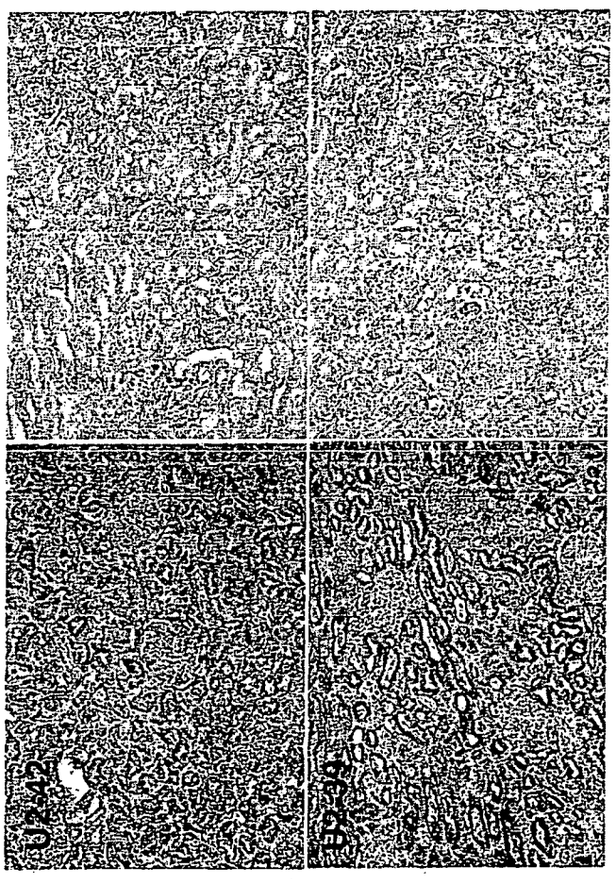


Fig 39 A

HBEGF detecting ELISA based on human antibodies

Fig 39 B

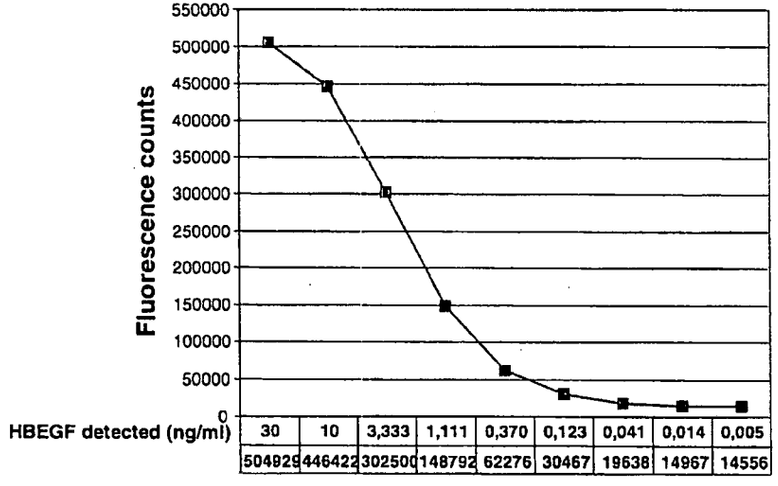


Fig 40A

Scratch assay
- Inhibition of HB-EGF-induced migration

CLS354 epithelial squamous carcinoma cells (mouth)

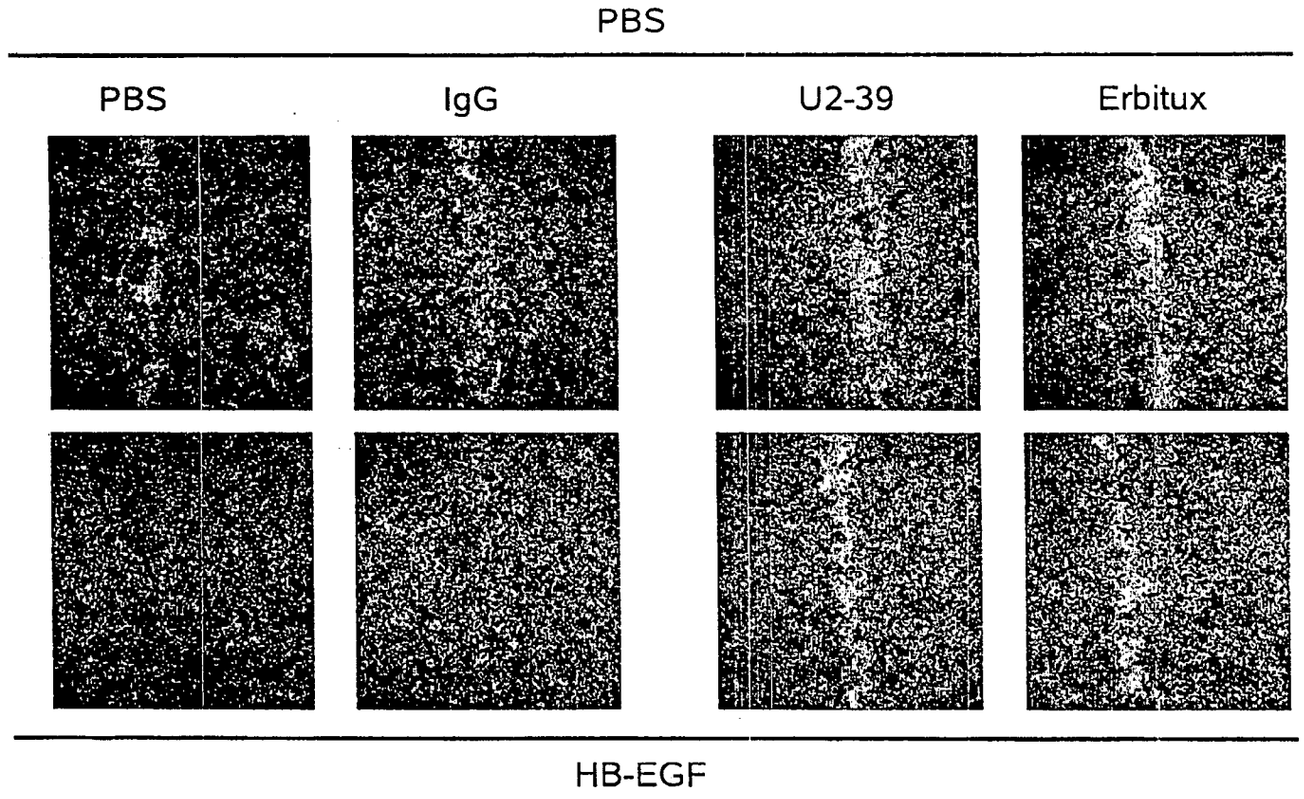
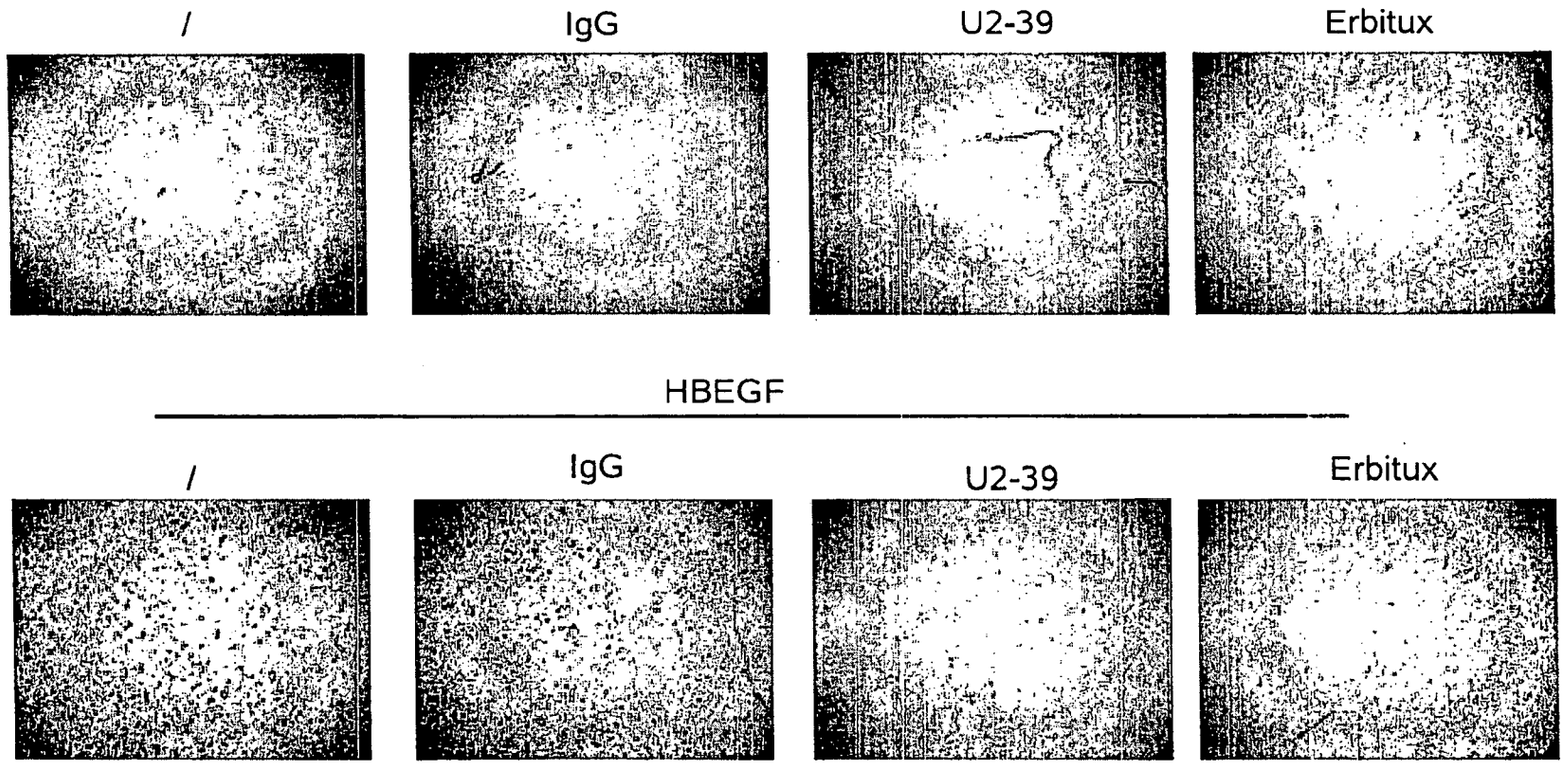


Fig 40B

Transmigration assay
- Inhibition of HB-EGF-induced migration

Detroit 562 epithelial carcinoma cells (pharynx)



Spheroid-based cellular angiogenesis assay – Inhibition of VEGF-stimulated endothelial cell sprouting

Fig 41A

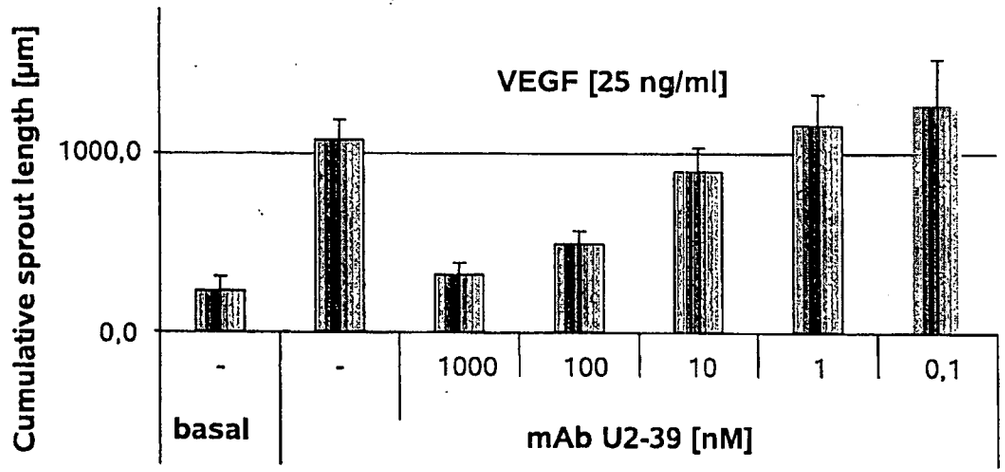


Fig 41B

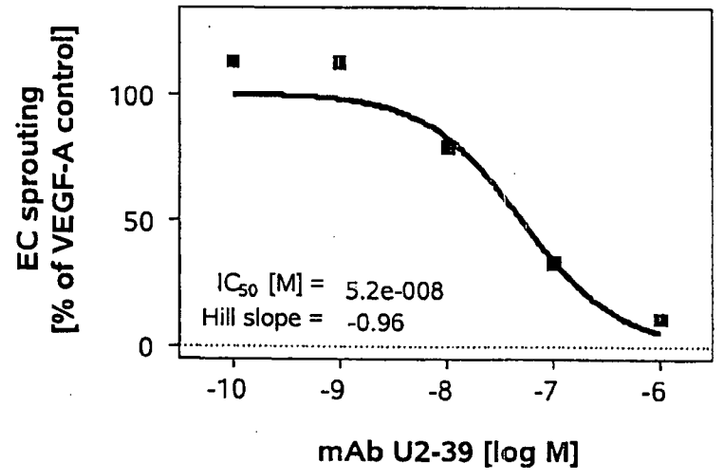


Fig 42

IHC analysis of tumor xenograft samples- Inhibition of CD31 staining of human tumor xenografts *in vivo*

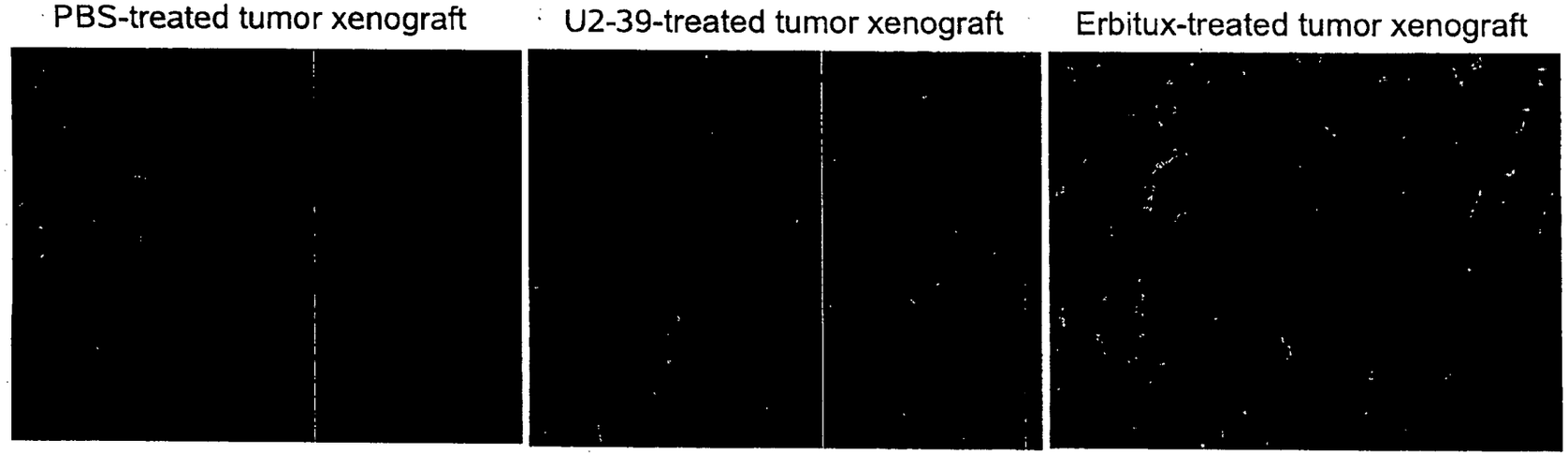


Fig 43A

In vivo ovarian tumor xenograft model- Combination treatment of U2-39 with Cisplatin

Subcutaneous EFO-27-HB-EGF ovarian cancer xenograft model

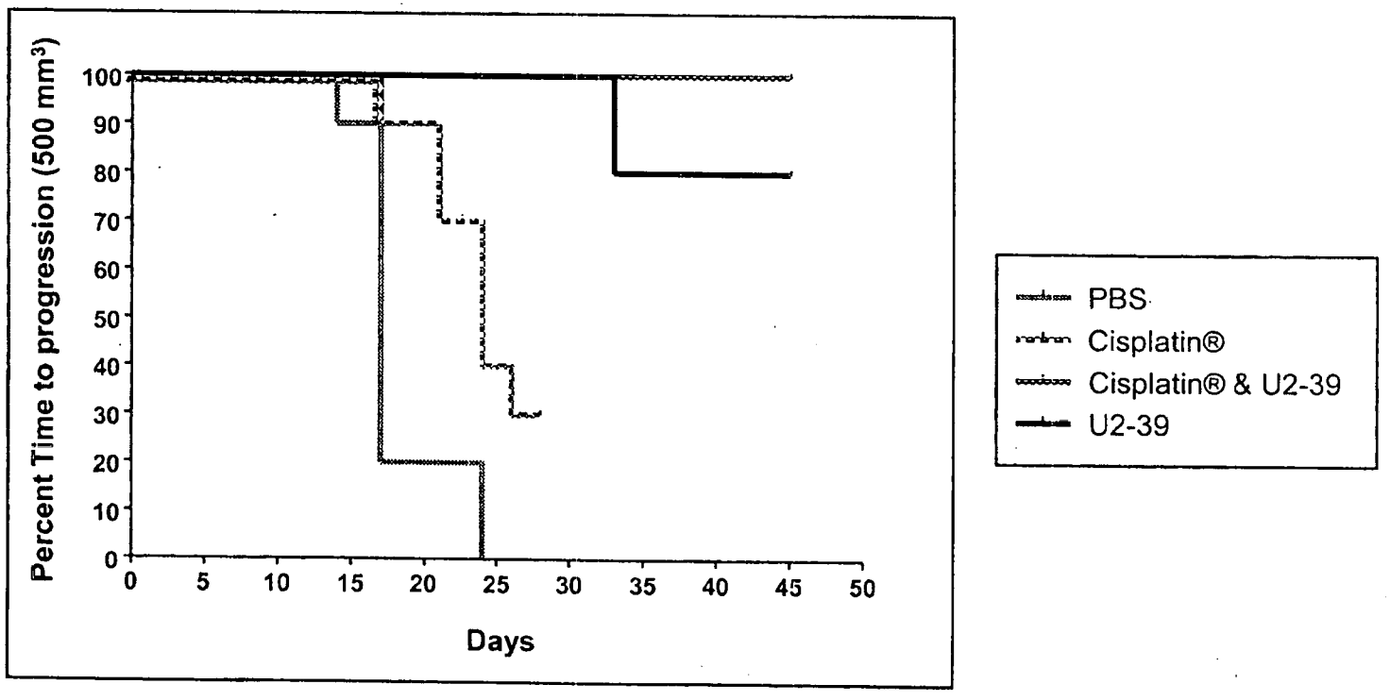
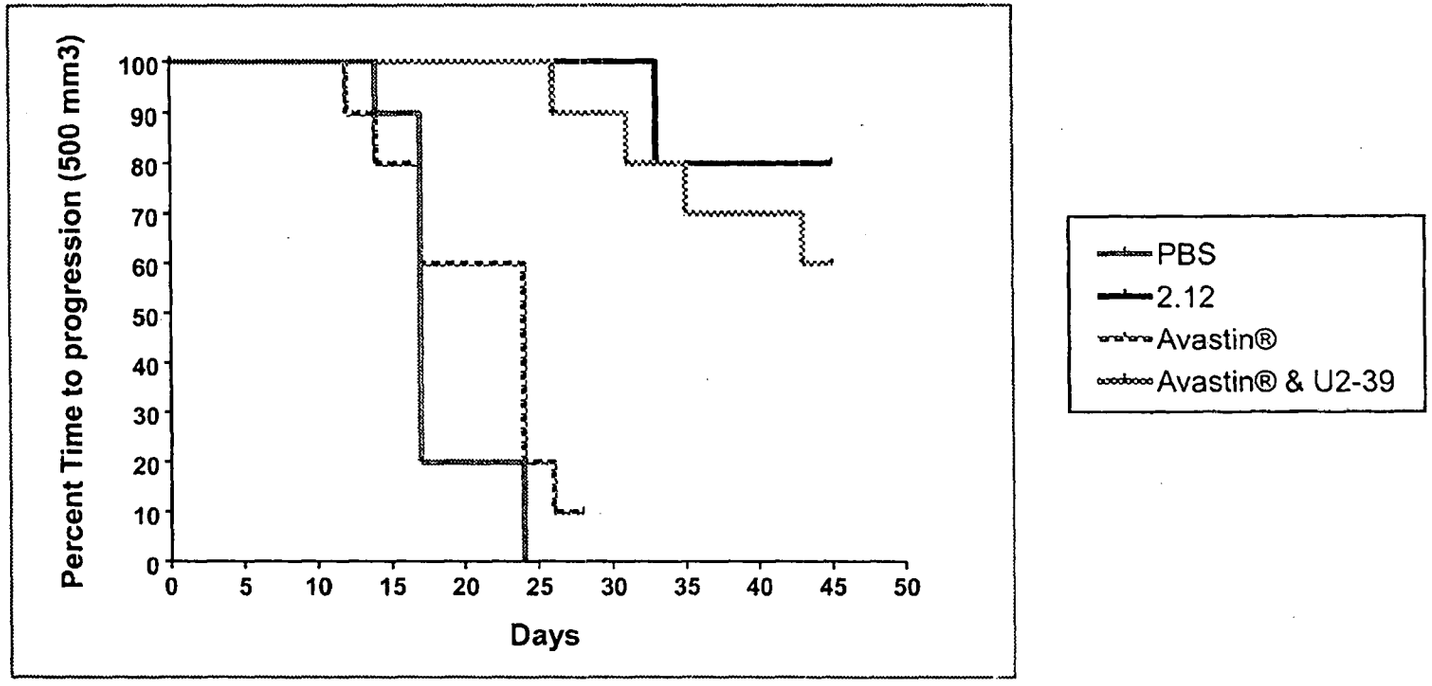


Fig 43B

In vivo ovarian tumor xenograft model- Combination treatment of U2-39 with Avastin

Subcutaneous EFO-27-HB-EGF ovarian cancer xenograft model



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            20                  25                  30

Asp Gly Asn Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
        35                  40                  45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Asp Ser Gly Val Pro
    50                  55                  60

Asp Arg Phe Asn Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ser
                85                  90                  95

Thr His Trp Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105                 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
        115                 120                 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
    130                 135                 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145                 150                 155                 160
```

```
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
                165                 170                 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
            180                 185                 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
        195                 200                 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215
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1               5                   10                  15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
            20                  25                  30

Asp Gly Asn Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
        35                  40                  45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Asp Ser Gly Val Pro
    50                  55                  60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ile Gln Gly
                85                  90                  95

Thr His Trp Pro Thr Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105                 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
        115                 120                 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
    130                 135                 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145                 150                 155                 160
```

```
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
                165                 170                 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
            180                 185                 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
        195                 200                 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215
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Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
            20                  25                  30

Asp Gly Asn Thr Tyr Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Ser
        35                  40                  45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Asp Ser Gly Val Pro
    50                  55                  60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
                85                  90                  95

Thr His Trp Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105                 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
        115                 120                 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
    130                 135                 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145                 150                 155                 160
```

```
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
                165                 170                 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
            180                 185                 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
        195                 200                 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215
```

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Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
            20                  25                  30

Asp Gly Lys Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Pro
        35                  40                  45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
                85                  90                  95

Ile Gln Leu Pro Cys Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
        115                 120                 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
    130                 135                 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
```

145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 5
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<212> PRT
<213> Homo Sapiens

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1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Pro
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ser
85 90 95

Ile Gln Leu Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

```
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145                 150                 155                 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
                165                 170                 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
            180                 185                 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
        195                 200                 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215
```

<210> 6
<211> 219
<212> PRT
<213> Homo Sapiens

<400> 6

```
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1               5                   10                  15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
            20                  25                  30

Asp Gly Lys Thr Tyr Leu Tyr Trp Phe Leu Gln Lys Pro Gly Gln Pro
        35                  40                  45

Pro Gln Pro Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ser
                85                  90                  95

Ile Gln Leu Pro Ile Thr Phe Gly His Gly Thr Arg Leu Glu Ile Lys
            100                 105                 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
        115                 120                 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
    130                 135                 140
```

```
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145                 150                 155                 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
                165                 170                 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
            180                 185                 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
        195                 200                 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215
```

<210> 7
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 7

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ala Asn Tyr
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Val Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Asn Tyr Asn Ser Ala Pro Phe
                85                  90                  95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140
```

```
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 8
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 8

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Ile Cys Arg Ala Ser Gln Gly Ile Ser Asn Asp
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Val Pro Leu
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
```

130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 9
<211> 219
<212> PRT
<213> Homo Sapiens

<400> 9

Asn Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
35 40 45

Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85 90 95

Thr Gln Phe Pro His Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

```
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
    130                 135                 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145                 150                 155                 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
                165                 170                 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
            180                 185                 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
        195                 200                 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215
```

<210> 10
<211> 219
<212> PRT
<213> Homo Sapiens

<400> 10

```
Glu Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
1               5                   10                  15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
            20                  25                  30

Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
        35                  40                  45

Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60

Asp Arg Phe Ser Gly Thr Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
                85                  90                  95

Thr Gln Phe Pro His Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
        115                 120                 125
```

```
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
    130                 135                 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145                 150                 155                 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
                165                 170                 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
            180                 185                 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
        195                 200                 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215
```

<210> 11
<211> 215
<212> PRT
<213> Homo Sapiens

<400> 11

```
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Thr Val Ile Ser Ser
            20                  25                  30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

Ile Ser Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
                85                  90                  95

Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
            100                 105                 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125
```

```
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
        195                 200                 205

Ser Phe Asn Arg Gly Glu Cys
    210                 215
```

<210> 12
<211> 213
<212> PRT
<213> Homo Sapiens

<400> 12

```
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Leu
            20                  25                  30

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
        35                  40                  45

Gly Ala Ser Arg Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
    50                  55                  60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
65                  70                  75                  80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Arg Ser
                85                  90                  95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
            100                 105                 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
```

115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 13
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 13

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

```
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 14
<211> 220
<212> PRT
<213> Homo Sapiens

<400> 14

```
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
            20                  25                  30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

Pro Pro Lys Leu Phe Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
                85                  90                  95

Tyr Tyr Ser Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
            100                 105                 110
```

```
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
        115                 120                 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    130                 135                 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145                 150                 155                 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165                 170                 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180                 185                 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
        195                 200                 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215                 220
```

<210> 15
<211> 220
<212> PRT
<213> Homo Sapiens

<400> 15

```
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
            20                  25                  30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
                85                  90                  95

Tyr Tyr Ser Thr Thr Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
            100                 105                 110
```

```
Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
        115                 120                 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    130                 135                 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145                 150                 155                 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165                 170                 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180                 185                 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
        195                 200                 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215                 220
```

<210> 16
<211> 220
<212> PRT
<213> Homo Sapiens

<400> 16

```
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Asn Val Leu Tyr Ser
            20                  25                  30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Phe Cys Gln Gln
                85                  90                  95

Tyr Tyr Gly Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
```

100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 17
<211> 220
<212> PRT
<213> Homo Sapiens

<400> 17

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Asn Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Phe Cys Gln Gln
85 90 95

```
Tyr Tyr Gly Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
            100                 105                 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
        115                 120                 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    130                 135                 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145                 150                 155                 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165                 170                 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180                 185                 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
        195                 200                 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215                 220
```

<210> 18
<211> 220
<212> PRT
<213> Homo Sapiens

<400> 18

```
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Thr Val Ser Leu Gly
1               5                   10                  15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
            20                  25                  30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

Pro Asp Arg Phe Gly Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
                85                  90                  95
```

```
Tyr Tyr Ser Ile Ser Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
            100                 105                 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
        115                 120                 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    130                 135                 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145                 150                 155                 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165                 170                 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180                 185                 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
        195                 200                 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215                 220
```

<210> 19
<211> 220
<212> PRT
<213> Homo Sapiens

<400> 19

```
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Asn
            20                  25                  30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80

Ile Ser Ser Leu Gln Ala Asp Asp Val Ala Val Tyr Tyr Cys Gln Gln
                85                  90                  95
```

```
Tyr Tyr Ser Thr Thr Trp Thr Phe Gly Pro Gly Thr Lys Val Glu Ile
            100                 105                 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
        115                 120                 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    130                 135                 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145                 150                 155                 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165                 170                 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180                 185                 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
        195                 200                 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215                 220
```

<210> 20
<211> 220
<212> PRT
<213> Homo Sapiens

<400> 20

```
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Asn
            20                  25                  30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80

Ile Ser Ser Leu Gln Ala Asp Asp Val Ala Val Tyr Tyr Cys Gln Gln
```

85 90 95

Tyr Tyr Ser Thr Thr Trp Thr Phe Gly Pro Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 21
<211> 220
<212> PRT
<213> Homo Sapiens

<400> 21

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Val Leu Ile Tyr Trp Ala Ser Thr Arg Lys Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

```
Ile Ser Gly Leu Gln Ala Glu Asp Val Ala Leu Tyr Tyr Cys Gln Gln
                85                  90                  95

Tyr Tyr Ser Thr Met Phe Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile
            100                 105                 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
        115                 120                 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    130                 135                 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145                 150                 155                 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165                 170                 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180                 185                 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
        195                 200                 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215                 220
```

<210> 22
<211> 220
<212> PRT
<213> Homo Sapiens

<400> 22

```
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Asp Ser
            20                  25                  30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80
```

```
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Phe Tyr Cys His Gln
                85                  90                  95

Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Ala Ile
            100                 105                 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
        115                 120                 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
    130                 135                 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145                 150                 155                 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
                165                 170                 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
            180                 185                 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
        195                 200                 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215                 220
```

<210> 23
<211> 220
<212> PRT
<213> Homo Sapiens

<400> 23

```
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Ile Leu Tyr Arg
            20                  25                  30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ala Arg Glu Ser Gly Val
    50                  55                  60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65                  70                  75                  80
```

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Phe Cys Gln Gln
85 90 95

Tyr Phe Ile Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 24
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 24

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser His Tyr
20 25 30

Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Lys Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Asn Tyr Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 25
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 25

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Ala Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Ala Trp Leu Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

```
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Thr Tyr Pro Phe
                85                  90                  95

Thr Phe Gly Pro Gly Thr Lys Met Asp Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 26
<211> 215
<212> PRT
<213> Homo Sapiens

<400> 26

```
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1               5                   10                  15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Asp Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45

Tyr Gly Ala Ser Arg Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60
```

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln His Asn Asn Trp Pro Pro
85 90 95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 27
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 27

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Arg Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

```
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Pro
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Phe Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 28
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 28

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Thr Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Phe Leu Ile
        35                  40                  45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
```

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Ala Tyr Tyr Cys Gln Gln Ser His Ser Ala Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 29
<211> 213
<212> PRT
<213> Homo Sapiens

<400> 29

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Ser Ile Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

```
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Thr
                85                  90                  95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
            100                 105                 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
        115                 120                 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
    130                 135                 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145                 150                 155                 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                165                 170                 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            180                 185                 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        195                 200                 205

Asn Arg Gly Glu Cys
    210
```

<210> 30
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 30

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Asn Ala Pro Lys Leu Leu Ile
        35                  40                  45
```

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Val Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Arg Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ile Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 31
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 31

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Arg Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Ser Arg Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

```
Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Leu Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ile Tyr Ser Thr Ser Ile
                85                  90                  95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 32
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 32

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Arg Ile Ser Ser Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
```

35 40 45

Tyr Ala Glu Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ile Thr Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Ile Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 33
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 33

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Arg Tyr
20 25 30

```
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asn Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Phe Thr Pro Ile
                85                  90                  95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 34
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 34

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
            20                  25                  30
```

```
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Phe Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Phe Ser Pro Ile
                85                  90                  95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 35
<211> 433
<212> PRT
<213> Homo Sapiens

<400> 35

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
            20                  25                  30
```

```
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Leu Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Ser Phe Tyr Thr Pro Ile
                85                  90                  95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Ala Ser Thr Lys Gly
            100                 105                 110

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
        115                 120                 125

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
    130                 135                 140

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
145                 150                 155                 160

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
                165                 170                 175

Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val
            180                 185                 190

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys
        195                 200                 205

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
    210                 215                 220

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
225                 230                 235                 240

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
                245                 250                 255

Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
            260                 265                 270
```

```
Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val
        275                 280                 285

Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu
    290                 295                 300

Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys
305                 310                 315                 320

Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
                325                 330                 335

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
            340                 345                 350

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
        355                 360                 365

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu
    370                 375                 380

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
385                 390                 395                 400

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
                405                 410                 415

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
            420                 425                 430

Lys
```

<210> 36
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 36

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
```

```
Tyr Thr Val Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Phe Thr Pro Ile
                85                  90                  95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 37
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 37

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45
```

```
Tyr Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Ser Phe Tyr Ala Pro Ile
                85                  90                  95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 38
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 38

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
```

35 40 45

Tyr Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Phe Thr Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 39
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 39

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Tyr Leu Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 40
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 40

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Ser
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Cys Asp Asp Leu Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 41
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 41

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asp Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln His Tyr Asp Asn Leu Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 42
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 42

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Ala Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr

20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 43
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 43

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

```
Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Ser
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Ile Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Glu Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Cys Asp Ile Leu Pro Leu
                85                  90                  95

Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 44
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 44

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15
```

```
Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Ser
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Leu
                85                  90                  95

Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Arg Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 45
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 45

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15
```

```
Asp Gly Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Thr Asn Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Ser Leu Pro Ile
                85                  90                  95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 46
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 46

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
```

```
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Leu Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

His Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Ile
                85                  90                  95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 47
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 47

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                  10                  15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asp Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln His Tyr Asp Asn Leu Pro Ile
                85                  90                  95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 48
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 48

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                  10                  15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Ser
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln His Tyr Asp Asn Leu Pro Ile
                85                  90                  95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```

<210> 49
<211> 446
<212> PRT
<213> Homo Sapiens

<400> 49

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                  10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Ile Ser Ala Ser Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu
    50                  55                  60

Gln Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Asp Asn Trp Asn Tyr Gly Phe Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val
    210                 215                 220

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
225                 230                 235                 240
```

```
Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            260                 265                 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val
    290                 295                 300

Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320

Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
                325                 330                 335

Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            340                 345                 350

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        355                 360                 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    370                 375                 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp
385                 390                 395                 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
```

<210> 50
<211> 443
<212> PRT
<213> Homo Sapiens

<400> 50

```
Gln Val His Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15
```

```
Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Gly His
            20                  25                  30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Cys Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Ile Ala Val Ala Leu Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
        115                 120                 125

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn
            180                 185                 190

Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro
225                 230                 235                 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
                245                 250                 255

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn
```

260 265 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
275 280 285

Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val
290 295 300

Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305 310 315 320

Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
325 330 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
340 345 350

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
355 360 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
370 375 380

Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe
385 390 395 400

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
405 410 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 51
<211> 443
<212> PRT
<213> Homo Sapiens

<400> 51

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

```
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn His Thr Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Ile Ala Val Ala Leu Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
        115                 120                 125

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
    130                 135                 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145                 150                 155                 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
                165                 170                 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn
            180                 185                 190

Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
        195                 200                 205

Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro
225                 230                 235                 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
                245                 250                 255

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn
            260                 265                 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
        275                 280                 285
```

```
Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val
    290                 295                 300

Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305                 310                 315                 320

Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
                325                 330                 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
            340                 345                 350

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
        355                 360                 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
    370                 375                 380

Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe
385                 390                 395                 400

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
                405                 410                 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
            420                 425                 430

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440
```

<210> 52
<211> 448
<212> PRT
<213> Homo Sapiens

<400> 52

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Arg Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Glu Leu
            20                  25                  30

Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
        35                  40                  45

Gly Ser Phe Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala Gln Lys Phe
```

```
    50                  55                  60

Gln Gly Arg Val Thr Met Leu Glu Asp Thr Ser Thr Asp Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Thr Glu Gly Asp Gly Gly Tyr Tyr Tyr Tyr Gly Met Asp Val Trp
            100                 105                 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
        115                 120                 125

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
    130                 135                 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145                 150                 155                 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                165                 170                 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180                 185                 190

Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp
        195                 200                 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys
    210                 215                 220

Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val
    290                 295                 300
```

Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr
325 330 335

Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 53
<211> 448
<212> PRT
<213> Homo Sapiens

<400> 53

Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Ser Gln Val
65 70 75 80

```
Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr
                325                 330                 335

Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp
385                 390                 395                 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
```

<210> 53
<211> 448
<212> PRT
<213> Homo Sapiens

<400> 53

```
Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
1               5                   10                  15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asn Ala
            20                  25                  30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
    50                  55                  60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Ser Gln Val
65                  70                  75                  80
```

```
Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala Arg Met Tyr Ser Ser Gly Trp Tyr Gly Val Phe Asp Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
        115                 120                 125

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
    130                 135                 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145                 150                 155                 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                165                 170                 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180                 185                 190

Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp
        195                 200                 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys
    210                 215                 220

Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320
```

Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr
325 330 335

Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 54
<211> 449
<212> PRT
<213> Homo Sapiens

<400> 54

Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Val Leu Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Ser Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

```
Cys Ala Arg Val Tyr Ser Ser Gly Trp Ser Phe Tyr Gly Met Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val
        195                 200                 205

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys
    210                 215                 220

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
```

340 345 350

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 55
<211> 444
<212> PRT
<213> Homo Sapiens

<400> 55

Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Gly
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

```
Cys Ala His Arg Arg Glu Leu Pro Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
            340                 345                 350
```

```
Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser
385                 390                 395                 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
                405                 410                 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            420                 425                 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440
```

<210> 56
<211> 444
<212> PRT
<213> Homo Sapiens

<400> 56

```
Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1               5                   10                  15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Gly
            20                  25                  30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
    50                  55                  60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Thr Gln Val
65                  70                  75                  80

Val Leu Thr Val Thr Asp Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala His Arg Asn Trp Thr Pro Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
```

```
        115                 120                 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365
```

```
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser
385                 390                 395                 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
                405                 410                 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            420                 425                 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440
```

<210> 57
<211> 444
<212> PRT
<213> Homo Sapiens

<400> 57

```
Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1               5                   10                  15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Asn Thr Gly
            20                  25                  30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
    50                  55                  60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala His Arg Leu Glu Leu Pro Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
    130                 135                 140
```

```
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380
```

```
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser
385                 390                 395                 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
                405                 410                 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            420                 425                 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440
```

<210> 58
<211> 444
<212> PRT
<213> Homo Sapiens

<400> 58

```
Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1               5                   10                  15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Gly
            20                  25                  30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
    50                  55                  60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80

Val Leu Thr Met Thr Asn Leu Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala His Arg Arg Glu Val Pro Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160
```

```
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser
385                 390                 395                 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
```

405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 59
<211> 444
<212> PRT
<213> Homo Sapiens

<400> 59

Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Gly
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asn Val Glu Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Arg Ser Arg Leu Thr Ile Thr Lys Ala Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala His Arg His Thr Asn Pro Phe Glu Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
210 215 220

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe
225 230 235 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
245 250 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe
260 265 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
275 280 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr
290 295 300

Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305 310 315 320

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
325 330 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
340 345 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
355 360 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
370 375 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser
385 390 395 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 60
<211> 444
<212> PRT
<213> Homo Sapiens

<400> 60

Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Gly
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala His Arg Gly Glu Leu Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser

195 200 205

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
210 215 220

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe
225 230 235 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
245 250 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe
260 265 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
275 280 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr
290 295 300

Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305 310 315 320

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
325 330 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
340 345 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
355 360 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
370 375 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser
385 390 395 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 61
<211> 447
<212> PRT
<213> Homo Sapiens

<400> 61

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser Arg Tyr
20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Val Gly Ala Thr Pro Asp Ala Phe Asp Ile Trp Gly
100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys
210 215 220

```
Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
225                 230                 235                 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
                245                 250                 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
            260                 265                 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
        275                 280                 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
    290                 295                 300

Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305                 310                 315                 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
                325                 330                 335

Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
            340                 345                 350

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
        355                 360                 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
    370                 375                 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
385                 390                 395                 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
                405                 410                 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
            420                 425                 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
```

<210> 62
<211> 454
<212> PRT
<213> Homo Sapiens

<400> 62

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Glu Gly Ile Ala Val Ala Gly Thr Ala Glu Tyr Tyr Tyr Tyr
            100                 105                 110

Tyr Ala Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
    130                 135                 140

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
145                 150                 155                 160

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
                165                 170                 175

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
            180                 185                 190

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
        195                 200                 205

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
    210                 215                 220

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
225                 230                 235                 240
```

```
Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                245                 250                 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
            260                 265                 270

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
        275                 280                 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
    290                 295                 300

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
305                 310                 315                 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
                325                 330                 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
            340                 345                 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
        355                 360                 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
    370                 375                 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
385                 390                 395                 400

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
                405                 410                 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
            420                 425                 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
        435                 440                 445

Ser Leu Ser Pro Gly Lys
    450
```

<210> 63
<211> 451
<212> PRT
<213> Homo Sapiens

<400> 63

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Glu Gly Ile Ala Ala Arg Asp Ser Tyr Tyr Tyr Tyr Ala Met
            100                 105                 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
        115                 120                 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser
    130                 135                 140

Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
145                 150                 155                 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
                165                 170                 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
            180                 185                 190

Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys
        195                 200                 205

Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu
    210                 215                 220

Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala
225                 230                 235                 240
```

```
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445

Pro Gly Lys
    450
```

<210> 64
<211> 451
<212> PRT
<213> Homo Sapiens

<400> 64

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Glu Tyr Tyr Cys
                85                  90                  95

Ala Lys Glu Gly Ile Ala Gly Arg Asp Ser Tyr Tyr Tyr Tyr Gly Met
            100                 105                 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
        115                 120                 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser
    130                 135                 140

Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
145                 150                 155                 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
                165                 170                 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
            180                 185                 190

Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys
        195                 200                 205

Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu
    210                 215                 220

Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
```

245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
290 295 300

Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 65
<211> 449
<212> PRT
<213> Homo Sapiens

<400> 65

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Phe Ile Ser Asp Asp Gly Ser Thr Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Met Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Tyr Tyr Asp Ser Ser Gly Tyr Tyr Tyr Gly Phe Asp Tyr
            100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val
        195                 200                 205

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys
    210                 215                 220

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
```

```
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu
385                 390                 395                 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445

Lys
```

<210> 66
<211> 440
<212> PRT
<213> Homo Sapiens

<400> 66

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
```

```
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asn Val Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
            100                 105                 110

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys
        115                 120                 125

Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys
    130                 135                 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
145                 150                 155                 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
                165                 170                 175

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr
            180                 185                 190

Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val
        195                 200                 205

Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro
    210                 215                 220

Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
225                 230                 235                 240

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
                245                 250                 255
```

```
Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
            260                 265                 270

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
        275                 280                 285

Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln
    290                 295                 300

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
305                 310                 315                 320

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro
                325                 330                 335

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
            340                 345                 350

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
        355                 360                 365

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
    370                 375                 380

Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
385                 390                 395                 400

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
                405                 410                 415

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
            420                 425                 430

Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440
```

<210> 67
<211> 446
<212> PRT
<213> Homo Sapiens

<400> 67

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30
```

```
Asp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Val Ile Trp Tyr Asp Gly Ser Ile Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Gly Ala Thr Gly Ala Glu Tyr Phe Gln His Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val
    210                 215                 220

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
225                 230                 235                 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            260                 265                 270
```

```
Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val
    290                 295                 300

Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320

Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
                325                 330                 335

Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            340                 345                 350

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        355                 360                 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    370                 375                 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp
385                 390                 395                 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
```

<210> 68
<211> 444
<212> PRT
<213> Homo Sapiens

<400> 68

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45
```

```
Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Val Leu Leu Trp Phe Gly Glu Thr Phe Asp Tyr Trp Gly Gln Gly Ser
            100                 105                 110

Leu Val Thr Val Ser Pro Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr
```

290 295 300

Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305 310 315 320

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
325 330 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
340 345 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
355 360 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
370 375 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser
385 390 395 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 69
<211> 441
<212> PRT
<213> Homo Sapiens

<400> 69

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Ser Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

```
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asn Leu Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
        115                 120                 125

Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val
    130                 135                 140

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145                 150                 155                 160

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
                165                 170                 175

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly
            180                 185                 190

Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys
        195                 200                 205

Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys
    210                 215                 220

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
225                 230                 235                 240

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
                245                 250                 255

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
            260                 265                 270

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
        275                 280                 285

Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His
    290                 295                 300

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
305                 310                 315                 320
```

Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
325 330 335

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
340 345 350

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
355 360 365

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
370 375 380

Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
385 390 395 400

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
405 410 415

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
420 425 430

Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 70
<211> 449
<212> PRT
<213> Homo Sapiens

<400> 70

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Asp Asp Gly Ser Asn Gln Tyr Tyr Thr Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

```
                85                  90                  95

Ala Arg Ser His Tyr Gly Gly Asp Tyr Asp Tyr Tyr Gly Met Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val
        195                 200                 205

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys
    210                 215                 220

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335
```

Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 71
<211> 446
<212> PRT
<213> Homo Sapiens

<400> 71

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Arg Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

```
Ala Arg Asp Gly Trp Gln Gln Gln Ala Pro Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val
    210                 215                 220

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
225                 230                 235                 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            260                 265                 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val
    290                 295                 300

Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320

Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
                325                 330                 335
```

```
Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            340                 345                 350

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        355                 360                 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    370                 375                 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp
385                 390                 395                 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
```

<210> 72
<211> 444
<212> PRT
<213> Homo Sapiens

<400> 72

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser His
            20                  25                  30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val
    50                  55                  60

Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Asp
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Trp Gly Ile Ser Ala Pro Phe Asp Cys Trp Gly Gln Gly Thr
            100                 105                 110
```

```
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
```

355 360 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
370 375 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser
385 390 395 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 73
<211> 441
<212> PRT
<213> Homo Sapiens

<400> 73

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Ser Gly Arg Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Phe
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Leu Trp Ala Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
115 120 125

```
Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val
    130                 135                 140

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145                 150                 155                 160

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
                165                 170                 175

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly
            180                 185                 190

Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys
        195                 200                 205

Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys
    210                 215                 220

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
225                 230                 235                 240

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
                245                 250                 255

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
            260                 265                 270

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
        275                 280                 285

Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His
    290                 295                 300

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
305                 310                 315                 320

Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
                325                 330                 335

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
            340                 345                 350

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
        355                 360                 365

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
    370                 375                 380
```

Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
385 390 395 400

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
405 410 415

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
420 425 430

Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 74
<211> 451
<212> PRT
<213> Homo Sapiens

<400> 74

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser His Ile Ser Ser Ser Ser Arg Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Asn Trp Asn Gly Gly Gly Asn Tyr Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser
130 135 140

Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu

```
145                 150                 155                 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
                165                 170                 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
            180                 185                 190

Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys
        195                 200                 205

Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu
    210                 215                 220

Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400
```

Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 75
<211> 451
<212> PRT
<213> Homo Sapiens

<400> 75

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser His Ile Ser Arg Ser Ser Arg Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Asn Trp Asn Asn Gly Gly Tyr Tyr Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser
130 135 140

Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
145 150 155 160

```
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
                165                 170                 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
            180                 185                 190

Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys
        195                 200                 205

Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu
    210                 215                 220

Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400
```

```
Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445

Pro Gly Lys
    450
```

<210> 76
<211> 444
<212> PRT
<213> Homo Sapiens

<400> 76

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Ser Gly
            20                  25                  30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile His Ser Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Asn Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Gly Pro Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr
            100                 105                 110

Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160
```

```
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser
385                 390                 395                 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
```

405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 77
<211> 453
<212> PRT
<213> Homo Sapiens

<400> 77

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Arg Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr His Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Asn Met Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Ala Leu Arg Gly Ile Val Leu Met Val Tyr Val Leu Gly
100 105 110

Ala Leu Asp Ile Trp Gly Gln Gly Thr Lys Val Thr Val Ser Ser Ala
115 120 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser
130 135 140

Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145 150 155 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
165 170 175

```
Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr
        195                 200                 205

Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr
    210                 215                 220

Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro
225                 230                 235                 240

Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
    290                 295                 300

Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430
```

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly Lys
450

<210> 78
<211> 453
<212> PRT
<213> Homo Sapiens

<400> 78

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Asp Glu Thr Val Val Arg Gly Leu Ile Arg Tyr Cys Tyr
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
115 120 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser
130 135 140

Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145 150 155 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
165 170 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu

```
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr
        195                 200                 205

Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr
    210                 215                 220

Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro
225                 230                 235                 240

Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
    290                 295                 300

Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala
                325                 330                 335

Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
        355                 360                 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430
```

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly Lys
450

<210> 79
<211> 448
<212> PRT
<213> Homo Sapiens

<400> 79

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Asn Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile His Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Ile Thr Ile Ser Ala Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Asp Arg Gly Gly Gly Asp Tyr Gly Arg Met Asp Val Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
130 135 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190

```
Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp
        195                 200                 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys
    210                 215                 220

Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr
                325                 330                 335

Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp
385                 390                 395                 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430
```

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 80
<211> 448
<212> PRT
<213> Homo Sapiens

<400> 80

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Asn Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile His Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Ile Thr Ile Ser Ala Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Asp Arg Gly Gly Gly Asp Tyr Gly Arg Met Asp Val Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
130 135 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190

Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp
195 200 205

```
His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys
    210                 215                 220

Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr
                325                 330                 335

Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp
385                 390                 395                 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
```

<210> 81

<211> 445
<212> PRT
<213> Homo Sapiens

<400> 81

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                  10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile His Ser Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Ile Thr Lys Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Ser Asn Asn Tyr Gly Cys Phe Ala Leu Trp Gly Arg Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
    130                 135                 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu
    210                 215                 220
```

```
Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu
225                 230                 235                 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                245                 250                 255

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln
            260                 265                 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        275                 280                 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu
    290                 295                 300

Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305                 310                 315                 320

Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335

Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            340                 345                 350

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        355                 360                 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    370                 375                 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly
385                 390                 395                 400

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                405                 410                 415

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            420                 425                 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
```

<210> 82
<211> 445
<212> PRT
<213> Homo Sapiens

<400> 82

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                  10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile His Ser Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Ile Thr Lys Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Ser Asn Asn Tyr Gly Cys Phe Ala Leu Trp Gly Arg Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
    130                 135                 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu
    210                 215                 220

Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu
225                 230                 235                 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
```

245 250 255

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln
260 265 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu
290 295 300

Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
325 330 335

Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
340 345 350

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 83
<211> 459
<212> PRT
<213> Homo Sapiens

<400> 83

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

```
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile His Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Ser Gly Tyr Asn Tyr Gly Leu Tyr Tyr Tyr Asp Ser Ser Gly
            100                 105                 110

Tyr Pro Ser Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
        115                 120                 125

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
    130                 135                 140

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
145                 150                 155                 160

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
                165                 170                 175

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
            180                 185                 190

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn
        195                 200                 205

Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
    210                 215                 220

Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro
225                 230                 235                 240

Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro
                245                 250                 255

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
            260                 265                 270
```

```
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn
        275                 280                 285

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
    290                 295                 300

Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val
305                 310                 315                 320

Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
                325                 330                 335

Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
            340                 345                 350

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
        355                 360                 365

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
    370                 375                 380

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
385                 390                 395                 400

Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe
                405                 410                 415

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
            420                 425                 430

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
        435                 440                 445

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    450                 455
```

<210> 84
<211> 451
<212> PRT
<213> Homo Sapiens

<400> 84

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
```

```
          20                  25                  30

Asp Tyr Tyr Trp Asn Trp Val Arg Gln His Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Gly Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Phe Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe
                85                  90                  95

Cys Ala Arg Thr Tyr Tyr Asp Ile Leu Thr Gly Tyr Pro Phe Tyr Phe
            100                 105                 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
        115                 120                 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser
    130                 135                 140

Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
145                 150                 155                 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
                165                 170                 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
            180                 185                 190

Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys
        195                 200                 205

Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu
    210                 215                 220

Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270
```

```
Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445

Pro Gly Lys
    450
```

<210> 85
<211> 451
<212> PRT
<213> Homo Sapiens

<400> 85

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30
```

```
Asp Tyr Tyr Trp Asn Trp Val Arg Gln His Pro Gly Lys Gly Leu Glu
         35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Gly Thr Tyr Tyr Asn Pro Ser
     50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Phe Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe
                 85                  90                  95

Cys Ala Arg Thr Tyr Tyr Asp Ile Leu Thr Gly Tyr Pro Phe Tyr Phe
            100                 105                 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
        115                 120                 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser
    130                 135                 140

Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
145                 150                 155                 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
                165                 170                 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
            180                 185                 190

Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys
        195                 200                 205

Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu
    210                 215                 220

Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270
```

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
290 295 300

Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 86
<211> 446
<212> PRT
<213> Homo Sapiens

<400> 86

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
20 25 30

SLS

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gly Gly Tyr Ser Ser Ser Trp Tyr Trp Phe Asp Pro Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val
210 215 220

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr

275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val
290 295 300

Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
325 330 335

Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 87
<211> 446
<212> PRT
<213> Homo Sapiens

<400> 87

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

```
Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
    50                  55                  60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65                  70                  75                  80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Gly Gly Tyr Ser Ser Ser Trp Phe Trp Phe Asp Pro Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val
    210                 215                 220

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
225                 230                 235                 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            260                 265                 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val
    290                 295                 300
```

```
Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320

Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
                325                 330                 335

Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            340                 345                 350

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        355                 360                 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    370                 375                 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp
385                 390                 395                 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445
```

<210> 88
<211> 449
<212> PRT
<213> Homo Sapiens

<400> 88

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
            20                  25                  30

Tyr Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45

Gly Arg Ile Tyr Thr Ser Gly Thr Thr Asn Tyr Asn Pro Ser Leu Lys
    50                  55                  60

Ser Arg Val Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
```

65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Gly Tyr Ser Tyr Gly His Tyr Tyr Tyr Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
180 185 190

Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val
195 200 205

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys
210 215 220

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val
290 295 300

Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys
325 330 335

Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 89
<211> 452
<212> PRT
<213> Homo Sapiens

<400> 89

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Ser Gly
20 25 30

Gly Ser Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Ile Val Thr Ser Arg Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Ser Ala Leu Arg Tyr Phe Asp Trp Leu Phe Ser Asp Val
100 105 110

Ser Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser
115 120 125

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr
130 135 140

Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
145 150 155 160

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
165 170 175

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
180 185 190

Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr
195 200 205

Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val
210 215 220

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
225 230 235 240

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
245 250 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
260 265 270

His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
275 280 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
290 295 300

Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn
305 310 315 320

```
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro
                325                 330                 335

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln
            340                 345                 350

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
        355                 360                 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
    370                 375                 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385                 390                 395                 400

Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
                405                 410                 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            420                 425                 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        435                 440                 445

Ser Pro Gly Lys
    450
```

<210> 90
<211> 446
<212> PRT
<213> Homo Sapiens

<400> 90

```
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Leu Lys Lys Pro Gly Glu
1               5                   10                  15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Arg Phe Thr Ser Tyr
            20                  25                  30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35                  40                  45

Gly Ile Ile Tyr Pro Asp Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
    50                  55                  60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80
```

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Gln Lys Ser Tyr Gly Tyr Ser Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val
210 215 220

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val
290 295 300

Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser

325 330 335

Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 91
<211> 447
<212> PRT
<213> Homo Sapiens

<400> 91

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Asp Asp Ser Asp Ala Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Tyr Gly Ser Gly Trp Gly Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys
210 215 220

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
290 295 300

Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
325 330 335

Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 92
<211> 453
<212> PRT
<213> Homo Sapiens

<400> 92

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Ile Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Leu Ala Val Ala Gly Thr Ser Tyr Tyr Tyr Tyr Tyr
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala

115 120 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser
130 135 140

Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145 150 155 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
165 170 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
180 185 190

Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr
195 200 205

Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr
210 215 220

Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro
225 230 235 240

Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
260 265 270

Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
275 280 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
290 295 300

Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu
305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala
325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro
340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385 390 395 400

Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly Lys
450

<210> 93
<211> 451
<212> PRT
<213> Homo Sapiens

<400> 93

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Tyr
20 25 30

Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
35 40 45

Trp Leu Gly Arg Thr Tyr Cys Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Ala Arg Asp Arg Ala Val Ala Gly Tyr Tyr Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser
130 135 140

Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
180 185 190

Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys
195 200 205

Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu
210 215 220

Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
290 295 300

Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 94
<211> 112
<212> PRT
<213> Homo Sapiens

<400> 94

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
20 25 30

Asp Gly Asn Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Asp Ser Gly Val Pro
50 55 60

Asp Arg Phe Asn Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ser
85 90 95

Thr His Trp Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105 110

<210> 95
<211> 112
<212> PRT

<213> Homo Sapiens

<400> 95

```
Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1               5                  10                  15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
            20                  25                  30

Asp Gly Asn Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
        35                  40                  45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Asp Ser Gly Val Pro
    50                  55                  60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ile Gln Gly
                85                  90                  95

Thr His Trp Pro Thr Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105                 110
```

<210> 96
<211> 112
<212> PRT
<213> Homo Sapiens

<400> 96

```
Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1               5                  10                  15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
            20                  25                  30

Asp Gly Asn Thr Tyr Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Ser
        35                  40                  45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Asp Ser Gly Val Pro
    50                  55                  60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
                85                  90                  95
```

Thr His Trp Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105 110

<210> 97
<211> 112
<212> PRT
<213> Homo Sapiens

<400> 97

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Pro
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
85 90 95

Ile Gln Leu Pro Cys Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 98
<211> 112
<212> PRT
<213> Homo Sapiens

<400> 98

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Pro
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ser
85 90 95

Ile Gln Leu Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 99
<211> 112
<212> PRT
<213> Homo Sapiens

<400> 99

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Tyr Trp Phe Leu Gln Lys Pro Gly Gln Pro
35 40 45

Pro Gln Pro Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ser
85 90 95

Ile Gln Leu Pro Ile Thr Phe Gly His Gly Thr Arg Leu Glu Ile Lys
100 105 110

<210> 100
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 100

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ala Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
35 40 45

Tyr Val Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Asn Tyr Asn Ser Ala Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 101
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 101

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Ile Cys Arg Ala Ser Gln Gly Ile Ser Asn Asp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Val Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 102
<211> 112
<212> PRT
<213> Homo Sapiens

<400> 102

```
Asn Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
1               5                  10                  15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
            20                  25                  30

Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
        35                  40                  45

Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60

Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
                85                  90                  95

Thr Gln Phe Pro His Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100                 105                 110
```

<210> 103
<211> 112
<212> PRT
<213> Homo Sapiens

<400> 103

```
Glu Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
1               5                  10                  15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
            20                  25                  30

Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
        35                  40                  45

Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60

Asp Arg Phe Ser Gly Thr Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
                85                  90                  95

Thr Gln Phe Pro His Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110
```

<210> 104
<211> 108
<212> PRT
<213> Homo Sapiens

<400> 104

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Thr Val Ile Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Ser Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 105
<211> 106
<212> PRT
<213> Homo Sapiens

<400> 105

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Leu
20 25 30

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
35 40 45

Gly Ala Ser Arg Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
65 70 75 80

```
Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Arg Ser
                85                  90                  95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

<210> 106
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 106

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                  10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
            20                  25                  30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
        35                  40                  45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Pro
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 107
<211> 113
<212> PRT
<213> Homo Sapiens

<400> 107

```
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                  10                  15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
            20                  25                  30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45
```

Pro Pro Lys Leu Phe Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 108
<211> 113
<212> PRT
<213> Homo Sapiens

<400> 108

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Thr Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 109

<211> 113
<212> PRT
<213> Homo Sapiens

<400> 109

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Asn Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Phe Cys Gln Gln
85 90 95

Tyr Tyr Gly Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 110
<211> 113
<212> PRT
<213> Homo Sapiens

<400> 110

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Asn Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr

65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Phe Cys Gln Gln
85 90 95

Tyr Tyr Gly Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 111
<211> 113
<212> PRT
<213> Homo Sapiens

<400> 111

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Thr Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Gly Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Ile Ser Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 112
<211> 113
<212> PRT
<213> Homo Sapiens

<400> 112

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly

1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Asn
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Asp Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Thr Trp Thr Phe Gly Pro Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 113
<211> 113
<212> PRT
<213> Homo Sapiens

<400> 113

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Asn
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Asp Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Thr Trp Thr Phe Gly Pro Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 114
<211> 113
<212> PRT
<213> Homo Sapiens

<400> 114

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Val Leu Ile Tyr Trp Ala Ser Thr Arg Lys Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Gly Leu Gln Ala Glu Asp Val Ala Leu Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Met Phe Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105 110

Lys

<210> 115
<211> 113
<212> PRT
<213> Homo Sapiens

<400> 115

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Asp Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Phe Tyr Cys His Gln
85 90 95

Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Ala Ile
100 105 110

Lys

<210> 116
<211> 113
<212> PRT
<213> Homo Sapiens

<400> 116

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Ile Leu Tyr Arg
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ala Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Phe Cys Gln Gln
85 90 95

Tyr Phe Ile Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 117
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 117

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser His Tyr
20 25 30

Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Lys Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Asn Tyr Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 118
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 118

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Ala Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Ala Trp Leu Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Thr Tyr Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Met Asp Ile Lys
100 105

<210> 119
<211> 108
<212> PRT
<213> Homo Sapiens

<400> 119

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Asp Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Arg Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln His Asn Asn Trp Pro Pro
85 90 95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 120
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 120

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Arg Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Phe Lys
100 105

<210> 121
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 121

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Thr Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Phe Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Ala Tyr Tyr Cys Gln Gln Ser His Ser Ala Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 122
<211> 106
<212> PRT
<213> Homo Sapiens

<400> 122

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Ser Ile Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 123
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 123

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Asn Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Val Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Arg Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ile Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 124
<211> 107

<212> PRT
<213> Homo Sapiens

<400> 124

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Arg Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Ser Arg Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Leu Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ile Tyr Ser Thr Ser Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 125
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 125

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Arg Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
35 40 45

Tyr Ala Glu Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ile Thr Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Ile
100 105

<210> 126
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 126

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Arg Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asn Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Phe Thr Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 127
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 127

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Phe Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Phe Ser Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 128
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 128

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Leu Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Ser Phe Tyr Thr Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 129
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 129

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

```
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Thr Val Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Phe Thr Pro Ile
                85                  90                  95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105
```

<210> 130
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 130

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Ser Phe Tyr Ala Pro Ile
                85                  90                  95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105
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<210> 131
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 131

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Phe Thr Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 132
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 132

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Tyr Leu Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys

100 105

<210> 133
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 133

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Ser
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Cys Asp Asp Leu Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 134
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 134

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asp Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln His Tyr Asp Asn Leu Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 135
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 135

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Ala Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 136
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 136

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Ser
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35 40 45

Tyr Asp Ala Ser Ile Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Glu Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Cys Asp Ile Leu Pro Leu
85 90 95

Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 137
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 137

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Ser
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Leu
85 90 95

Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Arg
100 105

<210> 138
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 138

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

```
1               5                   10                  15

Asp Gly Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Thr Asn Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Ser Leu Pro Ile
                85                  90                  95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105
```

<210> 139
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 139

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Leu Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

His Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Ile
                85                  90                  95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105
```

<210> 140
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 140

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asp Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln His Tyr Asp Asn Leu Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 141
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 141

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Ser
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln His Tyr Asp Asn Leu Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 142
<211> 120
<212> PRT
<213> Homo Sapiens

<400> 142

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Ser Ala Ser Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu
50 55 60

Gln Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Asp Asn Trp Asn Tyr Gly Phe Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 143
<211> 117
<212> PRT
<213> Homo Sapiens

<400> 143

Gln Val His Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Gly His
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Cys Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Ile Ala Val Ala Leu Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 144
<211> 117
<212> PRT
<213> Homo Sapiens

<400> 144

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn His Thr Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Ile Ala Val Ala Leu Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

S70

<210> 145
<211> 122
<212> PRT
<213> Homo Sapiens

<400> 145

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Arg Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Glu Leu
20 25 30

Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ser Phe Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Leu Glu Asp Thr Ser Thr Asp Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Thr Glu Gly Asp Gly Gly Tyr Tyr Tyr Tyr Gly Met Asp Val Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 146
<211> 122
<212> PRT
<213> Homo Sapiens

<400> 146

Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

```
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Ser Gln Val
65                  70                  75                  80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala Arg Met Tyr Ser Ser Gly Trp Tyr Gly Val Phe Asp Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 147
<211> 123
<212> PRT
<213> Homo Sapiens

<400> 147

```
Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
1               5                   10                  15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asn Ala
            20                  25                  30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45

Trp Leu Val Leu Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
    50                  55                  60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Ser Gln Val
65                  70                  75                  80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala Arg Val Tyr Ser Ser Gly Trp Ser Phe Tyr Gly Met Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 148
<211> 118
<212> PRT
<213> Homo Sapiens

<400> 148

Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Gly
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala His Arg Arg Glu Leu Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 149
<211> 118
<212> PRT
<213> Homo Sapiens

<400> 149

Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Gly
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Thr Gln Val
65 70 75 80

Val Leu Thr Val Thr Asp Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala His Arg Asn Trp Thr Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 150
<211> 118
<212> PRT
<213> Homo Sapiens

<400> 150

Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Asn Thr Gly
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala His Arg Leu Glu Leu Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 151
<211> 118
<212> PRT
<213> Homo Sapiens

<400> 151

Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Gly
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Leu Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala His Arg Arg Glu Val Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 152
<211> 118
<212> PRT
<213> Homo Sapiens

<400> 152

Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Gly
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asn Val Glu Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Arg Ser Arg Leu Thr Ile Thr Lys Ala Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala His Arg His Thr Asn Pro Phe Glu Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser

115

<210> 153
<211> 118
<212> PRT
<213> Homo Sapiens

<400> 153

Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Gly
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala His Arg Gly Glu Leu Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 154
<211> 121
<212> PRT
<213> Homo Sapiens

<400> 154

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser Arg Tyr
20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala Asp Ser Val

50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Val Gly Ala Thr Pro Asp Ala Phe Asp Ile Trp Gly
100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 155
<211> 128
<212> PRT
<213> Homo Sapiens

<400> 155

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Gly Ile Ala Val Ala Gly Thr Ala Glu Tyr Tyr Tyr Tyr
100 105 110

Tyr Ala Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 156
<211> 125
<212> PRT
<213> Homo Sapiens

<400> 156

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Gly Ile Ala Ala Arg Asp Ser Tyr Tyr Tyr Tyr Ala Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 157
<211> 125
<212> PRT
<213> Homo Sapiens

<400> 157

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

```
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Glu Tyr Tyr Cys
                85                  90                  95

Ala Lys Glu Gly Ile Ala Gly Arg Asp Ser Tyr Tyr Tyr Tyr Gly Met
            100                 105                 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125
```

<210> 158
<211> 123
<212> PRT
<213> Homo Sapiens

<400> 158

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Phe Ile Ser Asp Asp Gly Ser Thr Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Met Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Tyr Tyr Asp Ser Ser Gly Tyr Tyr Tyr Gly Phe Asp Tyr
            100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 159
<211> 114
<212> PRT
<213> Homo Sapiens

<400> 159

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asn Val Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
            100                 105                 110

Ser Ser
```

<210> 160
<211> 120
<212> PRT
<213> Homo Sapiens

<400> 160

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Asp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Val Ile Trp Tyr Asp Gly Ser Ile Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Gly Ala Thr Gly Ala Glu Tyr Phe Gln His Trp Gly Gln
            100                 105                 110
```

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 161
<211> 118
<212> PRT
<213> Homo Sapiens

<400> 161

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Leu Leu Trp Phe Gly Glu Thr Phe Asp Tyr Trp Gly Gln Gly Ser
100 105 110

Leu Val Thr Val Ser Pro
115

<210> 162
<211> 115
<212> PRT
<213> Homo Sapiens

<400> 162

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Ser Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asn Leu Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 163
<211> 123
<212> PRT
<213> Homo Sapiens

<400> 163

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Asp Asp Gly Ser Asn Gln Tyr Tyr Thr Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser His Tyr Gly Gly Asp Tyr Asp Tyr Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 164
<211> 120

<212> PRT
<213> Homo Sapiens

<400> 164

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Arg Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Trp Gln Gln Gln Ala Pro Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 165
<211> 118
<212> PRT
<213> Homo Sapiens

<400> 165

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser His
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val
50 55 60

Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Trp Gly Ile Ser Ala Pro Phe Asp Cys Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 166
<211> 115
<212> PRT
<213> Homo Sapiens

<400> 166

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Ser Gly Arg Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Phe
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Leu Trp Ala Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 167
<211> 125
<212> PRT
<213> Homo Sapiens

<400> 167

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser His Ile Ser Ser Ser Ser Arg Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Asn Trp Asn Gly Gly Gly Asn Tyr Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 168
<211> 125
<212> PRT
<213> Homo Sapiens

<400> 168

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser His Ile Ser Arg Ser Ser Arg Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Asn Trp Asn Asn Gly Gly Tyr Tyr Tyr Gly Met

100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 169
<211> 118
<212> PRT
<213> Homo Sapiens

<400> 169

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile His Ser Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Asn Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Gly Pro Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr
100 105 110

Thr Val Thr Val Ser Ser
115

<210> 170
<211> 127
<212> PRT
<213> Homo Sapiens

<400> 170

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Arg Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu

35 40 45

Trp Ile Gly Tyr Ile Tyr His Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Asn Met Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Ala Leu Arg Gly Ile Val Leu Met Val Tyr Val Leu Gly
100 105 110

Ala Leu Asp Ile Trp Gly Gln Gly Thr Lys Val Thr Val Ser Ser
115 120 125

<210> 171
<211> 127
<212> PRT
<213> Homo Sapiens

<400> 171

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Asp Glu Thr Val Val Arg Gly Leu Ile Arg Tyr Cys Tyr
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 172
<211> 122
<212> PRT
<213> Homo Sapiens

<400> 172

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Asn Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile His Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Ile Thr Ile Ser Ala Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Asp Arg Gly Gly Gly Asp Tyr Gly Arg Met Asp Val Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 173
<211> 122
<212> PRT
<213> Homo Sapiens

<400> 173

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Asn Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile His Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

```
Leu Lys Ser Arg Ile Thr Ile Ser Ala Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Asp Arg Gly Gly Gly Asp Tyr Gly Arg Met Asp Val Trp
            100                 105                 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 174
<211> 119
<212> PRT
<213> Homo Sapiens

<400> 174

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile His Ser Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Ile Thr Lys Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Ser Asn Asn Tyr Gly Cys Phe Ala Leu Trp Gly Arg Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser
        115
```

<210> 175
<211> 119
<212> PRT
<213> Homo Sapiens

<400> 175

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                  10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile His Ser Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Ile Thr Lys Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Ser Asn Asn Tyr Gly Cys Phe Ala Leu Trp Gly Arg Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser
        115
```

<210> 176
<211> 133
<212> PRT
<213> Homo Sapiens

<400> 176

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                  10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile His Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95
```

Cys Ala Ser Gly Tyr Asn Tyr Gly Leu Tyr Tyr Tyr Asp Ser Ser Gly
100 105 110

Tyr Pro Ser Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
115 120 125

Val Thr Val Ser Ser
130

<210> 177
<211> 125
<212> PRT
<213> Homo Sapiens

<400> 177

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Asp Tyr Tyr Trp Asn Trp Val Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Gly Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Phe Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe
85 90 95

Cys Ala Arg Thr Tyr Tyr Asp Ile Leu Thr Gly Tyr Pro Phe Tyr Phe
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 178
<211> 125
<212> PRT
<213> Homo Sapiens

<400> 178

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

```
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30

Asp Tyr Tyr Trp Asn Trp Val Arg Gln His Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Gly Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Phe Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe
                85                  90                  95

Cys Ala Arg Thr Tyr Tyr Asp Ile Leu Thr Gly Tyr Pro Phe Tyr Phe
            100                 105                 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125
```

<210> 179
<211> 120
<212> PRT
<213> Homo Sapiens

<400> 179

```
Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
            20                  25                  30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45

Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
    50                  55                  60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65                  70                  75                  80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Gly Gly Tyr Ser Ser Ser Trp Tyr Trp Phe Asp Pro Trp Gly Gln
            100                 105                 110
```

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 180
<211> 120
<212> PRT
<213> Homo Sapiens

<400> 180

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gly Gly Tyr Ser Ser Ser Trp Phe Trp Phe Asp Pro Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 181
<211> 123
<212> PRT
<213> Homo Sapiens

<400> 181

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Arg Ile Tyr Thr Ser Gly Thr Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Gly Tyr Ser Tyr Gly His Tyr Tyr Tyr Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 182
<211> 126
<212> PRT
<213> Homo Sapiens

<400> 182

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Ser Gly
20 25 30

Gly Ser Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Ile Val Thr Ser Arg Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Ser Ala Leu Arg Tyr Phe Asp Trp Leu Phe Ser Asp Val
100 105 110

Ser Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120 125

<210> 183

<211> 120
<212> PRT
<213> Homo Sapiens

<400> 183

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Leu Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Arg Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Asp Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Gln Lys Ser Tyr Gly Tyr Ser Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 184
<211> 121
<212> PRT
<213> Homo Sapiens

<400> 184

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Asp Asp Ser Asp Ala Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr Ala Tyr

65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Tyr Gly Ser Gly Trp Gly Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 185
<211> 127
<212> PRT
<213> Homo Sapiens

<400> 185

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Ile Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Leu Ala Val Ala Gly Thr Ser Tyr Tyr Tyr Tyr Tyr
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 186
<211> 125
<212> PRT
<213> Homo Sapiens

<400> 186

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln

```
1               5                   10                  15

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Tyr
            20                  25                  30

Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
        35                  40                  45

Trp Leu Gly Arg Thr Tyr Cys Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
    50                  55                  60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65                  70                  75                  80

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
                85                  90                  95

Tyr Tyr Cys Ala Arg Asp Arg Ala Val Ala Gly Tyr Tyr Tyr Gly Met
            100                 105                 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125
```

<210> 187
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 187

```
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1               5                   10                  15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
            20                  25                  30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
        35                  40                  45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
    50                  55                  60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65                  70                  75                  80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
                85                  90                  95
```

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 188
<211> 326
<212> PRT
<213> Homo Sapiens

<400> 188

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
1 5 10 15

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
100 105 110

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
115 120 125

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
130 135 140

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
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165 170 175

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
180 185 190

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
195 200 205

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Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
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Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
225                 230                 235                 240

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
                245                 250                 255

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
            260                 265                 270

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
        275                 280                 285

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
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Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
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Ser Leu Ser Pro Gly Lys
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Phe Gly His Gly Thr Arg Leu Glu Ile Lys
1 5 10

<210> 445

<211> 10
<212> PRT
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<400> 445

Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
1 5 10

<210> 446
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<400> 446

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 447
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<400> 447

Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 448
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<400> 448

Phe Gly Gly Gly Thr Lys Val Ala Ile Lys
1 5 10

<210> 449
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<212> PRT
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<400> 449

Phe Gly Pro Gly Thr Lys Met Asp Ile Lys
1 5 10

<210> 450
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<400> 450

Phe Gly Gln Gly Thr Lys Val Glu Phe Lys

1 5 10

<210> 451
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<212> PRT
<213> Homo Sapiens

<400> 451

Phe Gly Gly Gly Thr Lys Val Glu Ile Arg
1 5 10

<210> 452
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 452

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 453
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 453

Gln Val His Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Val Ser
20 25

<210> 454
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 454

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Arg Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Val Ser
20 25

<210> 455
<211> 25
<212> PRT

<213> Homo Sapiens

<400> 455

Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser
20 25

<210> 456
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 456

Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser
20 25

<210> 457
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 457

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 458
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 458

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 459
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 459

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser
20 25

<210> 460
<211> 25
<212> PRT
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<400> 460

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 461
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 461

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 462
<211> 25
<212> PRT
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<400> 462

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser
20 25

<210> 463
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 463

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Asn Cys Thr Val Ser
20 25

<210> 464
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 464

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr
20 25

<210> 465
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<212> PRT
<213> Homo Sapiens

<400> 465

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser
20 25

<210> 466
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 466

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Leu Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser
20 25

<210> 467
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 467

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser
20 25

<210> 468
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 468

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Ile Ser
20 25

<210> 469
<211> 14
<212> PRT
<213> Homo Sapiens

<400> 469

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1 5 10

<210> 470
<211> 14
<212> PRT
<213> Homo Sapiens

<400> 470

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met Gly
1 5 10

<210> 471
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<212> PRT
<213> Homo Sapiens

<400> 471

Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu Ala
1 5 10

<210> 472
<211> 14
<212> PRT
<213> Homo Sapiens

<400> 472

Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu Val

1 5 10

<210> 473
<211> 14
<212> PRT
<213> Homo Sapiens

<400> 473

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
1 5 10

<210> 474
<211> 14
<212> PRT
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<400> 474

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
1 5 10

<210> 475
<211> 14
<212> PRT
<213> Homo Sapiens

<400> 475

Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu Trp Ile Gly
1 5 10

<210> 476
<211> 14
<212> PRT
<213> Homo Sapiens

<400> 476

Trp Val Arg Gln His Pro Gly Lys Gly Leu Glu Trp Ile Gly
1 5 10

<210> 477
<211> 14
<212> PRT
<213> Homo Sapiens

<400> 477

Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
1 5 10

<210> 478
<211> 14
<212> PRT
<213> Homo Sapiens

<400> 478

Trp Ile Arg Gln Pro Ala Gly Lys Gly Leu Glu Trp Ile Gly
1 5 10

<210> 479
<211> 14
<212> PRT
<213> Homo Sapiens

<400> 479

Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
1 5 10

<210> 480
<211> 14
<212> PRT
<213> Homo Sapiens

<400> 480

Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu Gly
1 5 10

<210> 481
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 481

Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 482
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 482

Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 483
<211> 32
<212> PRT

<213> Homo Sapiens

<400> 483

Arg Val Thr Met Leu Glu Asp Thr Ser Thr Asp Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Thr
20 25 30

<210> 484
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 484

Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Ser Gln Val Val Leu Thr
1 5 10 15

Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala Arg
20 25 30

<210> 485
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 485

Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val Val Leu Thr
1 5 10 15

Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala His
20 25 30

<210> 486
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 486

Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Thr Gln Val Val Leu Thr
1 5 10 15

Val Thr Asp Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala His
20 25 30

<210> 487
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 487

Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val Val Leu Thr
1 5 10 15

Met Thr Asn Leu Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala His
20 25 30

<210> 488
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 488

Arg Leu Thr Ile Thr Lys Ala Thr Ser Lys Asn Gln Val Val Leu Thr
1 5 10 15

Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala His
20 25 30

<210> 489
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 489

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 490
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 490

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys
20 25 30

<210> 491
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 491

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Glu Tyr Tyr Cys Ala Lys
20 25 30

<210> 492
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 492

Arg Phe Thr Ile Ser Arg Asp Asn Ser Met Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 493
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 493

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 494
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 494

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val Leu
20 25 30

<210> 495
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 495

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Asp Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 496
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 496

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Phe Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys Ala Leu
20 25 30

<210> 497
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 497

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Val Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 498
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 498

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 499
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 499

Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Asn
1 5 10 15

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 500
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 500

Arg Val Asn Met Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys
1 5 10 15

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 501
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 501

Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys
1 5 10 15

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 502
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 502

Arg Ile Thr Ile Ser Ala Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys
1 5 10 15

Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 503
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 503

Arg Ile Thr Lys Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys
1 5 10 15

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 504
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 504

Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys
1 5 10 15

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Ser
20 25 30

<210> 505
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 505

Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys
1 5 10 15

Leu Phe Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala Arg
20 25 30

<210> 506
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 506

Arg Val Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys
1 5 10 15

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 507
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 507

Arg Val Thr Ile Ser Ile Val Thr Ser Arg Asn Gln Phe Ser Leu Lys
1 5 10 15

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 508
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 508

Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln
1 5 10 15

Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg
20 25 30

<210> 509
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 509

Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr Ala Tyr Leu Gln
1 5 10 15

Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg
20 25 30

<210> 510
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 510

Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Gln
1 5 10 15

Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 511
<211> 11
<212> PRT
<213> Homo Sapiens

<400> 511

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 512
<211> 11
<212> PRT
<213> Homo Sapiens

<400> 512

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> 513
<211> 11
<212> PRT
<213> Homo Sapiens

<400> 513

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
1 5 10

<210> 514
<211> 11
<212> PRT
<213> Homo Sapiens

<400> 514

Trp Gly Gln Gly Ser Leu Val Thr Val Ser Pro
1 5 10

<210> 515
<211> 11
<212> PRT
<213> Homo Sapiens

<400> 515

Trp Gly Gln Gly Thr Lys Val Thr Val Ser Ser
1 5 10

<210> 516
<211> 11
<212> PRT
<213> Homo Sapiens

<400> 516

Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 517
<211> 657
<212> PRT
<213> Homo Sapiens

<400> 517

Gly Ala Tyr Gly Thr Asn Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Met Thr Asn Trp Ser Asn Met Thr
20 25 30

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Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Met Thr Asn Gly Gly Asn
        35                  40                  45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
    50                  55                  60

Ser Asn Thr Gly Tyr Met Gly Asn Trp Ser Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Trp Ser Asn Met Thr Asn Gly Thr Asn Thr Ala Tyr Trp Ser Asn
                85                  90                  95

Gly Ala Tyr Gly Gly Asn Ala Ala Tyr Ala Cys Asn Thr Ala Tyr Met
            100                 105                 110

Thr Asn Ala Ala Tyr Thr Gly Gly Thr Thr Tyr Cys Ala Arg Cys Ala
        115                 120                 125

Arg Met Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala Arg Trp Ser Asn
    130                 135                 140

Cys Cys Asn Met Gly Asn Met Gly Asn Met Thr Asn Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Thr Gly
                165                 170                 175

Gly Gly Ala Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
            180                 185                 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Ala Ala Tyr Gly Gly Asn Trp
        195                 200                 205

Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly Ala
    210                 215                 220

Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Ala Arg Ala Thr His
225                 230                 235                 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
                245                 250                 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
            260                 265                 270
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Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Trp Ser Asn
        275                 280                 285

Ala Cys Asn Cys Ala Tyr Thr Gly Gly Cys Cys Asn Ala Thr His Ala
    290                 295                 300

Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys
305                 310                 315                 320

Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
                325                 330                 335

Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn Cys
            340                 345                 350

Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr Thr
        355                 360                 365

Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala Arg
    370                 375                 380

Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn Ala
385                 390                 395                 400

Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr Gly
                405                 410                 415

Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr Tyr
            420                 425                 430

Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn Ala
        435                 440                 445

Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly Thr
    450                 455                 460

Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala Arg
465                 470                 475                 480

Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg Gly
                485                 490                 495

Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys Ala
            500                 505                 510

Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser Asn
        515                 520                 525
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Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp
    530                 535                 540

Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp Ser
545                 550                 555                 560

Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala Arg
                565                 570                 575

Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr Gly
            580                 585                 590

Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys Ala
        595                 600                 605

Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
    610                 615                 620

Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn Thr
625                 630                 635                 640

Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr Gly
                645                 650                 655

Tyr
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<210> 518
<211> 657
<212> PRT
<213> Homo Sapiens

<400> 518

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Gly Ala Tyr Gly Thr Asn Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
1               5                   10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Met Thr Asn Trp Ser Asn Met Thr
            20                  25                  30

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Met Thr Asn Gly Gly Asn
        35                  40                  45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
    50                  55                  60

Ser Asn Thr Gly Tyr Met Gly Asn Trp Ser Asn Trp Ser Asn Cys Ala
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65                  70                  75                  80

Arg Trp Ser Asn Met Thr Asn Gly Thr Asn Thr Ala Tyr Trp Ser Asn
                85                  90                  95

Gly Ala Tyr Gly Gly Asn Ala Ala Tyr Ala Cys Asn Thr Ala Tyr Met
            100                 105                 110

Thr Asn Ala Ala Tyr Thr Gly Gly Thr Thr Tyr Cys Ala Arg Cys Ala
        115                 120                 125

Arg Met Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala Arg Trp Ser Asn
    130                 135                 140

Cys Cys Asn Met Gly Asn Met Gly Asn Met Thr Asn Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Thr Gly
                165                 170                 175

Gly Gly Ala Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
            180                 185                 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp
        195                 200                 205

Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly Ala
    210                 215                 220

Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Ala Arg Ala Thr His
225                 230                 235                 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
                245                 250                 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
            260                 265                 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr His Cys Ala Arg Gly Gly Asn
        275                 280                 285

Ala Cys Asn Cys Ala Tyr Thr Gly Gly Cys Cys Asn Ala Cys Asn Ala
    290                 295                 300

Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys
305                 310                 315                 320
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Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
325 330 335

Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn Cys
340 345 350

Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr Thr
355 360 365

Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala Arg
370 375 380

Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn Ala
385 390 395 400

Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr Gly
405 410 415

Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr Tyr
420 425 430

Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn Ala
435 440 445

Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly Thr
450 455 460

Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala Arg
465 470 475 480

Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg Gly
485 490 495

Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys Ala
500 505 510

Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser Asn
515 520 525

Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp
530 535 540

Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp Ser
545 550 555 560

Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala Arg

565 570 575

Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr Gly
580 585 590

Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys Ala
595 600 605

Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
610 615 620

Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn Thr
625 630 635 640

Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr Gly
645 650 655

Tyr

<210> 519
<211> 657
<212> PRT
<213> Homo Sapiens

<400> 519

Gly Ala Tyr Gly Thr Asn Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Met Thr Asn Trp Ser Asn Met Thr
20 25 30

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Met Thr Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr Met Gly Asn Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Met Thr Asn Gly Thr Asn Thr Ala Tyr Trp Ser Asn
85 90 95

Gly Ala Tyr Gly Gly Asn Ala Ala Tyr Ala Cys Asn Thr Ala Tyr Met
100 105 110

Thr Asn Ala Ala Tyr Thr Gly Gly Met Thr Asn Cys Ala Arg Cys Ala
115 120 125

Arg Met Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala Arg Trp Ser Asn
130 135 140

Cys Cys Asn Met Gly Asn Met Gly Asn Met Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Thr Gly
165 170 175

Gly Gly Ala Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
180 185 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp
195 200 205

Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly Ala
210 215 220

Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Ala Arg Ala Thr His
225 230 235 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
245 250 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
260 265 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Gly Gly Asn
275 280 285

Ala Cys Asn Cys Ala Tyr Thr Gly Gly Cys Cys Asn Ala Thr His Ala
290 295 300

Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys
305 310 315 320

Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
325 330 335

Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn Cys
340 345 350

Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr Thr
355 360 365

Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala Arg
370 375 380

Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn Ala
385 390 395 400

Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr Gly
405 410 415

Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr Tyr
420 425 430

Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn Ala
435 440 445

Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly Thr
450 455 460

Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala Arg
465 470 475 480

Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg Gly
485 490 495

Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys Ala
500 505 510

Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser Asn
515 520 525

Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp
530 535 540

Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp Ser
545 550 555 560

Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala Arg
565 570 575

Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr Gly
580 585 590

Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys Ala
595 600 605

Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
610 615 620

Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn Thr
625 630 635 640

Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr Gly
645 650 655

Tyr

<210> 520
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<400> 520

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
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Ala Arg Ala Cys Asn Cys Cys Asn Met Thr Asn Trp Ser Asn Met Thr
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Asn Trp Ser Asn Gly Thr Asn Ala Cys Asn Cys Cys Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Met Thr Asn Met Thr Asn Cys Ala Tyr Trp Ser Asn
85 90 95

Gly Ala Tyr Gly Gly Asn Ala Ala Arg Ala Cys Asn Thr Ala Tyr Met
100 105 110

Thr Asn Thr Ala Tyr Thr Gly Gly Thr Ala Tyr Met Thr Asn Cys Ala
115 120 125

Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn
130 135 140

Cys Cys Asn Cys Ala Arg Met Thr Asn Met Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Gly Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Met Gly
165 170 175

Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
180 185 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp
195 200 205

Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly Ala
210 215 220

Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Ala Arg Ala Thr His
225 230 235 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
245 250 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
260 265 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Gly Gly Asn
275 280 285

Ala Thr His Cys Ala Arg Met Thr Asn Cys Cys Asn Thr Gly Tyr Trp
290 295 300

Ser Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys
305 310 315 320

Asn Ala Ala Arg Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
325 330 335

Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn Cys
340 345 350

Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr Thr
355 360 365

Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala Arg
370 375 380

Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn Ala
385 390 395 400

Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr Gly

405 410 415

Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr Tyr
420 425 430

Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn Ala
435 440 445

Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly Thr
450 455 460

Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala Arg
465 470 475 480

Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg Gly
485 490 495

Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys Ala
500 505 510

Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser Asn
515 520 525

Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp
530 535 540

Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp Ser
545 550 555 560

Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala Arg
565 570 575

Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr Gly
580 585 590

Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys Ala
595 600 605

Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
610 615 620

Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn Thr
625 630 635 640

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645 650 655

Tyr

<210> 521
<211> 657
<212> PRT
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<400> 521

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Ala Arg Ala Cys Asn Cys Cys Asn Met Thr Asn Trp Ser Asn Met Thr
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Asn Trp Ser Asn Gly Thr Asn Ala Cys Asn Cys Cys Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Met Thr Asn Met Thr Asn Cys Ala Tyr Trp Ser Asn
85 90 95

Gly Ala Tyr Gly Gly Asn Ala Ala Arg Ala Cys Asn Thr Ala Tyr Met
100 105 110

Thr Asn Thr Ala Tyr Thr Gly Gly Thr Ala Tyr Met Thr Asn Cys Ala
115 120 125

Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn
130 135 140

Cys Cys Asn Cys Ala Arg Met Thr Asn Met Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Gly Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Met Gly
165 170 175

Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
180 185 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp
195 200 205

Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly Ala
210 215 220

Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Ala Arg Ala Thr His
225 230 235 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
245 250 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
260 265 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Trp Ser Asn
275 280 285

Ala Thr His Cys Ala Arg Met Thr Asn Cys Cys Asn Met Thr Asn Ala
290 295 300

Cys Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Ala Cys
305 310 315 320

Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
325 330 335

Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn Cys
340 345 350

Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr Thr
355 360 365

Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala Arg
370 375 380

Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn Ala
385 390 395 400

Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr Gly
405 410 415

Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr Tyr
420 425 430

Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn Ala
435 440 445

Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly Thr
450 455 460

Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala Arg
465 470 475 480

Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg Gly
485 490 495

Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys Ala
500 505 510

Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser Asn
515 520 525

Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp
530 535 540

Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp Ser
545 550 555 560

Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala Arg
565 570 575

Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr Gly
580 585 590

Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys Ala
595 600 605

Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
610 615 620

Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn Thr
625 630 635 640

Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr Gly
645 650 655

Tyr

<210> 522
<211> 657
<212> PRT
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<400> 522

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
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Ala Arg Ala Cys Asn Cys Cys Asn Met Thr Asn Trp Ser Asn Met Thr
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Asn Trp Ser Asn Gly Thr Asn Ala Cys Asn Cys Cys Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Met Thr Asn Met Thr Asn Cys Ala Tyr Trp Ser Asn
85 90 95

Gly Ala Tyr Gly Gly Asn Ala Ala Arg Ala Cys Asn Thr Ala Tyr Met
100 105 110

Thr Asn Thr Ala Tyr Thr Gly Gly Thr Thr Tyr Met Thr Asn Cys Ala
115 120 125

Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn
130 135 140

Cys Cys Asn Cys Ala Arg Cys Cys Asn Met Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Gly Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Met Gly
165 170 175

Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
180 185 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp
195 200 205

Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly Ala
210 215 220

Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Ala Arg Ala Thr His
225 230 235 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly

245 250 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
260 265 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Trp Ser Asn
275 280 285

Ala Thr His Cys Ala Arg Met Thr Asn Cys Cys Asn Ala Thr His Ala
290 295 300

Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Tyr Gly Gly Asn Ala Cys
305 310 315 320

Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
325 330 335

Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn Cys
340 345 350

Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr Thr
355 360 365

Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala Arg
370 375 380

Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn Ala
385 390 395 400

Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr Gly
405 410 415

Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr Tyr
420 425 430

Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn Ala
435 440 445

Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly Thr
450 455 460

Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala Arg
465 470 475 480

Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg Gly
485 490 495

Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys Ala
500 505 510

Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser Asn
515 520 525

Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp
530 535 540

Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp Ser
545 550 555 560

Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala Arg
565 570 575

Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr Gly
580 585 590

Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys Ala
595 600 605

Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
610 615 620

Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn Thr
625 630 635 640

Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr Gly
645 650 655

Tyr

<210> 523
<211> 642
<212> PRT
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<400> 523

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
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Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

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Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
    50                  55                  60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Gly Gly Asn Ala Thr His Gly Cys Asn Ala Ala Tyr Thr Ala Tyr
                85                  90                  95

Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Thr
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Thr Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Met
145                 150                 155                 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Ala Cys Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Ala Ala Tyr Thr Ala
            260                 265                 270

Tyr Ala Ala Tyr Trp Ser Asn Gly Cys Asn Cys Cys Asn Thr Thr Tyr
        275                 280                 285
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Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Ala
    290                 295                 300

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Thr His Ala Ala
305                 310                 315                 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
                325                 330                 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
            340                 345                 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
        355                 360                 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
    370                 375                 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385                 390                 395                 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
                405                 410                 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
            420                 425                 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
        435                 440                 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
    450                 455                 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465                 470                 475                 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
                485                 490                 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
            500                 505                 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
        515                 520                 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
    530                 535                 540
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Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

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1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Thr His Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Gly Asn Ala Thr His Trp Ser Asn Ala Ala Tyr Gly Ala Tyr
85 90 95

Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys

100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Thr
115 120 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Met
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Ala Cys Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Ala Ala Arg Thr Ala
260 265 270

Tyr Ala Ala Tyr Trp Ser Asn Gly Thr Asn Cys Cys Asn Met Thr Asn
275 280 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Ala
290 295 300

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
325 330 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
340 345 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
355 360 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
370 375 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385 390 395 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
405 410 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
420 425 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
435 440 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
450 455 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465 470 475 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
485 490 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
500 505 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser

595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 525
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<400> 525

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Ala Arg Ala Cys Asn Cys Cys Asn Met Thr Asn Trp Ser Asn Trp Ser
20 25 30

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Met Thr Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr Met Gly Asn Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Met Thr Asn Gly Thr Asn Cys Ala Tyr Trp Ser Asn
85 90 95

Gly Ala Tyr Gly Gly Asn Ala Ala Tyr Ala Cys Asn Thr Ala Tyr Met
100 105 110

Thr Asn Trp Ser Asn Thr Gly Gly Met Thr Asn Cys Ala Arg Cys Ala
115 120 125

Arg Met Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn
130 135 140

Cys Cys Asn Met Gly Asn Met Thr Asn Met Thr Asn Ala Thr His Thr
145 150 155 160

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Ala Tyr Ala Ala Arg Ala Thr His Trp Ser Asn Ala Ala Tyr Met Gly
                165                 170                 175

Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
            180                 185                 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp
        195                 200                 205

Ser Asn Gly Gly Asn Gly Cys Asn Gly Gly Asn Ala Cys Asn Gly Ala
    210                 215                 220

Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Ala Arg Ala Thr His
225                 230                 235                 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
                245                 250                 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
            260                 265                 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Gly Cys Asn
        275                 280                 285

Ala Cys Asn Cys Ala Arg Thr Thr Tyr Cys Cys Asn Cys Ala Tyr Ala
    290                 295                 300

Cys Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Ala Cys
305                 310                 315                 320

Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Thr His Ala Ala Arg
                325                 330                 335

Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn Cys
            340                 345                 350

Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr Thr
        355                 360                 365

Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala Arg
    370                 375                 380

Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn Ala
385                 390                 395                 400

Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr Gly
                405                 410                 415
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Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr Tyr
            420                 425                 430

Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn Ala
        435                 440                 445

Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly Thr
    450                 455                 460

Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala Arg
465                 470                 475                 480

Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg Gly
                485                 490                 495

Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys Ala
            500                 505                 510

Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser Asn
        515                 520                 525

Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp
    530                 535                 540

Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp Ser
545                 550                 555                 560

Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala Arg
                565                 570                 575

Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr Gly
            580                 585                 590

Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys Ala
        595                 600                 605

Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
    610                 615                 620

Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn Thr
625                 630                 635                 640

Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr Gly
                645                 650                 655
```

Tyr

<210> 526
<211> 657
<212> PRT
<213> Homo Sapiens

<400> 526

Gly Ala Arg Ala Thr His Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Ala Cys Asn Cys Cys Asn Met Thr Asn Trp Ser Asn Trp Ser
20 25 30

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Met Thr Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr Met Gly Asn Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Met Thr Asn Gly Thr Asn Cys Ala Tyr Trp Ser Asn
85 90 95

Gly Ala Tyr Gly Gly Asn Ala Ala Tyr Ala Cys Asn Thr Ala Tyr Met
100 105 110

Thr Asn Trp Ser Asn Thr Gly Gly Met Thr Asn Cys Ala Arg Cys Ala
115 120 125

Arg Met Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn
130 135 140

Cys Cys Asn Met Gly Asn Met Thr Asn Met Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Ala Ala Arg Ala Thr His Trp Ser Asn Ala Ala Tyr Met Gly
165 170 175

Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
180 185 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Ala
195 200 205

Cys Asn Gly Gly Asn Gly Cys Asn Gly Gly Asn Ala Cys Asn Gly Ala
210 215 220

Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Ala Arg Ala Thr His
225 230 235 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
245 250 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
260 265 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Gly Cys Asn
275 280 285

Ala Cys Asn Cys Ala Arg Thr Thr Tyr Cys Cys Asn Cys Ala Tyr Ala
290 295 300

Cys Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Ala Cys
305 310 315 320

Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
325 330 335

Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn Cys
340 345 350

Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr Thr
355 360 365

Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala Arg
370 375 380

Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn Ala
385 390 395 400

Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr Gly
405 410 415

Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr Tyr
420 425 430

Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn Ala
435 440 445

Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly Thr

```
    450                 455                 460

Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala Arg
465                 470                 475                 480

Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg Gly
                485                 490                 495

Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys Ala
            500                 505                 510

Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser Asn
        515                 520                 525

Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp
    530                 535                 540

Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp Ser
545                 550                 555                 560

Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala Arg
                565                 570                 575

Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr Gly
            580                 585                 590

Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys Ala
        595                 600                 605

Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
    610                 615                 620

Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn Thr
625                 630                 635                 640

Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr Gly
                645                 650                 655

Tyr
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<210> 527
<211> 645
<212> PRT
<213> Homo Sapiens

<400> 527

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Gly Ala Arg Ala Thr His Gly Thr Asn Met Thr Asn Ala Cys Asn Cys
1               5                   10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Gly Asn Ala Cys Asn Met Thr
            20                  25                  30

Asn Trp Ser Asn Met Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn
        35                  40                  45

Gly Ala Arg Met Gly Asn Gly Cys Asn Ala Cys Asn Met Thr Asn Trp
    50                  55                  60

Ser Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Ala Cys Asn Gly Thr Asn Ala Thr His Trp Ser Asn Trp Ser Asn
                85                  90                  95

Thr Ala Tyr Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys
            100                 105                 110

Ala Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala
        115                 120                 125

Arg Gly Cys Asn Cys Cys Asn Met Gly Asn Met Thr Asn Met Thr Asn
    130                 135                 140

Ala Thr His Trp Ser Asn Gly Gly Asn Gly Cys Asn Trp Ser Asn Trp
145                 150                 155                 160

Ser Asn Met Gly Asn Gly Cys Asn Ala Cys Asn Gly Gly Asn Ala Thr
                165                 170                 175

His Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn
            180                 185                 190

Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala
        195                 200                 205

Cys Asn Gly Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys
    210                 215                 220

Asn Ala Thr His Trp Ser Asn Met Gly Asn Met Thr Asn Gly Ala Arg
225                 230                 235                 240

Cys Cys Asn Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Gly
                245                 250                 255
```

```
Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala
            260                 265                 270

Arg Thr Ala Tyr Gly Gly Asn Trp Ser Asn Trp Ser Asn Cys Cys Asn
        275                 280                 285

Met Gly Asn Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly
    290                 295                 300

Gly Asn Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr
305                 310                 315                 320

His Ala Ala Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn
                325                 330                 335

Gly Cys Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala
            340                 345                 350

Thr His Thr Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala
        355                 360                 365

Tyr Gly Ala Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn
    370                 375                 380

Gly Gly Asn Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly
385                 390                 395                 400

Thr Asn Thr Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala
                405                 410                 415

Tyr Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg
            420                 425                 430

Gly Cys Asn Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala
        435                 440                 445

Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr
    450                 455                 460

Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn
465                 470                 475                 480

Cys Ala Arg Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly
                485                 490                 495
```

Ala Arg Cys Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala
500 505 510

Tyr Trp Ser Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn
515 520 525

Trp Ser Asn Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met
530 535 540

Thr Asn Trp Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala
545 550 555 560

Tyr Gly Ala Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn
565 570 575

Thr Ala Tyr Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala
580 585 590

Cys Asn Cys Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser
595 600 605

Asn Trp Ser Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg
610 615 620

Trp Ser Asn Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly
625 630 635 640

Ala Arg Thr Gly Tyr
645

<210> 528
<211> 639
<212> PRT
<213> Homo Sapiens

<400> 528

Gly Ala Arg Ala Thr His Gly Thr Asn Met Thr Asn Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Gly Asn Ala Cys Asn Met Thr
20 25 30

Asn Trp Ser Asn Met Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Ala Cys Asn Met Thr Asn Trp
50 55 60

Ser Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Gly Thr Asn Trp Ser Asn Met Gly Asn Met Thr Asn
85 90 95

Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala
100 105 110

Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys
115 120 125

Asn Met Gly Asn Met Thr Asn Met Thr Asn Ala Thr His Thr Ala Tyr
130 135 140

Gly Gly Asn Gly Cys Asn Trp Ser Asn Met Gly Asn Met Gly Asn Gly
145 150 155 160

Cys Asn Ala Cys Asn Gly Gly Asn Ala Thr His Cys Cys Asn Gly Ala
165 170 175

Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn
180 185 190

Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly Ala Tyr Thr
195 200 205

Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr His Trp Ser
210 215 220

Asn Met Gly Asn Met Thr Asn Gly Ala Arg Cys Cys Asn Gly Ala Arg
225 230 235 240

Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr
245 250 255

Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala Tyr Gly Gly
260 265 270

Asn Trp Ser Asn Trp Ser Asn Cys Cys Asn Met Gly Asn Trp Ser Asn
275 280 285

Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Ala
290 295 300

Ala Arg Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg Met Gly

305 310 315 320

Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn Cys Cys Asn
325 330 335

Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr Thr Tyr Cys
340 345 350

Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala Arg Cys Ala
355 360 365

Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn Ala Cys Asn
370 375 380

Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr Gly Tyr Met
385 390 395 400

Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr Tyr Thr Ala
405 410 415

Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn Ala Ala Arg
420 425 430

Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly Thr Asn Gly
435 440 445

Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala Arg Trp Ser
450 455 460

Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg Gly Ala Arg
465 470 475 480

Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys Ala Arg Gly
485 490 495

Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser Asn Ala Cys
500 505 510

Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
515 520 525

Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp Ser Asn Ala
530 535 540

Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala Arg Ala Ala
545 550 555 560

```
Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr Gly Cys Asn
                565                 570                 575

Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys Ala Tyr Cys
            580                 585                 590

Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Cys Cys
        595                 600                 605

Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn Thr Thr Tyr
    610                 615                 620

Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr Gly Tyr
625                 630                 635
```

<210> 529
<211> 642
<212> PRT
<213> Homo Sapiens

<400> 529

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Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1               5                   10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
            20                  25                  30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
    50                  55                  60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Gly Gly Asn Ala Thr His Met Gly Asn Ala Ala Tyr Gly Ala Tyr
                85                  90                  95

Met Thr Asn Gly Gly Asn Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Met Gly Asn Met Thr Asn Ala Thr His
    130                 135                 140
```

```
Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Met
145                 150                 155                 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
        195                 200                 205

Ala Arg Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Ala Cys Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Met Thr Asn Cys Ala Arg Cys Ala
            260                 265                 270

Tyr Ala Ala Tyr Trp Ser Asn Thr Ala Tyr Cys Cys Asn Cys Cys Asn
        275                 280                 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala
    290                 295                 300

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305                 310                 315                 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
                325                 330                 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
            340                 345                 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
        355                 360                 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
    370                 375                 380
```

```
Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385                 390                 395                 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
                405                 410                 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
            420                 425                 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
        435                 440                 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
    450                 455                 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465                 470                 475                 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
                485                 490                 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
            500                 505                 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
        515                 520                 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
    530                 535                 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545                 550                 555                 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
                565                 570                 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
            580                 585                 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
        595                 600                 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
    610                 615                 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625                 630                 635                 640
```

Gly Tyr

<210> 530
<211> 660
<212> PRT
<213> Homo Sapiens

<400> 530

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Met Thr
20 25 30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Met Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Gly Thr Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn
85 90 95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
100 105 110

Ala Tyr Met Thr Asn Gly Thr Asn Thr Gly Gly Thr Ala Tyr Cys Ala
115 120 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
130 135 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Thr Thr Tyr Ala
145 150 155 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Ala Cys
165 170 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
180 185 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Ala Cys Asn Gly

195 200 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys
210 215 220

Asn Gly Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn
225 230 235 240

Ala Thr His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Gly
245 250 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
260 265 270

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
275 280 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Thr Thr Tyr Cys Cys Asn Thr
290 295 300

Gly Gly Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly
305 310 315 320

Asn Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
325 330 335

Ala Ala Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly
340 345 350

Cys Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr
355 360 365

His Thr Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr
370 375 380

Gly Ala Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly
385 390 395 400

Gly Asn Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr
405 410 415

Asn Thr Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr
420 425 430

Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly
435 440 445

```
Cys Asn Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala
    450                 455                 460

Arg Gly Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn
465                 470                 475                 480

Cys Ala Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys
                485                 490                 495

Ala Arg Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala
            500                 505                 510

Arg Cys Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr
        515                 520                 525

Trp Ser Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp
    530                 535                 540

Ser Asn Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr
545                 550                 555                 560

Asn Trp Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr
                565                 570                 575

Gly Ala Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr
            580                 585                 590

Ala Tyr Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys
        595                 600                 605

Asn Cys Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn
    610                 615                 620

Trp Ser Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp
625                 630                 635                 640

Ser Asn Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala
                645                 650                 655

Arg Thr Gly Tyr
            660
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<210> 531
<211> 660
<212> PRT
<213> Homo Sapiens

<400> 531

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Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
1               5                  10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Met Thr
            20                  25                  30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Met Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Arg Met Gly Asn Gly Cys Asn Ala Cys Asn Ala Thr His Ala
    50                  55                  60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Trp Ser Asn Gly Thr Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn
                85                  90                  95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
            100                 105                 110

Ala Tyr Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
        115                 120                 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
    130                 135                 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala
145                 150                 155                 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Ala Cys
                165                 170                 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
            180                 185                 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
        195                 200                 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys
    210                 215                 220

Asn Gly Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn
225                 230                 235                 240
```

```
Ala Thr His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Gly
                245                 250                 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
            260                 265                 270

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
        275                 280                 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Ala Cys Asn Ala Cys Asn Thr
    290                 295                 300

Gly Gly Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly
305                 310                 315                 320

Asn Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
                325                 330                 335

Ala Ala Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly
            340                 345                 350

Cys Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr
        355                 360                 365

His Thr Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr
    370                 375                 380

Gly Ala Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly
385                 390                 395                 400

Gly Asn Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr
                405                 410                 415

Asn Thr Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr
            420                 425                 430

Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly
        435                 440                 445

Cys Asn Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala
    450                 455                 460

Arg Gly Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn
465                 470                 475                 480

Cys Ala Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys
                485                 490                 495
```

Ala Arg Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala
500 505 510

Arg Cys Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr
515 520 525

Trp Ser Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp
530 535 540

Ser Asn Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr
545 550 555 560

Asn Trp Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr
565 570 575

Gly Ala Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr
580 585 590

Ala Tyr Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys
595 600 605

Asn Cys Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn
610 615 620

Trp Ser Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp
625 630 635 640

Ser Asn Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala
645 650 655

Arg Thr Gly Tyr
660

<210> 532
<211> 660
<212> PRT
<213> Homo Sapiens

<400> 532

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Met Thr
20 25 30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Met Thr Asn Gly Gly Asn

35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Ala Ala Tyr Gly Thr Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn
85 90 95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
100 105 110

Ala Tyr Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
115 120 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
130 135 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala
145 150 155 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Ala Cys
165 170 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
180 185 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
195 200 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys
210 215 220

Asn Gly Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn
225 230 235 240

Ala Thr His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Gly
245 250 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
260 265 270

Asn Thr Ala Tyr Thr Thr Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
275 280 285

```
Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Cys Asn Cys Cys Asn Met
    290                 295                 300

Gly Asn Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly
305                 310                 315                 320

Asn Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
                325                 330                 335

Ala Ala Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly
            340                 345                 350

Cys Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr
        355                 360                 365

His Thr Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr
    370                 375                 380

Gly Ala Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly
385                 390                 395                 400

Gly Asn Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr
                405                 410                 415

Asn Thr Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr
            420                 425                 430

Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly
        435                 440                 445

Cys Asn Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala
    450                 455                 460

Arg Gly Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn
465                 470                 475                 480

Cys Ala Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys
                485                 490                 495

Ala Arg Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala
            500                 505                 510

Arg Cys Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr
        515                 520                 525

Trp Ser Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp
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530 535 540

Ser Asn Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr
545 550 555 560

Asn Trp Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr
565 570 575

Gly Ala Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr
580 585 590

Ala Tyr Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys
595 600 605

Asn Cys Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn
610 615 620

Trp Ser Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp
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Ser Asn Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala
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Arg Thr Gly Tyr
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Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Met Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

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Arg Ala Ala Tyr Gly Thr Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn
                85                  90                  95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
            100                 105                 110

Ala Tyr Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
        115                 120                 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
    130                 135                 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala
145                 150                 155                 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Ala Cys
                165                 170                 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
            180                 185                 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
        195                 200                 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys
    210                 215                 220

Asn Gly Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn
225                 230                 235                 240

Ala Thr His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Gly
                245                 250                 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
            260                 265                 270

Asn Thr Ala Tyr Thr Thr Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
        275                 280                 285

Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Cys Asn Cys Cys Asn Met
    290                 295                 300

Gly Asn Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly
305                 310                 315                 320

Asn Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
                325                 330                 335
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Ala Ala Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly
340 345 350

Cys Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr
355 360 365

His Thr Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr
370 375 380

Gly Ala Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly
385 390 395 400

Gly Asn Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr
405 410 415

Asn Thr Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr
420 425 430

Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly
435 440 445

Cys Asn Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala
450 455 460

Arg Gly Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn
465 470 475 480

Cys Ala Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys
485 490 495

Ala Arg Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala
500 505 510

Arg Cys Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr
515 520 525

Trp Ser Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp
530 535 540

Ser Asn Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr
545 550 555 560

Asn Trp Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr
565 570 575

Gly Ala Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr
580 585 590

Ala Tyr Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys
595 600 605

Asn Cys Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn
610 615 620

Trp Ser Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp
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Ser Asn Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala
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Arg Thr Gly Tyr
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Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Met Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Gly Thr Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn
85 90 95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
100 105 110

Ala Tyr Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
115 120 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
130 135 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala
145 150 155 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Ala Cys
165 170 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
180 185 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Gly Gly Asn Gly
195 200 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys
210 215 220

Asn Gly Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn
225 230 235 240

Ala Thr His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Gly
245 250 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
260 265 270

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
275 280 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Ala Thr His Trp Ser Asn Met
290 295 300

Gly Asn Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly
305 310 315 320

Asn Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
325 330 335

Ala Ala Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly
340 345 350

Cys Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr
355 360 365

His Thr Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr

370 375 380

Gly Ala Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly
385 390 395 400

Gly Asn Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr
405 410 415

Asn Thr Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr
420 425 430

Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly
435 440 445

Cys Asn Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala
450 455 460

Arg Gly Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn
465 470 475 480

Cys Ala Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys
485 490 495

Ala Arg Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala
500 505 510

Arg Cys Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr
515 520 525

Trp Ser Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp
530 535 540

Ser Asn Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr
545 550 555 560

Asn Trp Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr
565 570 575

Gly Ala Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr
580 585 590

Ala Tyr Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys
595 600 605

Asn Cys Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn
610 615 620

Trp Ser Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp
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Arg Thr Gly Tyr
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Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Met Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Gly Thr Asn Met Thr Asn Thr Ala Tyr Ala Ala Tyr
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Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
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Ala Tyr Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
115 120 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
130 135 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala
145 150 155 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Ala Cys
165 170 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
180 185 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
195 200 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys
210 215 220

Asn Gly Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn
225 230 235 240

Ala Thr His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Gly
245 250 255

Cys Asn Gly Ala Tyr Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
260 265 270

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
275 280 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Ala Cys Asn Ala Cys Asn Thr
290 295 300

Gly Gly Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly
305 310 315 320

Asn Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
325 330 335

Ala Ala Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly
340 345 350

Cys Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr
355 360 365

His Thr Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr
370 375 380

Gly Ala Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly
385 390 395 400

Gly Asn Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr
405 410 415

Asn Thr Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr
420 425 430

Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly
435 440 445

Cys Asn Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala
450 455 460

Arg Gly Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn
465 470 475 480

Cys Ala Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys
485 490 495

Ala Arg Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala
500 505 510

Arg Cys Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr
515 520 525

Trp Ser Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp
530 535 540

Ser Asn Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr
545 550 555 560

Asn Trp Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr
565 570 575

Gly Ala Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr
580 585 590

Ala Tyr Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys
595 600 605

Asn Cys Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn
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Trp Ser Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp
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Ser Asn Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala
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Arg Thr Gly Tyr
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Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Met Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Gly Thr Asn Met Thr Asn Thr Ala Tyr Ala Ala Tyr
85 90 95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
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Ala Tyr Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
115 120 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
130 135 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala
145 150 155 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Ala Cys
165 170 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
180 185 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
195 200 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys

210 215 220

Asn Gly Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn
225 230 235 240

Ala Thr His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Gly
245 250 255

Cys Asn Gly Ala Tyr Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
260 265 270

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
275 280 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Ala Cys Asn Ala Cys Asn Thr
290 295 300

Gly Gly Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly
305 310 315 320

Asn Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
325 330 335

Ala Ala Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly
340 345 350

Cys Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr
355 360 365

His Thr Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr
370 375 380

Gly Ala Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly
385 390 395 400

Gly Asn Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr
405 410 415

Asn Thr Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr
420 425 430

Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly
435 440 445

Cys Asn Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala
450 455 460

Arg Gly Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn
465 470 475 480

Cys Ala Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys
485 490 495

Ala Arg Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala
500 505 510

Arg Cys Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr
515 520 525

Trp Ser Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp
530 535 540

Ser Asn Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr
545 550 555 560

Asn Trp Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr
565 570 575

Gly Ala Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr
580 585 590

Ala Tyr Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys
595 600 605

Asn Cys Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn
610 615 620

Trp Ser Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp
625 630 635 640

Ser Asn Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala
645 650 655

Arg Thr Gly Tyr
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<210> 537
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<400> 537

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
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            20                  25                  30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Met Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Arg Met Gly Asn Gly Cys Asn Ala Cys Asn Ala Thr His Ala
    50                  55                  60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Trp Ser Asn Gly Thr Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn
                85                  90                  95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
            100                 105                 110

Ala Tyr Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
        115                 120                 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
    130                 135                 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Gly Thr Asn Met Thr Asn Ala
145                 150                 155                 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Ala Cys
                165                 170                 175

Asn Met Gly Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
            180                 185                 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
        195                 200                 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys
    210                 215                 220

Asn Gly Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn
225                 230                 235                 240

Ala Thr His Trp Ser Asn Gly Gly Asn Met Thr Asn Cys Ala Arg Gly
                245                 250                 255
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Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Met Thr
            260                 265                 270

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
        275                 280                 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Ala Cys Asn Ala Thr Gly Thr
    290                 295                 300

Thr Tyr Trp Ser Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly
305                 310                 315                 320

Asn Ala Cys Asn Ala Ala Arg Met Thr Asn Gly Ala Arg Ala Thr His
                325                 330                 335

Ala Ala Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly
            340                 345                 350

Cys Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr
        355                 360                 365

His Thr Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr
    370                 375                 380

Gly Ala Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly
385                 390                 395                 400

Gly Asn Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr
                405                 410                 415

Asn Thr Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr
            420                 425                 430

Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly
        435                 440                 445

Cys Asn Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala
    450                 455                 460

Arg Gly Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn
465                 470                 475                 480

Cys Ala Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys
                485                 490                 495

Ala Arg Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala
            500                 505                 510
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Arg Cys Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr
515 520 525

Trp Ser Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp
530 535 540

Ser Asn Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr
545 550 555 560

Asn Trp Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr
565 570 575

Gly Ala Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr
580 585 590

Ala Tyr Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys
595 600 605

Asn Cys Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn
610 615 620

Trp Ser Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp
625 630 635 640

Ser Asn Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala
645 650 655

Arg Thr Gly Tyr
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<210> 538
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<400> 538

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Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Met Thr
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Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Met Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Ala Cys Asn Ala Thr His Ala

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    50                  55                  60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Trp Ser Asn Gly Thr Asn Met Thr Asn Gly Ala Tyr Trp Ser Asn
                85                  90                  95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
            100                 105                 110

Ala Tyr Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
        115                 120                 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
    130                 135                 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala
145                 150                 155                 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Ala Cys
                165                 170                 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
            180                 185                 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
        195                 200                 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys
    210                 215                 220

Asn Gly Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn
225                 230                 235                 240

Ala Thr His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Gly
                245                 250                 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
            260                 265                 270

Asn Thr Thr Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Tyr Cys Ala Arg
        275                 280                 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Ala Cys Asn Cys Cys Asn Met
    290                 295                 300
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Thr Asn Ala Cys Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly
305 310 315 320

Asn Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Cys Asn Ala Thr His
325 330 335

Ala Ala Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly
340 345 350

Cys Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr
355 360 365

His Thr Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr
370 375 380

Gly Ala Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly
385 390 395 400

Gly Asn Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr
405 410 415

Asn Thr Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr
420 425 430

Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly
435 440 445

Cys Asn Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala
450 455 460

Arg Gly Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn
465 470 475 480

Cys Ala Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys
485 490 495

Ala Arg Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala
500 505 510

Arg Cys Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr
515 520 525

Trp Ser Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp
530 535 540

Ser Asn Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr

545 550 555 560

Asn Trp Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr
565 570 575

Gly Ala Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr
580 585 590

Ala Tyr Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys
595 600 605

Asn Cys Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn
610 615 620

Trp Ser Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp
625 630 635 640

Ser Asn Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala
645 650 655

Arg Thr Gly Tyr
660

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<400> 539

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1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Met Thr
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Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Met Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Ala Thr His Met Thr Asn Thr Ala Tyr Met Gly Asn
85 90 95

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Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
            100                 105                 110

Ala Tyr Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
        115                 120                 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
    130                 135                 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala
145                 150                 155                 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Gly Cys
                165                 170                 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
            180                 185                 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
        195                 200                 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys
    210                 215                 220

Asn Gly Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn
225                 230                 235                 240

Ala Thr His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Gly
                245                 250                 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
            260                 265                 270

Asn Thr Ala Tyr Thr Thr Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
        275                 280                 285

Thr Ala Tyr Thr Thr Tyr Ala Thr His Ala Cys Asn Cys Cys Asn Met
    290                 295                 300

Thr Asn Ala Cys Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly
305                 310                 315                 320

Asn Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
                325                 330                 335

Ala Ala Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly
            340                 345                 350
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Cys Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr
        355                 360                 365

His Thr Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr
    370                 375                 380

Gly Ala Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly
385                 390                 395                 400

Gly Asn Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr
                405                 410                 415

Asn Thr Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr
            420                 425                 430

Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly
        435                 440                 445

Cys Asn Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala
    450                 455                 460

Arg Gly Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn
465                 470                 475                 480

Cys Ala Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys
                485                 490                 495

Ala Arg Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala
            500                 505                 510

Arg Cys Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr
        515                 520                 525

Trp Ser Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp
    530                 535                 540

Ser Asn Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr
545                 550                 555                 560

Asn Trp Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr
                565                 570                 575

Gly Ala Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr
            580                 585                 590
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Ala Tyr Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys
595 600 605

Asn Cys Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn
610 615 620

Trp Ser Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp
625 630 635 640

Ser Asn Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala
645 650 655

Arg Thr Gly Tyr
660

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<400> 540

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Cys Ala Tyr Thr Ala Tyr
85 90 95

Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Thr Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Trp Ser Asn Met Thr Asn Ala Thr His
130 135 140

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Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Met
145                 150                 155                 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Ala Ala Arg Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Ala Cys Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala
            260                 265                 270

Tyr Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr Cys Cys Asn Thr Thr Tyr
        275                 280                 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Ala
    290                 295                 300

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Thr His Ala Ala
305                 310                 315                 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
                325                 330                 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
            340                 345                 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
        355                 360                 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
    370                 375                 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
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385 390 395 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
405 410 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
420 425 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
435 440 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
450 455 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465 470 475 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
485 490 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
500 505 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 541
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<400> 541

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Gly Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Thr Ala Tyr
85 90 95

Met Thr Asn Gly Cys Asn Thr Gly Gly Met Thr Asn Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Trp Ser Asn Met Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Met
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Ala Cys Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala
260 265 270

Tyr Ala Ala Tyr Ala Cys Asn Thr Ala Tyr Cys Cys Asn Thr Thr Tyr
275 280 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Ala
290 295 300

Cys Asn Ala Ala Arg Ala Thr Gly Gly Ala Tyr Ala Thr His Ala Ala
305 310 315 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
325 330 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
340 345 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
355 360 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
370 375 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385 390 395 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
405 410 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
420 425 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
435 440 445

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Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
    450                 455                 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465                 470                 475                 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
                485                 490                 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
            500                 505                 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
        515                 520                 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
    530                 535                 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545                 550                 555                 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
                565                 570                 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
            580                 585                 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
        595                 600                 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
    610                 615                 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625                 630                 635                 640

Gly Tyr
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<210> 542
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<212> PRT
<213> Homo Sapiens

<400> 542

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            20                  25                  30

Asn Trp Ser Asn Gly Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn
        35                  40                  45

Gly Ala Arg Met Gly Asn Gly Cys Asn Ala Cys Asn Met Thr Asn Trp
    50                  55                  60

Ser Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Trp Ser Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr
                85                  90                  95

Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Gly Ala Tyr Cys Cys Asn Gly Gly Asn Cys Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Met Gly Asn Met Thr Asn Met Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Gly Asn Gly Cys Asn Trp Ser Asn Met Gly Asn Met
145                 150                 155                 160

Gly Asn Gly Cys Asn Ala Cys Asn Gly Gly Asn Ala Thr His Cys Cys
                165                 170                 175

Asn Gly Cys Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
        195                 200                 205

Ala Arg Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Trp Ser Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Gly Thr Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Cys Ala
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260 265 270

Tyr Ala Ala Tyr Ala Ala Tyr Thr Gly Gly Cys Cys Asn Cys Cys Asn
275 280 285

Thr Gly Gly Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly
290 295 300

Gly Asn Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr
305 310 315 320

His Ala Ala Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn
325 330 335

Gly Cys Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala
340 345 350

Thr His Thr Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala
355 360 365

Tyr Gly Ala Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn
370 375 380

Gly Gly Asn Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly
385 390 395 400

Thr Asn Thr Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala
405 410 415

Tyr Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg
420 425 430

Gly Cys Asn Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala
435 440 445

Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr
450 455 460

Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn
465 470 475 480

Cys Ala Arg Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly
485 490 495

Ala Arg Cys Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala
500 505 510

Tyr Trp Ser Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn
515 520 525

Trp Ser Asn Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met
530 535 540

Thr Asn Trp Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala
545 550 555 560

Tyr Gly Ala Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn
565 570 575

Thr Ala Tyr Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala
580 585 590

Cys Asn Cys Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser
595 600 605

Asn Trp Ser Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg
610 615 620

Trp Ser Asn Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly
625 630 635 640

Ala Arg Thr Gly Tyr
645

<210> 543
<211> 642
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<400> 543

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Gly Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

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Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Met Gly Asn Thr Gly Gly
                85                  90                  95

Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Met
145                 150                 155                 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Ala Cys Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Gly Cys
            260                 265                 270

Asn Ala Ala Tyr Trp Ser Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn
        275                 280                 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala
    290                 295                 300

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Thr Thr Tyr Ala Ala
305                 310                 315                 320
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Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
                325                 330                 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
            340                 345                 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
        355                 360                 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
    370                 375                 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385                 390                 395                 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
                405                 410                 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
            420                 425                 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
        435                 440                 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
    450                 455                 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465                 470                 475                 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
                485                 490                 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
            500                 505                 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
        515                 520                 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
    530                 535                 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545                 550                 555                 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
                565                 570                 575
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Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 544
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<212> PRT
<213> Homo Sapiens

<400> 544

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
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Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Ala Thr His Trp Ser Asn Ala Cys Asn Thr Ala Tyr
85 90 95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Thr Thr Tyr Met Thr Asn Ala Thr His

130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Met
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Gly Cys Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
260 265 270

Asn Cys Ala Tyr Trp Ser Asn Gly Cys Asn Cys Cys Asn Thr Thr Tyr
275 280 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Ala
290 295 300

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Thr His Ala Ala
305 310 315 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
325 330 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
340 345 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
355 360 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
370 375 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385 390 395 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
405 410 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
420 425 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
435 440 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
450 455 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465 470 475 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
485 490 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
500 505 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr

625 630 635 640

Gly Tyr

<210> 545
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<212> PRT
<213> Homo Sapiens

<400> 545

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Met Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Ala Cys Asn Ala Thr His Trp Ser Asn Ala Thr His Thr Ala Tyr
85 90 95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Met
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

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Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Ala Cys Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
            260                 265                 270

Asn Thr Ala Tyr Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn
        275                 280                 285

Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Ala Cys Asn Ala
    290                 295                 300

Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg Met Gly
305                 310                 315                 320

Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn Cys Cys Asn
                325                 330                 335

Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr Thr Tyr Cys
            340                 345                 350

Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala Arg Cys Ala
        355                 360                 365

Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn Ala Cys Asn
    370                 375                 380

Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr Gly Tyr Met
385                 390                 395                 400

Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr Tyr Thr Ala
                405                 410                 415

Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn Ala Ala Arg
            420                 425                 430

Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly Thr Asn Gly
        435                 440                 445
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Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala Arg Trp Ser
450 455 460

Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg Gly Ala Arg
465 470 475 480

Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys Ala Arg Gly
485 490 495

Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser Asn Ala Cys
500 505 510

Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
515 520 525

Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp Ser Asn Ala
530 535 540

Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala Arg Ala Ala
545 550 555 560

Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr Gly Cys Asn
565 570 575

Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys Ala Tyr Cys
580 585 590

Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Cys Cys
595 600 605

Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn Thr Thr Tyr
610 615 620

Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr Gly Tyr
625 630 635

<210> 546
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Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr

20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Ala Thr His Met Gly Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Met Gly Asn Cys Cys Asn Gly Gly Asn Ala Ala Tyr Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Met
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
210 215 220

His Met Gly Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Ala Cys Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
260 265 270

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Asn Thr Ala Tyr Trp Ser Asn Ala Thr His Cys Cys Asn Met Thr Asn
        275                 280                 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Ala
    290                 295                 300

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305                 310                 315                 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
                325                 330                 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
            340                 345                 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
        355                 360                 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
    370                 375                 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385                 390                 395                 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
                405                 410                 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
            420                 425                 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
        435                 440                 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
    450                 455                 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465                 470                 475                 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
                485                 490                 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
            500                 505                 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
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515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 547
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<212> PRT
<213> Homo Sapiens

<400> 547

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Gly
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

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Arg Ala Cys Asn Ala Thr His Trp Ser Asn Met Gly Asn Thr Ala Tyr
                85                  90                  95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Met
145                 150                 155                 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr
    210                 215                 220

Asn Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Ala Cys Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Ala Thr
            260                 265                 270

His Thr Ala Tyr Trp Ser Asn Ala Cys Asn Trp Ser Asn Ala Thr His
        275                 280                 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala
    290                 295                 300

Cys Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305                 310                 315                 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
                325                 330                 335
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Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
340 345 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
355 360 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
370 375 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385 390 395 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
405 410 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
420 425 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
435 440 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
450 455 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465 470 475 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
485 490 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
500 505 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 548
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<212> PRT
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<400> 548

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
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Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Met Gly Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Gly Thr Asn Met Thr Asn Ala Thr His
130 135 140

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Thr Ala Tyr Gly Cys Asn Gly Ala Arg Trp Ser Asn Trp Ser Asn Met
145                 150                 155                 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Ala Cys Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
            260                 265                 270

Asn Thr Ala Tyr Ala Thr His Ala Cys Asn Cys Cys Asn Ala Thr His
        275                 280                 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala
    290                 295                 300

Cys Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Thr
305                 310                 315                 320

His Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
                325                 330                 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
            340                 345                 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
        355                 360                 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
    370                 375                 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
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385 390 395 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
405 410 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
420 425 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
435 440 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
450 455 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465 470 475 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
485 490 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
500 505 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 549
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<400> 549

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Ala Thr His Trp Ser Asn Met Gly Asn Thr Ala Tyr
85 90 95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Ala Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Met
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Ala Ala Tyr Thr Thr Tyr Gly Cys Asn Ala Cys Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
260 265 270

Asn Thr Ala Tyr Thr Thr Tyr Ala Cys Asn Cys Cys Asn Ala Thr His
275 280 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala
290 295 300

Cys Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
325 330 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
340 345 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
355 360 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
370 375 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385 390 395 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
405 410 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
420 425 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
435 440 445

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Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
    450                 455                 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465                 470                 475                 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
                485                 490                 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
            500                 505                 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
        515                 520                 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
    530                 535                 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545                 550                 555                 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
                565                 570                 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
            580                 585                 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
        595                 600                 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
    610                 615                 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625                 630                 635                 640

Gly Tyr
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<210> 550
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Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Ala Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Met
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Thr Thr
210 215 220

Tyr Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Ala Cys Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser

260 265 270

Asn Thr Ala Tyr Thr Thr Tyr Trp Ser Asn Cys Cys Asn Ala Thr His
275 280 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala
290 295 300

Cys Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
325 330 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
340 345 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
355 360 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
370 375 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385 390 395 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
405 410 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
420 425 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
435 440 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
450 455 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465 470 475 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
485 490 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
500 505 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 551
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<212> PRT
<213> Homo Sapiens

<400> 551

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

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Arg Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr
                85                  90                  95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Ala Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Met
145                 150                 155                 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr
    210                 215                 220

Asn Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Trp Ser Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
            260                 265                 270

Asn Thr Thr Tyr Thr Ala Tyr Ala Cys Asn Cys Cys Asn Ala Thr His
        275                 280                 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala
    290                 295                 300

Cys Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305                 310                 315                 320
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Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
                325                 330                 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
            340                 345                 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
        355                 360                 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
    370                 375                 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385                 390                 395                 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
                405                 410                 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
            420                 425                 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
        435                 440                 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
    450                 455                 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465                 470                 475                 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
                485                 490                 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
            500                 505                 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
        515                 520                 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
    530                 535                 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545                 550                 555                 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
                565                 570                 575
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Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 552
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<212> PRT
<213> Homo Sapiens

<400> 552

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His

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    130                 135                 140

Thr Ala Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Met
145                 150                 155                 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Ala Cys Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
            260                 265                 270

Asn Thr Ala Tyr Thr Thr Tyr Ala Cys Asn Cys Cys Asn Ala Thr His
        275                 280                 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala
    290                 295                 300

Cys Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305                 310                 315                 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
                325                 330                 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
            340                 345                 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
        355                 360                 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
    370                 375                 380
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Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385                 390                 395                 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
                405                 410                 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
            420                 425                 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
        435                 440                 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
    450                 455                 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465                 470                 475                 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
                485                 490                 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
            500                 505                 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
        515                 520                 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
    530                 535                 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545                 550                 555                 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
                565                 570                 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
            580                 585                 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
        595                 600                 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
    610                 615                 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
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625 630 635 640

Gly Tyr

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<400> 553

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
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Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Ala Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Met
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

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Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Trp Ser Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
            260                 265                 270

Asn Thr Thr Tyr Thr Ala Tyr Gly Cys Asn Cys Cys Asn Ala Thr His
        275                 280                 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala
    290                 295                 300

Cys Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305                 310                 315                 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
                325                 330                 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
            340                 345                 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
        355                 360                 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
    370                 375                 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385                 390                 395                 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
                405                 410                 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
            420                 425                 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
        435                 440                 445
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Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
450 455 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465 470 475 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
485 490 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
500 505 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 554
<211> 642
<212> PRT
<213> Homo Sapiens

<400> 554

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys

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Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
            20                  25                  30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
    50                  55                  60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr
                85                  90                  95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Ala Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Met
145                 150                 155                 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Ala Cys Asn Thr
                245                 250                 255
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Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
260 265 270

Asn Thr Ala Tyr Thr Thr Tyr Ala Cys Asn Cys Cys Asn Ala Thr His
275 280 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala
290 295 300

Cys Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
325 330 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
340 345 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
355 360 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
370 375 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385 390 395 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
405 410 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
420 425 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
435 440 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
450 455 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465 470 475 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
485 490 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser

500 505 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 555
<211> 642
<212> PRT
<213> Homo Sapiens

<400> 555

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

```
Cys Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Thr Ala Tyr
                85                  90                  95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Met
145                 150                 155                 160

Thr Asn Gly Ala Arg Ala Cys Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Thr Thr Tyr Ala Cys Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Ala Cys Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala
            260                 265                 270

Tyr Gly Ala Tyr Thr Ala Tyr Met Thr Asn Cys Cys Asn Thr Thr Tyr
        275                 280                 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Ala
    290                 295                 300

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Thr His Ala Ala
305                 310                 315                 320
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Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
325 330 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
340 345 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
355 360 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
370 375 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385 390 395 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
405 410 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
420 425 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
435 440 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
450 455 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465 470 475 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
485 490 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
500 505 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 556
<211> 642
<212> PRT
<213> Homo Sapiens

<400> 556

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Trp Ser Asn
85 90 95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Gly Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Met
145 150 155 160

Thr Asn Gly Ala Arg Ala Cys Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Thr Thr Tyr Ala Cys Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Ala Cys Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Gly
260 265 270

Tyr Gly Ala Tyr Gly Ala Tyr Met Thr Asn Cys Cys Asn Met Thr Asn
275 280 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Ala
290 295 300

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
325 330 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
340 345 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
355 360 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn

370 375 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385 390 395 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
405 410 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
420 425 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
435 440 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
450 455 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465 470 475 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
485 490 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
500 505 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 557
<211> 642
<212> PRT
<213> Homo Sapiens

<400> 557

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Gly Ala Tyr Thr Ala Tyr
85 90 95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Met
145 150 155 160

Thr Asn Gly Ala Arg Ala Cys Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

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Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Thr Thr Tyr Ala Cys Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Ala Cys Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Tyr Thr Ala
            260                 265                 270

Tyr Gly Ala Tyr Ala Ala Tyr Met Thr Asn Cys Cys Asn Met Thr Asn
        275                 280                 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Ala
    290                 295                 300

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305                 310                 315                 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
                325                 330                 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
            340                 345                 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
        355                 360                 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
    370                 375                 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385                 390                 395                 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
                405                 410                 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
            420                 425                 430
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Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
        435                 440                 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
    450                 455                 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465                 470                 475                 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
                485                 490                 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
            500                 505                 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
        515                 520                 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
    530                 535                 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545                 550                 555                 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
                565                 570                 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
            580                 585                 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
        595                 600                 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
    610                 615                 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625                 630                 635                 640

Gly Tyr
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<210> 558
<211> 642
<212> PRT
<213> Homo Sapiens

<400> 558

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Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1               5                  10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
            20                  25                  30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Gly Cys Asn Ala Thr His Ala
    50                  55                  60

Cys Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Thr Ala Tyr
                85                  90                  95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Met
145                 150                 155                 160

Thr Asn Gly Ala Arg Ala Cys Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Thr Thr Tyr Ala Cys Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Ala Cys Asn Thr
```

245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala
260 265 270

Tyr Gly Ala Tyr Ala Ala Tyr Met Thr Asn Cys Cys Asn Met Thr Asn
275 280 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Ala
290 295 300

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
325 330 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
340 345 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
355 360 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
370 375 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385 390 395 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
405 410 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
420 425 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
435 440 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
450 455 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465 470 475 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
485 490 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
500 505 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 559
<211> 642
<212> PRT
<213> Homo Sapiens

<400> 559

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

```
Cys Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Trp Ser Asn
                85                  90                  95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Thr His Met
145                 150                 155                 160

Thr Asn Gly Ala Arg Ala Cys Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Ala Arg Ala Cys Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Thr Thr Tyr Ala Cys Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Ala Cys Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Gly
            260                 265                 270

Tyr Gly Ala Tyr Ala Thr His Met Thr Asn Cys Cys Asn Met Thr Asn
        275                 280                 285

Trp Ser Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Ala
    290                 295                 300
```

```
Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305                 310                 315                 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
                325                 330                 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
            340                 345                 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
        355                 360                 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
    370                 375                 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385                 390                 395                 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
                405                 410                 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
            420                 425                 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
        435                 440                 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
    450                 455                 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465                 470                 475                 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
                485                 490                 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
            500                 505                 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
        515                 520                 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
    530                 535                 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545                 550                 555                 560
```

```
Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
                565                 570                 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
            580                 585                 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
        595                 600                 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
    610                 615                 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625                 630                 635                 640

Gly Tyr
```

<210> 560
<211> 642
<212> PRT
<213> Homo Sapiens

<400> 560

```
Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1               5                   10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
            20                  25                  30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
    50                  55                  60

Cys Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Trp Ser Asn
                85                  90                  95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
```

```
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Met
145                 150                 155                 160

Thr Asn Gly Ala Arg Ala Cys Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Thr Thr Tyr Ala Cys Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Ala Cys Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala
            260                 265                 270

Tyr Gly Ala Tyr Ala Ala Tyr Met Thr Asn Cys Cys Asn Met Thr Asn
        275                 280                 285

Gly Cys Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Ala
    290                 295                 300

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Met Gly
305                 310                 315                 320

Asn Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
                325                 330                 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
            340                 345                 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
        355                 360                 365
```

```
Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
    370                 375                 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385                 390                 395                 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
                405                 410                 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
            420                 425                 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
        435                 440                 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
    450                 455                 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465                 470                 475                 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
                485                 490                 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
            500                 505                 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
        515                 520                 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
    530                 535                 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545                 550                 555                 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
                565                 570                 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
            580                 585                 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
        595                 600                 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
```

610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 561
<211> 642
<212> PRT
<213> Homo Sapiens

<400> 561

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Gly Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Ala Cys Asn Ala Ala Tyr Thr Ala Tyr
85 90 95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Met
145 150 155 160

Thr Asn Gly Ala Arg Ala Cys Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

```
Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Thr Thr Tyr Ala Cys Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Ala Cys Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala
            260                 265                 270

Tyr Gly Ala Tyr Trp Ser Asn Met Thr Asn Cys Cys Asn Ala Thr His
        275                 280                 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala
    290                 295                 300

Cys Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305                 310                 315                 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
                325                 330                 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
            340                 345                 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
        355                 360                 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
    370                 375                 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385                 390                 395                 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
                405                 410                 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
            420                 425                 430
```

```
Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
        435                 440                 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
    450                 455                 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465                 470                 475                 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
                485                 490                 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
            500                 505                 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
        515                 520                 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
    530                 535                 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545                 550                 555                 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
                565                 570                 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
            580                 585                 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
        595                 600                 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
    610                 615                 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625                 630                 635                 640

Gly Tyr
```

<210> 562
<211> 642
<212> PRT
<213> Homo Sapiens

<400> 562

```
Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1               5                  10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
            20                  25                  30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
    50                  55                  60

Cys Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Thr Ala Tyr
                85                  90                  95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Met Thr Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
    130                 135                 140

Cys Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Met
145                 150                 155                 160

Thr Asn Gly Ala Arg Ala Cys Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Thr Thr Tyr Ala Cys Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240
```

```
Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Ala Cys Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala
            260                 265                 270

Tyr Gly Ala Tyr Ala Ala Tyr Met Thr Asn Cys Cys Asn Ala Thr His
        275                 280                 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala
    290                 295                 300

Cys Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305                 310                 315                 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
                325                 330                 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
            340                 345                 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
        355                 360                 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
    370                 375                 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385                 390                 395                 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
                405                 410                 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
            420                 425                 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
        435                 440                 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
    450                 455                 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465                 470                 475                 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
```

485 490 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
500 505 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 563
<211> 642
<212> PRT
<213> Homo Sapiens

<400> 563

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

```
Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
    50                  55                  60

Cys Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Gly Ala Tyr Thr Ala Tyr
                85                  90                  95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Met
145                 150                 155                 160

Thr Asn Gly Ala Arg Ala Cys Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Thr Thr Tyr Ala Cys Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Ala Cys Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Tyr Thr Ala
            260                 265                 270

Tyr Gly Ala Tyr Ala Ala Tyr Met Thr Asn Cys Cys Asn Ala Thr His
        275                 280                 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala
    290                 295                 300
```

```
Cys Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305                 310                 315                 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
                325                 330                 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
            340                 345                 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
        355                 360                 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
    370                 375                 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385                 390                 395                 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
                405                 410                 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
            420                 425                 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
        435                 440                 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
    450                 455                 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465                 470                 475                 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
                485                 490                 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
            500                 505                 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
        515                 520                 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
    530                 535                 540
```

```
Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545                 550                 555                 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
                565                 570                 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
            580                 585                 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
        595                 600                 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
    610                 615                 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625                 630                 635                 640

Gly Tyr
```

<210> 564
<211> 642
<212> PRT
<213> Homo Sapiens

<400> 564

```
Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1               5                   10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
            20                  25                  30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
    50                  55                  60

Cys Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Trp Ser Asn
                85                  90                  95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110
```

```
Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Met
145                 150                 155                 160

Thr Asn Gly Ala Arg Ala Cys Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Thr Thr Tyr Ala Cys Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Ala Cys Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Tyr Thr Ala
            260                 265                 270

Tyr Gly Ala Tyr Ala Ala Tyr Met Thr Asn Cys Cys Asn Ala Thr His
        275                 280                 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala
    290                 295                 300

Cys Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305                 310                 315                 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
                325                 330                 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
            340                 345                 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
```

355 360 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
370 375 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385 390 395 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
405 410 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
420 425 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
435 440 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
450 455 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465 470 475 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
485 490 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
500 505 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 565
<211> 1338
<212> PRT
<213> Homo Sapiens

<400> 565

Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
20 25 30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Cys Asn
35 40 45

Trp Ser Asn Gly Thr Asn Ala Ala Arg Gly Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Ala
65 70 75 80

Tyr Ala Cys Asn Thr Thr Tyr Ala Cys Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Gly Asn Ala Thr His Trp Ser Asn Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Cys Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
130 135 140

Gly Gly Asn Thr Gly Gly Ala Thr His Trp Ser Asn Gly Cys Asn Trp
145 150 155 160

Ser Asn Ala Ala Tyr Gly Gly Asn Ala Ala Tyr Ala Cys Asn Ala Ala
165 170 175

```
Tyr Thr Ala Tyr Gly Cys Asn Cys Ala Arg Ala Ala Arg Met Thr Asn
            180                 185                 190

Cys Ala Arg Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala
        195                 200                 205

Thr Gly Ala Cys Asn Ala Cys Asn Gly Ala Tyr Ala Cys Asn Trp Ser
    210                 215                 220

Asn Ala Cys Asn Trp Ser Asn Ala Cys Asn Gly Cys Asn Thr Ala Tyr
225                 230                 235                 240

Ala Thr Gly Gly Ala Arg Met Thr Asn Met Gly Asn Trp Ser Asn Met
                245                 250                 255

Thr Asn Met Gly Asn Trp Ser Asn Gly Ala Tyr Gly Ala Tyr Ala Cys
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Tyr Ala Ala Tyr Thr
    290                 295                 300

Gly Gly Ala Ala Tyr Thr Ala Tyr Gly Gly Asn Thr Thr Tyr Thr Thr
305                 310                 315                 320

Tyr Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg
                325                 330                 335

Gly Gly Asn Ala Cys Asn Met Thr Asn Gly Thr Asn Ala Cys Asn Gly
            340                 345                 350

Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys
        355                 360                 365

Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn
    370                 375                 380

Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr
385                 390                 395                 400

Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser
                405                 410                 415
```

```
Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn
            420                 425                 430

Met Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala
        435                 440                 445

Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala
    450                 455                 460

Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn
465                 470                 475                 480

Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met
                485                 490                 495

Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala
            500                 505                 510

Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn
        515                 520                 525

Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met
    530                 535                 540

Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser
545                 550                 555                 560

Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn
                565                 570                 575

Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala
            580                 585                 590

Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly
        595                 600                 605

Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg
    610                 615                 620

Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly
625                 630                 635                 640

Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala
                645                 650                 655

Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn
            660                 665                 670
```

Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys
675 680 685

Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys
690 695 700

Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr
705 710 715 720

Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys
725 730 735

Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr
740 745 750

Gly Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn
755 760 765

Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly
770 775 780

Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala
785 790 795 800

Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn
805 810 815

Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly
820 825 830

Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr
835 840 845

Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn
850 855 860

Ala Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys
865 870 875 880

Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr
885 890 895

Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn
900 905 910

Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys
915 920 925

Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly
930 935 940

Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr
945 950 955 960

Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly
965 970 975

Gly Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr
980 985 990

His Gly Ala Arg Ala Ala Arg Ala Cys Asn Ala Thr His Trp Ser Asn
995 1000 1005

Ala Ala Arg Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Ala Arg
1010 1015 1020

Cys Cys Asn Met Gly Asn Gly Ala Arg Cys Cys Asn Cys Ala Arg
1025 1030 1035

Gly Thr Asn Thr Ala Tyr Ala Cys Asn Met Thr Asn Cys Cys Asn
1040 1045 1050

Cys Cys Asn Trp Ser Asn Met Gly Asn Gly Ala Arg Gly Ala Arg
1055 1060 1065

Ala Thr Gly Ala Cys Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg
1070 1075 1080

Gly Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr Gly Tyr
1085 1090 1095

Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Gly Asn Thr Thr Tyr
1100 1105 1110

Thr Ala Tyr Cys Cys Asn Trp Ser Asn Gly Ala Tyr Ala Thr His
1115 1120 1125

Gly Cys Asn Gly Thr Asn Gly Ala Arg Thr Gly Gly Gly Ala Arg
1130 1135 1140

Trp Ser Asn Ala Ala Tyr Gly Gly Asn Cys Ala Arg Cys Cys Asn
1145 1150 1155

```
Gly Ala  Arg Ala Ala Tyr Ala  Ala Tyr Thr Ala Tyr  Ala Ala Arg
    1160                 1165                 1170

Ala Cys  Asn Ala Cys Asn Cys  Cys Asn Cys Cys Asn  Ala Thr Gly
    1175                 1180                 1185

Met Thr  Asn Gly Ala Tyr Trp  Ser Asn Gly Ala Tyr  Gly Gly Asn
    1190                 1195                 1200

Trp Ser  Asn Thr Thr Tyr Thr  Thr Tyr Met Thr Asn  Thr Ala Tyr
    1205                 1210                 1215

Trp Ser  Asn Ala Ala Arg Met  Thr Asn Ala Cys Asn  Gly Thr Asn
    1220                 1225                 1230

Gly Ala  Tyr Ala Ala Arg Trp  Ser Asn Met Gly Asn  Thr Gly Gly
    1235                 1240                 1245

Cys Ala  Arg Cys Ala Arg Gly  Gly Asn Ala Ala Tyr  Gly Thr Asn
    1250                 1255                 1260

Thr Thr  Tyr Trp Ser Asn Thr  Gly Tyr Trp Ser Asn  Gly Thr Asn
    1265                 1270                 1275

Ala Thr  Gly Cys Ala Tyr Gly  Ala Arg Gly Cys Asn  Met Thr Asn
    1280                 1285                 1290

Cys Ala  Tyr Ala Ala Tyr Cys  Ala Tyr Thr Ala Tyr  Ala Cys Asn
    1295                 1300                 1305

Cys Ala  Arg Ala Ala Arg Trp  Ser Asn Met Thr Asn  Trp Ser Asn
    1310                 1315                 1320

Met Thr  Asn Trp Ser Asn Cys  Cys Asn Gly Gly Asn  Ala Ala Arg
    1325                 1330                 1335
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<210> 566
<211> 1329
<212> PRT
<213> Homo Sapiens

<400> 566

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Cys Ala Arg Gly Thr Asn Cys Ala Tyr Met Thr Asn Gly Thr Asn Cys
1               5                  10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
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```
            20                  25                  30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Cys Asn
        35                  40                  45

Trp Ser Asn Gly Thr Asn Ala Ala Arg Gly Thr Asn Trp Ser Asn Thr
    50                  55                  60

Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Gly Gly Asn Thr Ala
65                  70                  75                  80

Tyr Ala Cys Asn Thr Thr Tyr Ala Cys Asn Gly Gly Asn Cys Ala Tyr
                85                  90                  95

Thr Ala Tyr Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
            100                 105                 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Cys Ala
        115                 120                 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
    130                 135                 140

Gly Gly Asn Thr Gly Gly Ala Thr His Ala Ala Tyr Cys Cys Asn Ala
145                 150                 155                 160

Ala Tyr Trp Ser Asn Gly Gly Asn Gly Gly Asn Ala Cys Asn Ala Ala
                165                 170                 175

Tyr Thr Gly Tyr Gly Cys Asn Cys Ala Arg Ala Ala Arg Thr Thr Tyr
            180                 185                 190

Cys Ala Arg Gly Gly Asn Met Gly Asn Gly Thr Asn Ala Cys Asn Ala
        195                 200                 205

Thr Gly Ala Cys Asn Met Gly Asn Gly Ala Tyr Ala Cys Asn Trp Ser
    210                 215                 220

Asn Ala Thr His Trp Ser Asn Ala Cys Asn Gly Cys Asn Thr Ala Tyr
225                 230                 235                 240

Ala Thr Gly Gly Ala Arg Met Thr Asn Trp Ser Asn Met Gly Asn Met
                245                 250                 255

Thr Asn Met Gly Asn Trp Ser Asn Gly Ala Tyr Gly Ala Tyr Ala Cys
            260                 265                 270
```

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Trp Ser Asn Ala Thr His Gly Cys Asn Gly
290 295 300

Thr Asn Gly Cys Asn Met Thr Asn Gly Ala Tyr Thr Ala Tyr Thr Gly
305 310 315 320

Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Met Thr Asn
325 330 335

Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly
340 345 350

Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys
355 360 365

Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn
370 375 380

Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp
385 390 395 400

Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys
405 410 415

Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr
420 425 430

Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr
435 440 445

Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys
450 455 460

Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn
465 470 475 480

Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser Asn Gly
485 490 495

Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys
500 505 510

Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp Ser Asn

515 520 525

Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn Met
530 535 540

Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys
545 550 555 560

Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr
565 570 575

Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr
580 585 590

Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala
595 600 605

Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr
610 615 620

Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala
625 630 635 640

Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg Thr Gly
645 650 655

Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn
660 665 670

Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys
675 680 685

Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser
690 695 700

Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn
705 710 715 720

Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala
725 730 735

Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn Met Gly
740 745 750

Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn
755 760 765

```
Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly
    770                 775                 780

Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys
785                 790                 795                 800

Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr
                805                 810                 815

Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly
            820                 825                 830

Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys
        835                 840                 845

Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met Gly Asn
    850                 855                 860

Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp
865                 870                 875                 880

Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr
                885                 890                 895

Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly Thr Asn
            900                 905                 910

Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met
        915                 920                 925

Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala
    930                 935                 940

Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn
945                 950                 955                 960

Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys Cys Asn Gly
                965                 970                 975

Cys Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala Arg Ala Cys
            980                 985                 990

Asn Ala Thr His Trp Ser Asn Ala  Ala Arg Ala Cys Asn  Ala Ala Arg
        995                 1000                1005

Gly Gly  Asn Cys Ala Arg Cys  Cys Asn Met Gly Asn  Gly Ala Arg
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1010 1015 1020

Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr Ala Cys Asn
1025 1030 1035

Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn Met Gly Asn
1040 1045 1050

Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn Ala Ala Arg
1055 1060 1065

Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn Met Thr Asn
1070 1075 1080

Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg
1085 1090 1095

Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Trp Ser Asn
1100 1105 1110

Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn Gly Ala Arg
1115 1120 1125

Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr Gly Gly Asn
1130 1135 1140

Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr Ala Ala Tyr
1145 1150 1155

Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn Cys Cys Asn
1160 1165 1170

Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr Trp Ser Asn
1175 1180 1185

Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr Thr Thr Tyr
1190 1195 1200

Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg Met Thr Asn
1205 1210 1215

Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg Trp Ser Asn
1220 1225 1230

Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg Gly Gly Asn
1235 1240 1245

Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn Thr Gly Tyr
1250 1255 1260

Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr Gly Ala Arg
1265 1270 1275

Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr
1280 1285 1290

Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg Trp Ser Asn
1295 1300 1305

Met Thr Asn Trp Ser Asn Met Thr Asn Trp Ser Asn Cys Cys Asn
1310 1315 1320

Gly Gly Asn Ala Ala Arg
1325

<210> 567
<211> 1329
<212> PRT
<213> Homo Sapiens

<400> 567

Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
20 25 30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Cys Asn
35 40 45

Trp Ser Asn Gly Thr Asn Ala Ala Arg Gly Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Ala
65 70 75 80

Tyr Ala Cys Asn Thr Thr Tyr Ala Cys Asn Gly Gly Asn Thr Ala Tyr
85 90 95

Thr Ala Tyr Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Cys Ala
115 120 125

```
Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
    130                 135                 140

Gly Gly Asn Thr Gly Gly Ala Thr His Ala Ala Tyr Cys Cys Asn Ala
145                 150                 155                 160

Ala Tyr Trp Ser Asn Gly Gly Asn Gly Gly Asn Ala Cys Asn Ala Ala
                165                 170                 175

Tyr Cys Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg Thr Thr Tyr
            180                 185                 190

Cys Ala Arg Gly Gly Asn Met Gly Asn Gly Thr Asn Ala Cys Asn Ala
        195                 200                 205

Thr Gly Ala Cys Asn Met Gly Asn Gly Ala Tyr Ala Cys Asn Trp Ser
    210                 215                 220

Asn Ala Thr His Trp Ser Asn Ala Cys Asn Gly Cys Asn Thr Ala Tyr
225                 230                 235                 240

Ala Thr Gly Gly Ala Arg Met Thr Asn Trp Ser Asn Met Gly Asn Met
                245                 250                 255

Thr Asn Met Gly Asn Trp Ser Asn Gly Ala Tyr Gly Ala Tyr Ala Cys
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Met Gly Asn Trp Ser Asn Ala Thr His Gly Cys Asn Gly
    290                 295                 300

Thr Asn Gly Cys Asn Met Thr Asn Gly Ala Tyr Thr Ala Tyr Thr Gly
305                 310                 315                 320

Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Met Thr Asn
                325                 330                 335

Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly
            340                 345                 350

Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys
        355                 360                 365
```

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Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn
    370                 375                 380

Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp
385                 390                 395                 400

Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys
                405                 410                 415

Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr
            420                 425                 430

Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr
        435                 440                 445

Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys
    450                 455                 460

Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn
465                 470                 475                 480

Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser Asn Gly
                485                 490                 495

Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys
            500                 505                 510

Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp Ser Asn
        515                 520                 525

Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn Met
    530                 535                 540

Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys
545                 550                 555                 560

Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr
                565                 570                 575

Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr
            580                 585                 590

Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala
        595                 600                 605

Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr
    610                 615                 620
```

```
Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala
625                 630                 635                 640

Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg Thr Gly
                645                 650                 655

Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn
            660                 665                 670

Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys
        675                 680                 685

Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser
    690                 695                 700

Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn
705                 710                 715                 720

Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala
                725                 730                 735

Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn Met Gly
            740                 745                 750

Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn
        755                 760                 765

Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly
    770                 775                 780

Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys
785                 790                 795                 800

Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr
                805                 810                 815

Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly
            820                 825                 830

Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys
        835                 840                 845

Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met Gly Asn
    850                 855                 860
```

```
Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp
865                 870                 875                 880

Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr
                885                 890                 895

Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly Thr Asn
            900                 905                 910

Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met
        915                 920                 925

Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala
    930                 935                 940

Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn
945                 950                 955                 960

Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys Cys Asn Gly
                965                 970                 975

Cys Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala Arg Ala Cys
            980                 985                 990

Asn Ala Thr His Trp Ser Asn Ala  Ala Arg Ala Cys Asn  Ala Ala Arg
        995                 1000                1005

Gly Gly  Asn Cys Ala Arg Cys  Cys Asn Met Gly Asn  Gly Ala Arg
    1010                1015                1020

Cys Cys  Asn Cys Ala Arg Gly  Thr Asn Thr Ala Tyr  Ala Cys Asn
    1025                1030                1035

Met Thr  Asn Cys Cys Asn Cys  Cys Asn Trp Ser Asn  Met Gly Asn
    1040                1045                1050

Gly Ala  Arg Gly Ala Arg Ala  Thr Gly Ala Cys Asn  Ala Ala Arg
    1055                1060                1065

Ala Ala  Tyr Cys Ala Arg Gly  Thr Asn Trp Ser Asn  Met Thr Asn
    1070                1075                1080

Ala Cys  Asn Thr Gly Tyr Met  Thr Asn Gly Thr Asn  Ala Ala Arg
    1085                1090                1095

Gly Gly  Asn Thr Thr Tyr Thr  Ala Tyr Cys Cys Asn  Trp Ser Asn
    1100                1105                1110
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Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn Gly Ala Arg
1115 1120 1125

Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr Gly Gly Asn
1130 1135 1140

Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr Ala Ala Tyr
1145 1150 1155

Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn Cys Cys Asn
1160 1165 1170

Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr Trp Ser Asn
1175 1180 1185

Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr Thr Thr Tyr
1190 1195 1200

Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg Met Thr Asn
1205 1210 1215

Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg Trp Ser Asn
1220 1225 1230

Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg Gly Gly Asn
1235 1240 1245

Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn Thr Gly Tyr
1250 1255 1260

Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr Gly Ala Arg
1265 1270 1275

Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr
1280 1285 1290

Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg Trp Ser Asn
1295 1300 1305

Met Thr Asn Trp Ser Asn Met Thr Asn Trp Ser Asn Cys Cys Asn
1310 1315 1320

Gly Gly Asn Ala Ala Arg
1325

<210> 568
<211> 1344
<212> PRT
<213> Homo Sapiens

<400> 568

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Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Gly Thr Asn Cys
1               5                  10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
            20                  25                  30

Asn Met Gly Asn Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Cys Asn
        35                  40                  45

Trp Ser Asn Gly Thr Asn Ala Ala Arg Gly Thr Asn Trp Ser Asn Thr
    50                  55                  60

Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Gly Gly Asn Thr Ala
65                  70                  75                  80

Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Gly Ala Arg Met Thr Asn
                85                  90                  95

Trp Ser Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
            100                 105                 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
        115                 120                 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
    130                 135                 140

Gly Gly Asn Trp Ser Asn Thr Thr Tyr Gly Ala Tyr Cys Cys Asn Gly
145                 150                 155                 160

Ala Arg Gly Ala Tyr Gly Gly Asn Gly Ala Arg Ala Cys Asn Ala Thr
                165                 170                 175

His Thr Ala Tyr Gly Cys Asn Cys Ala Arg Ala Ala Arg Thr Thr Tyr
            180                 185                 190

Cys Ala Arg Gly Gly Asn Met Gly Asn Gly Thr Asn Ala Cys Asn Ala
        195                 200                 205

Thr Gly Met Thr Asn Gly Ala Arg Gly Ala Tyr Ala Cys Asn Trp Ser
    210                 215                 220
```

Asn Ala Cys Asn Gly Ala Tyr Ala Cys Asn Gly Cys Asn Thr Ala Tyr
225 230 235 240

Ala Thr Gly Gly Ala Arg Met Thr Asn Trp Ser Asn Trp Ser Asn Met
245 250 255

Thr Asn Met Gly Asn Trp Ser Asn Gly Ala Arg Gly Ala Tyr Ala Cys
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Ala Cys Asn Gly Ala Arg Gly Gly Asn Gly Ala Tyr Gly
290 295 300

Gly Asn Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala
305 310 315 320

Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr Gly Gly
325 330 335

Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Ala Cys Asn Gly
340 345 350

Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys
355 360 365

Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn
370 375 380

Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly
385 390 395 400

Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser
405 410 415

Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn
420 425 430

Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr Met
435 440 445

Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr
450 455 460

Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn

```
465                 470                 475                 480

Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly
                485                 490                 495

Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly
            500                 505                 510

Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn
        515                 520                 525

Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp Ser Asn Trp
    530                 535                 540

Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr
545                 550                 555                 560

Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn
                565                 570                 575

Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr
            580                 585                 590

Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala
        595                 600                 605

Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr
    610                 615                 620

Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala
625                 630                 635                 640

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys
                645                 650                 655

Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr
            660                 665                 670

Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys
        675                 680                 685

Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys
    690                 695                 700

Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn
705                 710                 715                 720
```

Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys
725 730 735

Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys
740 745 750

Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn Met Gly Asn
755 760 765

Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr
770 775 780

Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr
785 790 795 800

Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn
805 810 815

Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr
820 825 830

Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr
835 840 845

Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn
850 855 860

Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met Gly Asn Gly
865 870 875 880

Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser
885 890 895

Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn
900 905 910

Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly Thr Asn Gly
915 920 925

Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr
930 935 940

Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr
945 950 955 960

Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala

965 970 975

Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys Cys Asn Gly Cys
980 985 990

Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala Arg Ala Cys Asn
995 1000 1005

Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg
1010 1015 1020

Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg
1025 1030 1035

Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr Ala Cys Asn
1040 1045 1050

Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn Met Gly Asn
1055 1060 1065

Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn Ala Ala Arg
1070 1075 1080

Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn Met Thr Asn
1085 1090 1095

Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg
1100 1105 1110

Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Trp Ser Asn
1115 1120 1125

Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn Gly Ala Arg
1130 1135 1140

Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr Gly Gly Asn
1145 1150 1155

Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr Ala Ala Tyr
1160 1165 1170

Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn Cys Cys Asn
1175 1180 1185

Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr Trp Ser Asn
1190 1195 1200

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Gly Ala  Tyr Gly Gly Asn Trp  Ser Asn Thr Thr Tyr  Thr Thr Tyr
    1205                 1210                 1215

Met Thr  Asn Thr Ala Tyr Trp  Ser Asn Ala Ala Arg  Met Thr Asn
    1220                 1225                 1230

Ala Cys  Asn Gly Thr Asn Gly  Ala Tyr Ala Ala Arg  Trp Ser Asn
    1235                 1240                 1245

Met Gly  Asn Thr Gly Gly Cys  Ala Arg Cys Ala Arg  Gly Gly Asn
    1250                 1255                 1260

Ala Ala  Tyr Gly Thr Asn Thr  Thr Tyr Trp Ser Asn  Thr Gly Tyr
    1265                 1270                 1275

Trp Ser  Asn Gly Thr Asn Ala  Thr Gly Cys Ala Tyr  Gly Ala Arg
    1280                 1285                 1290

Gly Cys  Asn Met Thr Asn Cys  Ala Tyr Ala Ala Tyr  Cys Ala Tyr
    1295                 1300                 1305

Thr Ala  Tyr Ala Cys Asn Cys  Ala Arg Ala Ala Arg  Trp Ser Asn
    1310                 1315                 1320

Met Thr  Asn Trp Ser Asn Met  Thr Asn Trp Ser Asn  Cys Cys Asn
    1325                 1330                 1335

Gly Gly  Asn Ala Ala Arg
    1340
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<210> 569
<211> 1344
<212> PRT
<213> Homo Sapiens

<400> 569

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Cys Ala Arg Gly Thr Asn Ala Cys Asn Met Thr Asn Ala Ala Arg Gly
1               5                  10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Thr Asn Met Thr
            20                  25                  30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Ala Cys Asn Gly Ala Arg
        35                  40                  45

Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Thr
    50                  55                  60
```

Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Ala Ala Tyr Gly Cys Asn
85 90 95

Met Gly Asn Ala Thr Gly Gly Gly Asn Gly Thr Asn Trp Ser Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Met Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Met Thr Asn Gly Cys Asn Cys Ala Tyr Ala Thr His Thr
145 150 155 160

Thr Tyr Trp Ser Asn Ala Ala Tyr Gly Ala Tyr Gly Ala Arg Ala Ala
165 170 175

Arg Trp Ser Asn Thr Ala Tyr Trp Ser Asn Ala Cys Asn Trp Ser Asn
180 185 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Met Thr Asn Ala
195 200 205

Cys Asn Ala Thr His Trp Ser Asn Ala Ala Arg Gly Ala Tyr Ala Cys
210 215 220

Asn Trp Ser Asn Ala Ala Arg Trp Ser Asn Cys Ala Arg Gly Thr Asn
225 230 235 240

Gly Thr Asn Met Thr Asn Ala Cys Asn Ala Thr Gly Ala Cys Asn Ala
245 250 255

Ala Tyr Ala Thr Gly Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
260 265 270

Tyr Ala Cys Asn Gly Cys Asn Ala Cys Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Ala Thr Gly Thr Ala Tyr Trp
290 295 300

Ser Asn Trp Ser Asn Gly Gly Asn Thr Gly Gly Thr Ala Tyr Gly Gly
305 310 315 320

Asn Gly Thr Asn Thr Thr Tyr Gly Ala Tyr Thr Ala Tyr Thr Gly Gly
325 330 335

Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Met Thr Asn Gly
340 345 350

Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys
355 360 365

Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn
370 375 380

Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly
385 390 395 400

Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser
405 410 415

Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn
420 425 430

Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr Met
435 440 445

Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr
450 455 460

Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn
465 470 475 480

Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly
485 490 495

Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly
500 505 510

Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn
515 520 525

Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp Ser Asn Trp
530 535 540

Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr
545 550 555 560

```
Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn
                565                 570                 575

Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr
            580                 585                 590

Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala
        595                 600                 605

Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr
    610                 615                 620

Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala
625                 630                 635                 640

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys
                645                 650                 655

Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr
            660                 665                 670

Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys
        675                 680                 685

Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys
    690                 695                 700

Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn
705                 710                 715                 720

Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys
                725                 730                 735

Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys
            740                 745                 750

Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn Met Gly Asn
        755                 760                 765

Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr
    770                 775                 780

Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr
785                 790                 795                 800
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Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn
805 810 815

Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr
820 825 830

Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr
835 840 845

Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn
850 855 860

Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met Gly Asn Gly
865 870 875 880

Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser
885 890 895

Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn
900 905 910

Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly Thr Asn Gly
915 920 925

Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr
930 935 940

Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr
945 950 955 960

Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala
965 970 975

Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys Cys Asn Gly Cys
980 985 990

Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala Arg Ala Cys Asn
995 1000 1005

Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg
1010 1015 1020

Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg
1025 1030 1035

Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr Ala Cys Asn
1040 1045 1050

Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn Met Gly Asn
1055 1060 1065

Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn Ala Ala Arg
1070 1075 1080

Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn Met Thr Asn
1085 1090 1095

Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg
1100 1105 1110

Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Trp Ser Asn
1115 1120 1125

Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn Gly Ala Arg
1130 1135 1140

Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr Gly Gly Asn
1145 1150 1155

Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr Ala Ala Tyr
1160 1165 1170

Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn Cys Cys Asn
1175 1180 1185

Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr Trp Ser Asn
1190 1195 1200

Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr Thr Thr Tyr
1205 1210 1215

Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg Met Thr Asn
1220 1225 1230

Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg Trp Ser Asn
1235 1240 1245

Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg Gly Gly Asn
1250 1255 1260

Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn Thr Gly Tyr
1265 1270 1275

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Trp Ser  Asn Gly Thr Asn Ala  Thr Gly Cys Ala Tyr  Gly Ala Arg
    1280                 1285                 1290

Gly Cys  Asn Met Thr Asn Cys  Ala Tyr Ala Ala Tyr  Cys Ala Tyr
    1295                 1300                 1305

Thr Ala  Tyr Ala Cys Asn Cys  Ala Arg Ala Ala Arg  Trp Ser Asn
    1310                 1315                 1320

Met Thr  Asn Trp Ser Asn Met  Thr Asn Trp Ser Asn  Cys Cys Asn
    1325                 1330                 1335

Gly Gly  Asn Ala Ala Arg
    1340
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<210> 570
<211> 1347
<212> PRT
<213> Homo Sapiens

<400> 570

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Cys Ala Arg Gly Thr Asn Ala Cys Asn Met Thr Asn Ala Ala Arg Gly
1               5                  10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Thr Asn Met Thr
            20                  25                  30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Ala Cys Asn Gly Ala Arg
        35                  40                  45

Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Thr
    50                  55                  60

Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Thr Thr
65                  70                  75                  80

Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Ala Ala Tyr Gly Cys Asn
                85                  90                  95

Met Gly Asn Ala Thr Gly Gly Gly Asn Gly Thr Asn Trp Ser Asn Thr
            100                 105                 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Met Thr Asn Gly Ala Arg
    130                 135                 140
```

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Thr Gly Gly Met Thr Asn Gly Thr Asn Met Thr Asn Ala Thr His Thr
145                 150                 155                 160

Thr Tyr Trp Ser Asn Ala Ala Tyr Gly Ala Tyr Gly Ala Arg Ala Ala
                165                 170                 175

Arg Trp Ser Asn Thr Ala Tyr Trp Ser Asn Ala Cys Asn Trp Ser Asn
            180                 185                 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Met Thr Asn Ala
        195                 200                 205

Cys Asn Ala Thr His Trp Ser Asn Ala Ala Arg Gly Ala Tyr Ala Cys
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Trp Ser Asn Cys Ala Arg Gly Thr Asn
225                 230                 235                 240

Gly Thr Asn Met Thr Asn Ala Cys Asn Ala Thr Gly Ala Cys Asn Ala
                245                 250                 255

Ala Tyr Ala Thr Gly Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
            260                 265                 270

Tyr Ala Cys Asn Gly Cys Asn Ala Cys Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Gly Thr Asn Thr Ala Tyr Trp
    290                 295                 300

Ser Asn Trp Ser Asn Gly Gly Asn Thr Gly Gly Trp Ser Asn Thr Thr
305                 310                 315                 320

Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn
                325                 330                 335

Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Ala
            340                 345                 350

Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser
        355                 360                 365

Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn
    370                 375                 380

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met
```

385 390 395 400

Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly
405 410 415

Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn
420 425 430

Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr
435 440 445

Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala
450 455 460

Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn
465 470 475 480

Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp
485 490 495

Ser Asn Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser
500 505 510

Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr
515 520 525

Cys Cys Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp
530 535 540

Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser
545 550 555 560

Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn
565 570 575

Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala
580 585 590

Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys
595 600 605

Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn
610 615 620

Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala
625 630 635 640

Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala
645 650 655

Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg
660 665 670

Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys
675 680 685

Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys
690 695 700

Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn
705 710 715 720

Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys
725 730 735

Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala
740 745 750

Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn
755 760 765

Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala
770 775 780

Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala
785 790 795 800

Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr
805 810 815

Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala
820 825 830

Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly
835 840 845

Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr
850 855 860

Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met
865 870 875 880

Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala

885 890 895

Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn
900 905 910

Gly Thr Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly
915 920 925

Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly
930 935 940

Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg
945 950 955 960

Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp
965 970 975

Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys Cys
980 985 990

Asn Gly Cys Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala Arg
995 1000 1005

Ala Cys Asn Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn
1010 1015 1020

Ala Ala Arg Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn
1025 1030 1035

Gly Ala Arg Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr
1040 1045 1050

Ala Cys Asn Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn
1055 1060 1065

Met Gly Asn Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn
1070 1075 1080

Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn
1085 1090 1095

Met Thr Asn Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn
1100 1105 1110

Ala Ala Arg Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn
1115 1120 1125

Trp Ser Asn Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn
1130 1135 1140

Gly Ala Arg Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr
1145 1150 1155

Gly Gly Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr
1160 1165 1170

Ala Ala Tyr Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn
1175 1180 1185

Cys Cys Asn Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr
1190 1195 1200

Trp Ser Asn Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr
1205 1210 1215

Thr Thr Tyr Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg
1220 1225 1230

Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg
1235 1240 1245

Trp Ser Asn Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg
1250 1255 1260

Gly Gly Asn Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn
1265 1270 1275

Thr Gly Tyr Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr
1280 1285 1290

Gly Ala Arg Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr
1295 1300 1305

Cys Ala Tyr Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg
1310 1315 1320

Trp Ser Asn Met Thr Asn Trp Ser Asn Met Thr Asn Trp Ser Asn
1325 1330 1335

Cys Cys Asn Gly Gly Asn Ala Ala Arg
1340 1345

<210> 571

<211> 1332
<212> PRT
<213> Homo Sapiens

<400> 571

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Cys Ala Arg Ala Thr His Ala Cys Asn Met Thr Asn Ala Ala Arg Gly
1               5                  10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Ala Cys Asn Met Thr
            20                  25                  30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Ala Cys Asn Cys Ala Arg
        35                  40                  45

Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Thr
    50                  55                  60

Gly Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Thr
65                  70                  75                  80

Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Ala Cys Asn Gly Gly Asn
                85                  90                  95

Gly Gly Asn Gly Thr Asn Gly Gly Asn Gly Thr Asn Gly Gly Asn Thr
            100                 105                 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Met Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Met Thr Asn Gly Cys Asn Met Thr Asn Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Thr Gly Gly Ala Ala Tyr Gly Ala Tyr Gly Ala Tyr Ala Ala
                165                 170                 175

Arg Met Gly Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn
            180                 185                 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Met Thr Asn Ala
        195                 200                 205

Cys Asn Ala Thr His Ala Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys
    210                 215                 220
```

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Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn
225                 230                 235                 240

Gly Thr Asn Met Thr Asn Ala Cys Asn Ala Thr Gly Ala Cys Asn Ala
                245                 250                 255

Ala Tyr Ala Thr Gly Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
            260                 265                 270

Tyr Ala Cys Asn Gly Cys Asn Ala Cys Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Cys Ala Tyr Met Gly Asn Met Gly Asn Gly
    290                 295                 300

Ala Arg Met Thr Asn Cys Cys Asn Thr Thr Tyr Gly Ala Tyr Thr Ala
305                 310                 315                 320

Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn
                325                 330                 335

Met Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp
            340                 345                 350

Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly
        355                 360                 365

Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn
    370                 375                 380

Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met
385                 390                 395                 400

Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser
                405                 410                 415

Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn
            420                 425                 430

Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr
        435                 440                 445

Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr
    450                 455                 460

Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr
465                 470                 475                 480
```

```
Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp
                485                 490                 495

Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr
            500                 505                 510

Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg
        515                 520                 525

Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp
    530                 535                 540

Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr
545                 550                 555                 560

Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn
                565                 570                 575

Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala
            580                 585                 590

Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr
        595                 600                 605

Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn
    610                 615                 620

Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala
625                 630                 635                 640

Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala
                645                 650                 655

Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr
            660                 665                 670

Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys
        675                 680                 685

Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys
    690                 695                 700

Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr
705                 710                 715                 720
```

Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly
725 730 735

Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser
740 745 750

Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn
755 760 765

Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly
770 775 780

Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala
785 790 795 800

Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr
805 810 815

Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly
820 825 830

Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala
835 840 845

Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn
850 855 860

Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala
865 870 875 880

Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr
885 890 895

Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn
900 905 910

Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr
915 920 925

Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala
930 935 940

Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn
945 950 955 960

Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys
965 970 975

Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala
980 985 990

Arg Ala Cys Asn Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn
995 1000 1005

Ala Ala Arg Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn
1010 1015 1020

Gly Ala Arg Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr
1025 1030 1035

Ala Cys Asn Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn
1040 1045 1050

Met Gly Asn Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn
1055 1060 1065

Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn
1070 1075 1080

Met Thr Asn Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn
1085 1090 1095

Ala Ala Arg Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn
1100 1105 1110

Trp Ser Asn Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn
1115 1120 1125

Gly Ala Arg Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr
1130 1135 1140

Gly Gly Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr
1145 1150 1155

Ala Ala Tyr Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn
1160 1165 1170

Cys Cys Asn Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr
1175 1180 1185

Trp Ser Asn Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr
1190 1195 1200

Thr Thr Tyr Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg
1205 1210 1215

Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg
1220 1225 1230

Trp Ser Asn Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg
1235 1240 1245

Gly Gly Asn Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn
1250 1255 1260

Thr Gly Tyr Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr
1265 1270 1275

Gly Ala Arg Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr
1280 1285 1290

Cys Ala Tyr Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg
1295 1300 1305

Trp Ser Asn Met Thr Asn Trp Ser Asn Met Thr Asn Trp Ser Asn
1310 1315 1320

Cys Cys Asn Gly Gly Asn Ala Ala Arg
1325 1330

<210> 572
<211> 1332
<212> PRT
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<400> 572

Cys Ala Arg Ala Thr His Ala Cys Asn Met Thr Asn Ala Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Ala Cys Asn Met Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Ala Cys Asn Cys Ala Arg
35 40 45

Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Thr
50 55 60

Gly Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

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Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Ala Cys Asn Gly Gly Asn
                85                  90                  95

Gly Gly Asn Gly Thr Asn Gly Gly Asn Gly Thr Asn Gly Gly Asn Thr
            100                 105                 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Met Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Met Thr Asn Gly Cys Asn Met Thr Asn Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Thr Gly Gly Ala Ala Tyr Gly Ala Tyr Gly Ala Tyr Ala Ala
                165                 170                 175

Arg Met Gly Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn
            180                 185                 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Met Thr Asn Ala
        195                 200                 205

Cys Asn Ala Thr His Ala Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Cys Asn Cys Ala Arg Gly Thr Asn
225                 230                 235                 240

Gly Thr Asn Met Thr Asn Ala Cys Asn Gly Thr Asn Ala Cys Asn Gly
                245                 250                 255

Ala Tyr Ala Thr Gly Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
            260                 265                 270

Tyr Ala Cys Asn Gly Cys Asn Ala Cys Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Cys Ala Tyr Met Gly Asn Ala Ala Tyr Thr
    290                 295                 300

Gly Gly Ala Cys Asn Cys Cys Asn Thr Thr Tyr Gly Ala Tyr Thr Ala
305                 310                 315                 320

Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn
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325 330 335

Met Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp
340 345 350

Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly
355 360 365

Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn
370 375 380

Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met
385 390 395 400

Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser
405 410 415

Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn
420 425 430

Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr
435 440 445

Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr
450 455 460

Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr
465 470 475 480

Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp
485 490 495

Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr
500 505 510

Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg
515 520 525

Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp
530 535 540

Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr
545 550 555 560

Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn
565 570 575

Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala
580 585 590

Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr
595 600 605

Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn
610 615 620

Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala
625 630 635 640

Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala
645 650 655

Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr
660 665 670

Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys
675 680 685

Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys
690 695 700

Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr
705 710 715 720

Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly
725 730 735

Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser
740 745 750

Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn
755 760 765

Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly
770 775 780

Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala
785 790 795 800

Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr
805 810 815

Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly

820 825 830

Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala
835 840 845

Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn
850 855 860

Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala
865 870 875 880

Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr
885 890 895

Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn
900 905 910

Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr
915 920 925

Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala
930 935 940

Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn
945 950 955 960

Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys
965 970 975

Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala
980 985 990

Arg Ala Cys Asn Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn
995 1000 1005

Ala Ala Arg Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn
1010 1015 1020

Gly Ala Arg Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr
1025 1030 1035

Ala Cys Asn Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn
1040 1045 1050

Met Gly Asn Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn
1055 1060 1065

Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn
1070 1075 1080

Met Thr Asn Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn
1085 1090 1095

Ala Ala Arg Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn
1100 1105 1110

Trp Ser Asn Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn
1115 1120 1125

Gly Ala Arg Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr
1130 1135 1140

Gly Gly Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr
1145 1150 1155

Ala Ala Tyr Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn
1160 1165 1170

Cys Cys Asn Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr
1175 1180 1185

Trp Ser Asn Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr
1190 1195 1200

Thr Thr Tyr Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg
1205 1210 1215

Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg
1220 1225 1230

Trp Ser Asn Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg
1235 1240 1245

Gly Gly Asn Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn
1250 1255 1260

Thr Gly Tyr Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr
1265 1270 1275

Gly Ala Arg Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr
1280 1285 1290

Cys Ala Tyr Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg

1295 1300 1305

Trp Ser Asn Met Thr Asn Trp Ser Asn Met Thr Asn Trp Ser Asn
1310 1315 1320

Cys Cys Asn Gly Gly Asn Ala Ala Arg
1325 1330

<210> 573
<211> 1332
<212> PRT
<213> Homo Sapiens

<400> 573

Cys Ala Arg Ala Thr His Ala Cys Asn Met Thr Asn Ala Ala Arg Gly
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Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Ala Cys Asn Met Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Ala Cys Asn Cys Ala Arg
35 40 45

Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Thr
50 55 60

Gly Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Trp Ser Asn Met Thr Asn Ala Ala Tyr Ala Cys Asn Gly Gly Asn
85 90 95

Gly Gly Asn Gly Thr Asn Gly Gly Asn Gly Thr Asn Gly Gly Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Met Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Met Thr Asn Gly Cys Asn Met Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Thr Gly Gly Ala Ala Tyr Gly Ala Tyr Gly Ala Tyr Ala Ala
165 170 175

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Arg Met Gly Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn
            180                 185                 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Met Thr Asn Ala
        195                 200                 205

Cys Asn Ala Thr His Ala Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn
225                 230                 235                 240

Gly Thr Asn Met Thr Asn Ala Cys Asn Ala Thr Gly Ala Cys Asn Ala
                245                 250                 255

Ala Tyr Ala Thr Gly Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
            260                 265                 270

Tyr Ala Cys Asn Gly Cys Asn Ala Cys Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Cys Ala Tyr Met Gly Asn Met Thr Asn Gly
    290                 295                 300

Ala Arg Met Thr Asn Cys Cys Asn Thr Thr Tyr Gly Ala Tyr Thr Ala
305                 310                 315                 320

Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn
                325                 330                 335

Met Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp
            340                 345                 350

Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly
        355                 360                 365

Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn
    370                 375                 380

Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met
385                 390                 395                 400

Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser
                405                 410                 415

Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn
            420                 425                 430
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Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr
435 440 445

Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr
450 455 460

Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr
465 470 475 480

Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp
485 490 495

Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr
500 505 510

Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg
515 520 525

Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp
530 535 540

Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr
545 550 555 560

Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn
565 570 575

Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala
580 585 590

Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr
595 600 605

Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn
610 615 620

Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala
625 630 635 640

Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala
645 650 655

Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr
660 665 670

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Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys
        675                 680                 685

Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys
    690                 695                 700

Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr
705                 710                 715                 720

Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly
                725                 730                 735

Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser
            740                 745                 750

Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn
        755                 760                 765

Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly
    770                 775                 780

Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala
785                 790                 795                 800

Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr
                805                 810                 815

Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly
            820                 825                 830

Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala
        835                 840                 845

Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn
    850                 855                 860

Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala
865                 870                 875                 880

Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr
                885                 890                 895

Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn
            900                 905                 910

Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr
        915                 920                 925
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Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala
    930                 935                 940

Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn
945                 950                 955                 960

Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys
                965                 970                 975

Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala
            980                 985                 990

Arg Ala Cys Asn Ala Thr His Trp  Ser Asn Ala Ala Arg  Ala Cys Asn
        995                 1000                1005

Ala Ala  Arg Gly Gly Asn Cys  Ala Arg Cys Cys Asn  Met Gly Asn
    1010                1015                1020

Gly Ala  Arg Cys Cys Asn Cys  Ala Arg Gly Thr Asn  Thr Ala Tyr
    1025                1030                1035

Ala Cys  Asn Met Thr Asn Cys  Cys Asn Cys Cys Asn  Trp Ser Asn
    1040                1045                1050

Met Gly  Asn Gly Ala Arg Gly  Ala Arg Ala Thr Gly  Ala Cys Asn
    1055                1060                1065

Ala Ala  Arg Ala Ala Tyr Cys  Ala Arg Gly Thr Asn  Trp Ser Asn
    1070                1075                1080

Met Thr  Asn Ala Cys Asn Thr  Gly Tyr Met Thr Asn  Gly Thr Asn
    1085                1090                1095

Ala Ala  Arg Gly Gly Asn Thr  Thr Tyr Thr Ala Tyr  Cys Cys Asn
    1100                1105                1110

Trp Ser  Asn Gly Ala Tyr Ala  Thr His Gly Cys Asn  Gly Thr Asn
    1115                1120                1125

Gly Ala  Arg Thr Gly Gly Gly  Ala Arg Trp Ser Asn  Ala Ala Tyr
    1130                1135                1140

Gly Gly  Asn Cys Ala Arg Cys  Cys Asn Gly Ala Arg  Ala Ala Tyr
    1145                1150                1155
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Ala Ala  Tyr Thr Ala Tyr Ala  Ala Arg Ala Cys Asn  Ala Cys Asn
    1160                 1165                 1170

Cys Cys  Asn Cys Cys Asn Ala  Thr Gly Met Thr Asn  Gly Ala Tyr
    1175                 1180                 1185

Trp Ser  Asn Gly Ala Tyr Gly  Gly Asn Trp Ser Asn  Thr Thr Tyr
    1190                 1195                 1200

Thr Thr  Tyr Met Thr Asn Thr  Ala Tyr Trp Ser Asn  Ala Ala Arg
    1205                 1210                 1215

Met Thr  Asn Ala Cys Asn Gly  Thr Asn Gly Ala Tyr  Ala Ala Arg
    1220                 1225                 1230

Trp Ser  Asn Met Gly Asn Thr  Gly Gly Cys Ala Arg  Cys Ala Arg
    1235                 1240                 1245

Gly Gly  Asn Ala Ala Tyr Gly  Thr Asn Thr Thr Tyr  Trp Ser Asn
    1250                 1255                 1260

Thr Gly  Tyr Trp Ser Asn Gly  Thr Asn Ala Thr Gly  Cys Ala Tyr
    1265                 1270                 1275

Gly Ala  Arg Gly Cys Asn Met  Thr Asn Cys Ala Tyr  Ala Ala Tyr
    1280                 1285                 1290

Cys Ala  Tyr Thr Ala Tyr Ala  Cys Asn Cys Ala Arg  Ala Ala Arg
    1295                 1300                 1305

Trp Ser  Asn Met Thr Asn Trp  Ser Asn Met Thr Asn  Trp Ser Asn
    1310                 1315                 1320

Cys Cys  Asn Gly Gly Asn Ala  Ala Arg
    1325                 1330
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<210> 574
<211> 1332
<212> PRT
<213> Homo Sapiens

<400> 574

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Cys Ala Arg Ala Thr His Ala Cys Asn Met Thr Asn Ala Ala Arg Gly
1               5                  10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Ala Cys Asn Met Thr
            20                  25                  30
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Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Ala Cys Asn Cys Ala Arg
        35                  40                  45

Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Thr
    50                  55                  60

Gly Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Thr
65                  70                  75                  80

Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Ala Cys Asn Gly Gly Asn
                85                  90                  95

Gly Gly Asn Gly Thr Asn Gly Gly Asn Gly Thr Asn Gly Gly Asn Thr
            100                 105                 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Met Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Met Thr Asn Gly Cys Asn Met Thr Asn Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Thr Gly Gly Ala Ala Tyr Gly Ala Tyr Gly Ala Tyr Ala Ala
                165                 170                 175

Arg Met Gly Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn
            180                 185                 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Met Thr Asn Ala
        195                 200                 205

Cys Asn Ala Thr His Ala Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn
225                 230                 235                 240

Gly Thr Asn Met Thr Asn Ala Cys Asn Ala Thr Gly Ala Cys Asn Ala
                245                 250                 255

Ala Tyr Met Thr Asn Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
            260                 265                 270

Tyr Ala Cys Asn Gly Cys Asn Ala Cys Asn Thr Ala Tyr Thr Ala Tyr
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275 280 285

Thr Gly Tyr Gly Cys Asn Cys Ala Tyr Met Gly Asn Met Gly Asn Gly
290 295 300

Ala Arg Gly Thr Asn Cys Cys Asn Thr Thr Tyr Gly Ala Tyr Thr Ala
305 310 315 320

Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn
325 330 335

Met Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp
340 345 350

Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly
355 360 365

Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn
370 375 380

Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met
385 390 395 400

Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser
405 410 415

Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn
420 425 430

Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr
435 440 445

Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr
450 455 460

Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr
465 470 475 480

Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp
485 490 495

Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr
500 505 510

Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg
515 520 525

Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp
530 535 540

Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr
545 550 555 560

Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn
565 570 575

Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala
580 585 590

Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr
595 600 605

Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn
610 615 620

Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala
625 630 635 640

Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala
645 650 655

Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr
660 665 670

Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys
675 680 685

Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys
690 695 700

Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr
705 710 715 720

Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly
725 730 735

Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser
740 745 750

Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn
755 760 765

Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly

770 775 780

Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala
785 790 795 800

Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr
805 810 815

Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly
820 825 830

Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala
835 840 845

Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn
850 855 860

Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala
865 870 875 880

Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr
885 890 895

Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn
900 905 910

Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr
915 920 925

Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala
930 935 940

Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn
945 950 955 960

Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys
965 970 975

Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala
980 985 990

Arg Ala Cys Asn Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn
995 1000 1005

Ala Ala Arg Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn
1010 1015 1020

Gly Ala Arg Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr
1025 1030 1035

Ala Cys Asn Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn
1040 1045 1050

Met Gly Asn Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn
1055 1060 1065

Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn
1070 1075 1080

Met Thr Asn Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn
1085 1090 1095

Ala Ala Arg Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn
1100 1105 1110

Trp Ser Asn Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn
1115 1120 1125

Gly Ala Arg Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr
1130 1135 1140

Gly Gly Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr
1145 1150 1155

Ala Ala Tyr Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn
1160 1165 1170

Cys Cys Asn Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr
1175 1180 1185

Trp Ser Asn Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr
1190 1195 1200

Thr Thr Tyr Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg
1205 1210 1215

Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg
1220 1225 1230

Trp Ser Asn Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg
1235 1240 1245

Gly Gly Asn Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn

1250 1255 1260

Thr Gly Tyr Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr
1265 1270 1275

Gly Ala Arg Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr
1280 1285 1290

Cys Ala Tyr Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg
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Trp Ser Asn Met Thr Asn Trp Ser Asn Met Thr Asn Trp Ser Asn
1310 1315 1320

Cys Cys Asn Gly Gly Asn Ala Ala Arg
1325 1330

<210> 575
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<400> 575

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1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Ala Cys Asn Met Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Ala Cys Asn Cys Ala Arg
35 40 45

Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Thr
50 55 60

Gly Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Ala Cys Asn Gly Gly Asn
85 90 95

Gly Gly Asn Gly Thr Asn Gly Gly Asn Gly Thr Asn Gly Gly Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Met Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Met Thr Asn Gly Cys Asn Met Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Thr Gly Gly Ala Ala Tyr Gly Thr Asn Gly Ala Arg Ala Ala
165 170 175

Arg Met Gly Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn
180 185 190

Met Thr Asn Met Gly Asn Trp Ser Asn Met Gly Asn Met Thr Asn Ala
195 200 205

Cys Asn Ala Thr His Ala Cys Asn Ala Ala Arg Gly Cys Asn Ala Cys
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn
225 230 235 240

Gly Thr Asn Met Thr Asn Ala Cys Asn Ala Thr Gly Ala Cys Asn Ala
245 250 255

Ala Tyr Ala Thr Gly Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
260 265 270

Tyr Ala Cys Asn Gly Cys Asn Ala Cys Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Cys Ala Tyr Met Gly Asn Cys Ala Tyr Ala
290 295 300

Cys Asn Ala Ala Tyr Cys Cys Asn Thr Thr Tyr Gly Ala Arg Thr Ala
305 310 315 320

Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn
325 330 335

Met Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp
340 345 350

Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly
355 360 365

Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn
370 375 380

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Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met
385                 390                 395                 400

Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser
                405                 410                 415

Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn
            420                 425                 430

Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr
        435                 440                 445

Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr
    450                 455                 460

Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr
465                 470                 475                 480

Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp
                485                 490                 495

Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr
            500                 505                 510

Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg
        515                 520                 525

Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp
    530                 535                 540

Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr
545                 550                 555                 560

Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn
                565                 570                 575

Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala
            580                 585                 590

Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr
        595                 600                 605

Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn
    610                 615                 620
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Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala
625 630 635 640

Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala
645 650 655

Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr
660 665 670

Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys
675 680 685

Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys
690 695 700

Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr
705 710 715 720

Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly
725 730 735

Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser
740 745 750

Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn
755 760 765

Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly
770 775 780

Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala
785 790 795 800

Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr
805 810 815

Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly
820 825 830

Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala
835 840 845

Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn
850 855 860

Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala
865 870 875 880

Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr
885 890 895

Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn
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Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr
915 920 925

Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala
930 935 940

Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn
945 950 955 960

Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys
965 970 975

Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala
980 985 990

Arg Ala Cys Asn Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn
995 1000 1005

Ala Ala Arg Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn
1010 1015 1020

Gly Ala Arg Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr
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Ala Cys Asn Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn
1040 1045 1050

Met Gly Asn Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn
1055 1060 1065

Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn
1070 1075 1080

Met Thr Asn Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn
1085 1090 1095

Ala Ala Arg Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn
1100 1105 1110

Trp Ser Asn Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn
1115 1120 1125

Gly Ala Arg Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr
1130 1135 1140

Gly Gly Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr
1145 1150 1155

Ala Ala Tyr Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn
1160 1165 1170

Cys Cys Asn Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr
1175 1180 1185

Trp Ser Asn Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr
1190 1195 1200

Thr Thr Tyr Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg
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Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg
1220 1225 1230

Trp Ser Asn Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg
1235 1240 1245

Gly Gly Asn Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn
1250 1255 1260

Thr Gly Tyr Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr
1265 1270 1275

Gly Ala Arg Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr
1280 1285 1290

Cys Ala Tyr Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg
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Trp Ser Asn Met Thr Asn Trp Ser Asn Met Thr Asn Trp Ser Asn
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Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Ala Cys Asn Cys Ala Arg
        35                  40                  45

Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Thr
    50                  55                  60

Gly Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Thr
65                  70                  75                  80

Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Ala Cys Asn Gly Gly Asn
                85                  90                  95

Gly Gly Asn Gly Thr Asn Gly Gly Asn Gly Thr Asn Gly Gly Asn Thr
            100                 105                 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Met Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Met Thr Asn Gly Cys Asn Met Thr Asn Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Thr Gly Gly Ala Ala Tyr Gly Ala Tyr Gly Ala Tyr Ala Ala
                165                 170                 175

Arg Met Gly Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn
            180                 185                 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Met Thr Asn Ala
        195                 200                 205

Cys Asn Ala Thr His Ala Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys
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Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn
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225 230 235 240

Gly Thr Asn Met Thr Asn Ala Cys Asn Ala Thr Gly Ala Cys Asn Ala
245 250 255

Ala Tyr Ala Thr Gly Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
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Tyr Ala Cys Asn Gly Cys Asn Ala Cys Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Cys Ala Tyr Met Gly Asn Gly Gly Asn Gly
290 295 300

Ala Arg Met Thr Asn Cys Cys Asn Thr Thr Tyr Gly Ala Tyr Thr Ala
305 310 315 320

Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn
325 330 335

Met Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp
340 345 350

Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly
355 360 365

Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn
370 375 380

Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met
385 390 395 400

Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser
405 410 415

Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn
420 425 430

Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr
435 440 445

Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr
450 455 460

Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr
465 470 475 480

Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp
485 490 495

Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr
500 505 510

Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg
515 520 525

Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp
530 535 540

Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr
545 550 555 560

Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn
565 570 575

Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala
580 585 590

Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr
595 600 605

Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn
610 615 620

Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala
625 630 635 640

Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala
645 650 655

Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr
660 665 670

Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys
675 680 685

Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys
690 695 700

Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr
705 710 715 720

Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly

725 730 735

Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser
740 745 750

Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn
755 760 765

Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly
770 775 780

Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala
785 790 795 800

Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr
805 810 815

Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly
820 825 830

Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala
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Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn
850 855 860

Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala
865 870 875 880

Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr
885 890 895

Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn
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Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr
915 920 925

Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala
930 935 940

Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn
945 950 955 960

Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys
965 970 975

Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala
980 985 990

Arg Ala Cys Asn Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn
995 1000 1005

Ala Ala Arg Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn
1010 1015 1020

Gly Ala Arg Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr
1025 1030 1035

Ala Cys Asn Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn
1040 1045 1050

Met Gly Asn Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn
1055 1060 1065

Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn
1070 1075 1080

Met Thr Asn Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn
1085 1090 1095

Ala Ala Arg Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn
1100 1105 1110

Trp Ser Asn Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn
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Gly Ala Arg Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr
1130 1135 1140

Gly Gly Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr
1145 1150 1155

Ala Ala Tyr Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn
1160 1165 1170

Cys Cys Asn Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr
1175 1180 1185

Trp Ser Asn Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr
1190 1195 1200

Thr Thr Tyr Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg

1205 1210 1215

Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg
1220 1225 1230

Trp Ser Asn Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg
1235 1240 1245

Gly Gly Asn Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn
1250 1255 1260

Thr Gly Tyr Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr
1265 1270 1275

Gly Ala Arg Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr
1280 1285 1290

Cys Ala Tyr Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg
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20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
35 40 45

Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

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Tyr Cys Cys Asn Thr Thr Tyr Trp Ser Asn Met Gly Asn Thr Ala Tyr
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Trp Ser Asn Ala Thr Gly Ala Ala Tyr Thr Gly Gly Gly Thr Asn Met
            100                 105                 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
        115                 120                 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
    130                 135                 140

Trp Ser Asn Gly Cys Asn Ala Thr His Trp Ser Asn Trp Ser Asn Trp
145                 150                 155                 160

Ser Asn Trp Ser Asn Trp Ser Asn Thr Ala Tyr Ala Thr His Thr Ala
                165                 170                 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
            180                 185                 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Ala Cys Asn Ala
        195                 200                 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Gly Cys
    210                 215                 220

Asn Ala Ala Arg Ala Ala Tyr Trp Ser Asn Met Thr Asn Thr Ala Tyr
225                 230                 235                 240

Met Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Met
                245                 250                 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Ala Cys
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Met Gly Asn Gly Ala Tyr Met Gly Asn Gly Thr Asn Gly
    290                 295                 300

Gly Asn Gly Cys Asn Ala Cys Asn Cys Cys Asn Gly Ala Tyr Gly Cys
305                 310                 315                 320

Asn Thr Thr Tyr Gly Ala Tyr Ala Thr His Thr Gly Gly Gly Gly Asn
                325                 330                 335
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Cys Ala Arg Gly Gly Asn Ala Cys Asn Ala Thr Gly Gly Thr Asn Ala
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Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser
        355                 360                 365

Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn
    370                 375                 380

Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys
385                 390                 395                 400

Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys
                405                 410                 415

Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn
            420                 425                 430

Gly Cys Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly
        435                 440                 445

Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys
    450                 455                 460

Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn
465                 470                 475                 480

Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly
                485                 490                 495

Cys Asn Met Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr
            500                 505                 510

Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn
        515                 520                 525

Gly Thr Asn Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly
    530                 535                 540

Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser
545                 550                 555                 560

Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn
                565                 570                 575
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Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly
            580                 585                 590

Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys
        595                 600                 605

Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr
    610                 615                 620

Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala
625                 630                 635                 640

Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr
                645                 650                 655

Asn Gly Ala Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr
            660                 665                 670

Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr
        675                 680                 685

Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr
    690                 695                 700

Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn
705                 710                 715                 720

Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala
                725                 730                 735

Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr
            740                 745                 750

Asn Ala Thr Gly Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn
        755                 760                 765

Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly
    770                 775                 780

Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser
785                 790                 795                 800

Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg
                805                 810                 815

Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr
            820                 825                 830
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Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala
835 840 845

Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg
850 855 860

Ala Cys Asn Ala Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly
865 870 875 880

Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys
885 890 895

Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn
900 905 910

Gly Thr Asn Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys
915 920 925

Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala
930 935 940

Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg
945 950 955 960

Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala
965 970 975

Ala Arg Gly Gly Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys
980 985 990

Asn Ala Thr His Gly Ala Arg Ala Ala Arg Ala Cys Asn Ala Thr His
995 1000 1005

Trp Ser Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Gly Gly Asn
1010 1015 1020

Cys Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Cys Cys Asn
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Cys Ala Arg Gly Thr Asn Thr Ala Tyr Ala Cys Asn Met Thr Asn
1040 1045 1050

Cys Cys Asn Cys Cys Asn Trp Ser Asn Met Gly Asn Gly Ala Arg
1055 1060 1065

Gly Ala Arg Ala Thr Gly Ala Cys Asn Ala Ala Arg Ala Ala Tyr
1070 1075 1080

Cys Ala Arg Gly Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn
1085 1090 1095

Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Gly Asn
1100 1105 1110

Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Trp Ser Asn Gly Ala Tyr
1115 1120 1125

Ala Thr His Gly Cys Asn Gly Thr Asn Gly Ala Arg Thr Gly Gly
1130 1135 1140

Gly Ala Arg Trp Ser Asn Ala Ala Tyr Gly Gly Asn Cys Ala Arg
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Cys Cys Asn Gly Ala Arg Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr
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Ala Ala Arg Ala Cys Asn Ala Cys Asn Cys Cys Asn Cys Cys Asn
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Ala Thr Gly Met Thr Asn Gly Ala Tyr Trp Ser Asn Gly Ala Tyr
1190 1195 1200

Gly Gly Asn Trp Ser Asn Thr Thr Tyr Thr Thr Tyr Met Thr Asn
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Thr Ala Tyr Trp Ser Asn Ala Ala Arg Met Thr Asn Ala Cys Asn
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Gly Thr Asn Gly Ala Tyr Ala Ala Arg Trp Ser Asn Met Gly Asn
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Thr Gly Gly Cys Ala Arg Cys Ala Arg Gly Gly Asn Ala Ala Tyr
1250 1255 1260

Gly Thr Asn Thr Thr Tyr Trp Ser Asn Thr Gly Tyr Trp Ser Asn
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Gly Thr Asn Ala Thr Gly Cys Ala Tyr Gly Ala Arg Gly Cys Asn
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Met Thr Asn Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr Thr Ala Tyr
1295 1300 1305

Ala Cys Asn Cys Ala Arg Ala Ala Arg Trp Ser Asn Met Thr Asn
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Trp Ser Asn Met Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn
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Ala Ala Arg
1340

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20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
35 40 45

Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Cys Asn Ala Thr Gly Ala Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Trp Ser Asn Gly Cys Asn Ala Thr His Trp Ser Asn Gly Gly Asn Trp
145 150 155 160

Ser Asn Gly Gly Asn Gly Gly Asn Trp Ser Asn Ala Cys Asn Thr Ala

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                165                 170                 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
            180                 185                 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Ala Cys Asn Ala
        195                 200                 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
    210                 215                 220

Asn Ala Ala Arg Ala Ala Tyr Ala Cys Asn Met Thr Asn Thr Ala Tyr
225                 230                 235                 240

Met Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Met
                245                 250                 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Ala Cys
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Ala Ala Arg Gly Ala Arg Gly Gly Asn Ala Thr His Gly
    290                 295                 300

Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Ala Cys Asn Gly Cys
305                 310                 315                 320

Asn Gly Ala Arg Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr
                325                 330                 335

Thr Ala Tyr Gly Cys Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr
            340                 345                 350

Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Ala Cys
        355                 360                 365

Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
    370                 375                 380

Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys
385                 390                 395                 400

Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr
                405                 410                 415
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Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn
420 425 430

Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala
435 440 445

Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr Gly
450 455 460

Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr
465 470 475 480

Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala
485 490 495

Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser
500 505 510

Asn Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser Asn
515 520 525

Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys
530 535 540

Cys Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp Ser
545 550 555 560

Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn
565 570 575

Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala
580 585 590

Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala
595 600 605

Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn
610 615 620

Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly
625 630 635 640

Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala
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Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg

660 665 670

Ala Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg Thr
675 680 685

Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys
690 695 700

Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn
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Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp
725 730 735

Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys
740 745 750

Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr
755 760 765

Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn Met
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Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys
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Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr
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Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys
820 825 830

Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala
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Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn
850 855 860

Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly
865 870 875 880

Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met Gly
885 890 895

Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr
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Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly
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Thr Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly Thr
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Ala Cys Asn Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn
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Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn
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Ala Ala Arg Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn
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Trp Ser Asn Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn

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Thr Thr Tyr Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg
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Trp Ser Asn Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg
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Thr Gly Tyr Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr
1295 1300 1305

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Cys Ala Tyr Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg
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Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
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Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
    50                  55                  60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65                  70                  75                  80

Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
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Gly Cys Asn Ala Thr Gly Trp Ser Asn Thr Gly Gly Gly Thr Asn Met
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Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
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Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
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Trp Ser Asn Gly Cys Asn Ala Thr His Trp Ser Asn Gly Gly Asn Trp
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Ser Asn Gly Gly Asn Gly Gly Asn Trp Ser Asn Ala Cys Asn Thr Ala
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Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
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Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Ala Cys Asn Ala
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Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
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Asn Ala Ala Arg Ala Ala Tyr Ala Cys Asn Met Thr Asn Thr Ala Tyr
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Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Cys Asn Ala Thr Gly
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Gly Asn Ala Cys Asn Ala Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr
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Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn
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Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr
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Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn
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Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala
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Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg
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Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr
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Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met
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Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr
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Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
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Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp
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Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys
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Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr
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Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys
625                 630                 635                 640

Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr
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Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg
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Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly
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Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys
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Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn
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Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly
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Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr
785                 790                 795                 800

Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr
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Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys
            820                 825                 830

Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr
        835                 840                 845

Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn
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Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala
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Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala
                885                 890                 895

Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr
            900                 905                 910

Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met
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Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala
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Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn
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Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala
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Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His
995 1000 1005

Gly Ala Arg Ala Ala Arg Ala Cys Asn Ala Thr His Trp Ser Asn
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Cys Cys Asn Met Gly Asn Gly Ala Arg Cys Cys Asn Cys Ala Arg
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Cys Cys Asn Trp Ser Asn Met Gly Asn Gly Ala Arg Gly Ala Arg
1070 1075 1080

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Gly Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr Gly Tyr
1100 1105 1110

Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Gly Asn Thr Thr Tyr
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Thr Ala Tyr Cys Cys Asn Trp Ser Asn Gly Ala Tyr Ala Thr His
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Gly Cys Asn Gly Thr Asn Gly Ala Arg Thr Gly Gly Gly Ala Arg
1145 1150 1155

Trp Ser Asn Ala Ala Tyr Gly Gly Asn Cys Ala Arg Cys Cys Asn
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Gly Ala Arg Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr Ala Ala Arg
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Ala Cys Asn Ala Cys Asn Cys Cys Asn Cys Cys Asn Ala Thr Gly
1190 1195 1200

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Trp Ser Asn Thr Thr Tyr Thr Thr Tyr Met Thr Asn Thr Ala Tyr
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Trp Ser Asn Ala Ala Arg Met Thr Asn Ala Cys Asn Gly Thr Asn
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Gly Ala Tyr Ala Ala Arg Trp Ser Asn Met Gly Asn Thr Gly Gly
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Cys Ala Arg Cys Ala Arg Gly Gly Asn Ala Ala Tyr Gly Thr Asn
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Thr Thr Tyr Trp Ser Asn Thr Gly Tyr Trp Ser Asn Gly Thr Asn
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Ala Thr Gly Cys Ala Tyr Gly Ala Arg Gly Cys Asn Met Thr Asn
1295 1300 1305

Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr Thr Ala Tyr Ala Cys Asn
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Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
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Gly Tyr Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr

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Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
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Gly Cys Asn Ala Thr Gly Trp Ser Asn Thr Gly Gly Gly Thr Asn Met
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Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
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Trp Ser Asn Gly Cys Asn Ala Thr His Trp Ser Asn Gly Gly Asn Trp
145 150 155 160

Ser Asn Gly Gly Asn Gly Gly Asn Trp Ser Asn Ala Cys Asn Thr Ala
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Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
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Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Ala Cys Asn Ala
195 200 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
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Asn Ala Ala Arg Ala Ala Tyr Ala Cys Asn Met Thr Asn Thr Ala Tyr
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Met Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Met
245 250 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Ala Cys
260 265 270

Asn Gly Cys Asn Gly Ala Arg Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Ala Ala Arg Gly Ala Arg Gly Gly Asn Ala Thr His Gly
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Cys Asn Gly Gly Asn Met Gly Asn Gly Ala Tyr Trp Ser Asn Thr Ala
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Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly
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Gly Ala Tyr Gly Thr Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly
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Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr
385 390 395 400

Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly
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Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn
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Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met
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Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala
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Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg
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Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr
485 490 495

Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr
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Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr
515 520 525

Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met
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Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr
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Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn

565 570 575

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Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys
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Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr
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Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly
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Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn
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Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met
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Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr
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Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn
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Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala
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Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr
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Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala
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Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly
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Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His
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Trp Ser Asn Ala Ala Tyr Gly Gly Asn Cys Ala Arg Cys Cys Asn
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Trp Ser Asn Ala Ala Arg Met Thr Asn Ala Cys Asn Gly Thr Asn
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Cys Ala Arg Cys Ala Arg Gly Gly Asn Ala Ala Tyr Gly Thr Asn
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Ala Thr Gly Cys Ala Tyr Gly Ala Arg Gly Cys Asn Met Thr Asn
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35 40 45

Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
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Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
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Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
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Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
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Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
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Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
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Gly Cys Asn Thr Thr Tyr Ala Thr His Trp Ser Asn Gly Ala Tyr Gly
145 150 155 160

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Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
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Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
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Met Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Met
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Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Ala Cys
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Ala Tyr Trp Ser Asn Trp Ser Asn Gly Gly Asn Thr Ala Tyr Thr Ala
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Tyr Thr Ala Tyr Gly Gly Asn Thr Thr Tyr Gly Ala Tyr Thr Ala Tyr
                325                 330                 335

Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Met
            340                 345                 350

Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser
        355                 360                 365

Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn
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Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met
385                 390                 395                 400
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Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly
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Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr
        435                 440                 445

Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala
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Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn
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Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp
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Ser Asn Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser
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Cys Cys Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp
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Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser
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Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn
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Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn
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Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn
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Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys
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Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala
            740                 745                 750

Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn
        755                 760                 765

Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala
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Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala
785                 790                 795                 800

Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr
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Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala
            820                 825                 830

Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly
        835                 840                 845

Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr
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Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met
865                 870                 875                 880

Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala
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Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn
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Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly
    930                 935                 940

Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg
945                 950                 955                 960

Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp
                965                 970                 975

Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys Cys
            980                 985                 990

Asn Gly Cys Asn Cys Cys Asn Ala  Thr His Gly Ala Arg  Ala Ala Arg
        995                 1000                1005

Ala Cys  Asn Ala Thr His Trp  Ser Asn Ala Ala Arg  Ala Cys Asn
    1010                1015                1020

Ala Ala  Arg Gly Gly Asn Cys  Ala Arg Cys Cys Asn  Met Gly Asn
    1025                1030                1035

Gly Ala  Arg Cys Cys Asn Cys  Ala Arg Gly Thr Asn  Thr Ala Tyr
    1040                1045                1050

Ala Cys  Asn Met Thr Asn Cys  Cys Asn Cys Cys Asn  Trp Ser Asn
    1055                1060                1065

Met Gly  Asn Gly Ala Arg Gly  Ala Arg Ala Thr Gly  Ala Cys Asn
    1070                1075                1080

Ala Ala  Arg Ala Ala Tyr Cys  Ala Arg Gly Thr Asn  Trp Ser Asn
    1085                1090                1095

Met Thr  Asn Ala Cys Asn Thr  Gly Tyr Met Thr Asn  Gly Thr Asn
    1100                1105                1110

Ala Ala  Arg Gly Gly Asn Thr  Thr Tyr Thr Ala Tyr  Cys Cys Asn
    1115                1120                1125

Trp Ser  Asn Gly Ala Tyr Ala  Thr His Gly Cys Asn  Gly Thr Asn
    1130                1135                1140
```

```
Gly Ala  Arg Thr Gly Gly Gly  Ala Arg Trp Ser Asn  Ala Ala Tyr
    1145                 1150                 1155

Gly Gly  Asn Cys Ala Arg Cys  Cys Asn Gly Ala Arg  Ala Ala Tyr
    1160                 1165                 1170

Ala Ala  Tyr Thr Ala Tyr Ala  Ala Arg Ala Cys Asn  Ala Cys Asn
    1175                 1180                 1185

Cys Cys  Asn Cys Cys Asn Ala  Thr Gly Met Thr Asn  Gly Ala Tyr
    1190                 1195                 1200

Trp Ser  Asn Gly Ala Tyr Gly  Gly Asn Trp Ser Asn  Thr Thr Tyr
    1205                 1210                 1215

Thr Thr  Tyr Met Thr Asn Thr  Ala Tyr Trp Ser Asn  Ala Ala Arg
    1220                 1225                 1230

Met Thr  Asn Ala Cys Asn Gly  Thr Asn Gly Ala Tyr  Ala Ala Arg
    1235                 1240                 1245

Trp Ser  Asn Met Gly Asn Thr  Gly Gly Cys Ala Arg  Cys Ala Arg
    1250                 1255                 1260

Gly Gly  Asn Ala Ala Tyr Gly  Thr Asn Thr Thr Tyr  Trp Ser Asn
    1265                 1270                 1275

Thr Gly  Tyr Trp Ser Asn Gly  Thr Asn Ala Thr Gly  Cys Ala Tyr
    1280                 1285                 1290

Gly Ala  Arg Gly Cys Asn Met  Thr Asn Cys Ala Tyr  Ala Ala Tyr
    1295                 1300                 1305

Cys Ala  Tyr Thr Ala Tyr Ala  Cys Asn Cys Ala Arg  Ala Ala Arg
    1310                 1315                 1320

Trp Ser  Asn Met Thr Asn Trp  Ser Asn Met Thr Asn  Trp Ser Asn
    1325                 1330                 1335

Cys Cys  Asn Gly Gly Asn Ala  Ala Arg
    1340                 1345
```

<210> 582
<211> 1320
<212> PRT
<213> Homo Sapiens

<400> 582

```
Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Gly Thr Asn Gly
1               5                  10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
            20                  25                  30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
        35                  40                  45

Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
    50                  55                  60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65                  70                  75                  80

Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
                85                  90                  95

Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
            100                 105                 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
        115                 120                 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
    130                 135                 140

Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly
145                 150                 155                 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Thr Ala
                165                 170                 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
            180                 185                 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Ala Cys Asn Ala
        195                 200                 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
    210                 215                 220

Asn Ala Ala Arg Ala Ala Tyr Ala Cys Asn Met Thr Asn Thr Ala Tyr
225                 230                 235                 240
```

Met Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Met
245 250 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Ala Cys
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Ala Ala Tyr Gly Thr Asn Ala Thr His Gly
290 295 300

Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly
305 310 315 320

Asn Ala Cys Asn Met Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn
325 330 335

Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala
340 345 350

Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr
355 360 365

Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr
370 375 380

Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly
385 390 395 400

Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr
405 410 415

Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg
420 425 430

Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys
435 440 445

Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly
450 455 460

Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr Asn
465 470 475 480

Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala

485 490 495

Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met Thr
500 505 510

Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn
515 520 525

Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly
530 535 540

Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser
545 550 555 560

Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn
565 570 575

Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala
580 585 590

Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys
595 600 605

Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn
610 615 620

Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg Met
625 630 635 640

Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala
645 650 655

Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn
660 665 670

Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly
675 680 685

Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr
690 695 700

Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn
705 710 715 720

Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala
725 730 735

```
Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala
            740                 745                 750

Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn
        755                 760                 765

Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly
    770                 775                 780

Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala
785                 790                 795                 800

Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn
                805                 810                 815

Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys
            820                 825                 830

Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala
        835                 840                 845

Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg
    850                 855                 860

Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met
865                 870                 875                 880

Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met Thr
                885                 890                 895

Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg
            900                 905                 910

Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala
        915                 920                 925

Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala
    930                 935                 940

Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn
945                 950                 955                 960

Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His Gly
                965                 970                 975

Ala Arg Ala Ala Arg Ala Cys Asn Ala Thr His Trp Ser Asn Ala Ala
```

980 985 990

Arg Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Ala Arg Cys Cys Asn
995 1000 1005

Met Gly Asn Gly Ala Arg Cys Cys Asn Cys Ala Arg Gly Thr Asn
1010 1015 1020

Thr Ala Tyr Ala Cys Asn Met Thr Asn Cys Cys Asn Cys Cys Asn
1025 1030 1035

Trp Ser Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Ala Thr Gly
1040 1045 1050

Ala Cys Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn
1055 1060 1065

Trp Ser Asn Met Thr Asn Ala Cys Asn Thr Gly Tyr Met Thr Asn
1070 1075 1080

Gly Thr Asn Ala Ala Arg Gly Gly Asn Thr Thr Tyr Thr Ala Tyr
1085 1090 1095

Cys Cys Asn Trp Ser Asn Gly Ala Tyr Ala Thr His Gly Cys Asn
1100 1105 1110

Gly Thr Asn Gly Ala Arg Thr Gly Gly Gly Ala Arg Trp Ser Asn
1115 1120 1125

Ala Ala Tyr Gly Gly Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg
1130 1135 1140

Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr Ala Ala Arg Ala Cys Asn
1145 1150 1155

Ala Cys Asn Cys Cys Asn Cys Cys Asn Ala Thr Gly Met Thr Asn
1160 1165 1170

Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Gly Asn Trp Ser Asn
1175 1180 1185

Thr Thr Tyr Thr Thr Tyr Met Thr Asn Thr Ala Tyr Trp Ser Asn
1190 1195 1200

Ala Ala Arg Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Ala Tyr
1205 1210 1215

```
Ala Ala  Arg Trp Ser Asn Met  Gly Asn Thr Gly Gly  Cys Ala Arg
    1220                 1225                 1230

Cys Ala  Arg Gly Gly Asn Ala  Ala Tyr Gly Thr Asn  Thr Thr Tyr
    1235                 1240                 1245

Trp Ser  Asn Thr Gly Tyr Trp  Ser Asn Gly Thr Asn  Ala Thr Gly
    1250                 1255                 1260

Cys Ala  Tyr Gly Ala Arg Gly  Cys Asn Met Thr Asn  Cys Ala Tyr
    1265                 1270                 1275

Ala Ala  Tyr Cys Ala Tyr Thr  Ala Tyr Ala Cys Asn  Cys Ala Arg
    1280                 1285                 1290

Ala Ala  Arg Trp Ser Asn Met  Thr Asn Trp Ser Asn  Met Thr Asn
    1295                 1300                 1305

Trp Ser  Asn Cys Cys Asn Gly  Gly Asn Ala Ala Arg
    1310                 1315                 1320
```

<210> 583
<211> 1338
<212> PRT
<213> Homo Sapiens

<400> 583

```
Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Gly Thr Asn Gly
1               5                  10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
            20                  25                  30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
        35                  40                  45

Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
    50                  55                  60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65                  70                  75                  80

Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
                85                  90                  95

Gly Ala Tyr Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
            100                 105                 110
```

```
Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
        115                 120                 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
    130                 135                 140

Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly
145                 150                 155                 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Thr His Ala Ala Arg Thr Ala
                165                 170                 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
            180                 185                 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Ala Cys Asn Ala
        195                 200                 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
    210                 215                 220

Asn Ala Ala Arg Ala Ala Tyr Ala Cys Asn Met Thr Asn Thr Ala Tyr
225                 230                 235                 240

Met Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Met
                245                 250                 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Ala Cys
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Met Gly Asn Gly Gly Asn Gly Gly Asn Gly Cys Asn Ala
    290                 295                 300

Cys Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Thr Ala Tyr Thr Thr
305                 310                 315                 320

Tyr Cys Ala Arg Cys Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg
                325                 330                 335

Gly Gly Asn Ala Cys Asn Met Thr Asn Gly Thr Asn Ala Cys Asn Gly
            340                 345                 350
```

```
Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys
        355                 360                 365

Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn
    370                 375                 380

Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr
385                 390                 395                 400

Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser
                405                 410                 415

Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn
            420                 425                 430

Met Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala
        435                 440                 445

Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala
    450                 455                 460

Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn
465                 470                 475                 480

Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met
                485                 490                 495

Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala
            500                 505                 510

Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn
        515                 520                 525

Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met
    530                 535                 540

Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser
545                 550                 555                 560

Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn
                565                 570                 575

Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala
            580                 585                 590

Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly
        595                 600                 605
```

Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg
610 615 620

Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly
625 630 635 640

Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala
645 650 655

Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn
660 665 670

Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys
675 680 685

Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys
690 695 700

Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr
705 710 715 720

Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys
725 730 735

Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr
740 745 750

Gly Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn
755 760 765

Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly
770 775 780

Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala
785 790 795 800

Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn
805 810 815

Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly
820 825 830

Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr
835 840 845

```
Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn
    850                 855                 860

Ala Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys
865                 870                 875                 880

Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr
                885                 890                 895

Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn
            900                 905                 910

Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys
        915                 920                 925

Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly
    930                 935                 940

Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr
945                 950                 955                 960

Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly
                965                 970                 975

Gly Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr
            980                 985                 990

His Gly Ala Arg Ala Ala Arg Ala  Cys Asn Ala Thr His  Trp Ser Asn
        995                 1000                1005

Ala Ala  Arg Ala Cys Asn Ala  Ala Arg Gly Gly Asn  Cys Ala Arg
    1010                1015                1020

Cys Cys  Asn Met Gly Asn Gly  Ala Arg Cys Cys Asn  Cys Ala Arg
    1025                1030                1035

Gly Thr  Asn Thr Ala Tyr Ala  Cys Asn Met Thr Asn  Cys Cys Asn
    1040                1045                1050

Cys Cys  Asn Trp Ser Asn Met  Gly Asn Gly Ala Arg  Gly Ala Arg
    1055                1060                1065

Ala Thr  Gly Ala Cys Asn Ala  Ala Arg Ala Ala Tyr  Cys Ala Arg
    1070                1075                1080

Gly Thr  Asn Trp Ser Asn Met  Thr Asn Ala Cys Asn  Thr Gly Tyr
    1085                1090                1095
```

```
Met Thr  Asn Gly Thr Asn Ala  Ala Arg Gly Gly Asn  Thr Thr Tyr
    1100                 1105                 1110

Thr Ala  Tyr Cys Cys Asn Trp  Ser Asn Gly Ala Tyr  Ala Thr His
    1115                 1120                 1125

Gly Cys  Asn Gly Thr Asn Gly  Ala Arg Thr Gly Gly  Gly Ala Arg
    1130                 1135                 1140

Trp Ser  Asn Ala Ala Tyr Gly  Gly Asn Cys Ala Arg  Cys Cys Asn
    1145                 1150                 1155

Gly Ala  Arg Ala Ala Tyr Ala  Ala Tyr Thr Ala Tyr  Ala Ala Arg
    1160                 1165                 1170

Ala Cys  Asn Ala Cys Asn Cys  Cys Asn Cys Cys Asn  Ala Thr Gly
    1175                 1180                 1185

Met Thr  Asn Gly Ala Tyr Trp  Ser Asn Gly Ala Tyr  Gly Gly Asn
    1190                 1195                 1200

Trp Ser  Asn Thr Thr Tyr Thr  Thr Tyr Met Thr Asn  Thr Ala Tyr
    1205                 1210                 1215

Trp Ser  Asn Ala Ala Arg Met  Thr Asn Ala Cys Asn  Gly Thr Asn
    1220                 1225                 1230

Gly Ala  Tyr Ala Ala Arg Trp  Ser Asn Met Gly Asn  Thr Gly Gly
    1235                 1240                 1245

Cys Ala  Arg Cys Ala Arg Gly  Gly Asn Ala Ala Tyr  Gly Thr Asn
    1250                 1255                 1260

Thr Thr  Tyr Trp Ser Asn Thr  Gly Tyr Trp Ser Asn  Gly Thr Asn
    1265                 1270                 1275

Ala Thr  Gly Cys Ala Tyr Gly  Ala Arg Gly Cys Asn  Met Thr Asn
    1280                 1285                 1290

Cys Ala  Tyr Ala Ala Tyr Cys  Ala Tyr Thr Ala Tyr  Ala Cys Asn
    1295                 1300                 1305

Cys Ala  Arg Ala Ala Arg Trp  Ser Asn Met Thr Asn  Trp Ser Asn
    1310                 1315                 1320
```

Met Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn Ala Ala Arg
1325 1330 1335

<210> 584
<211> 1332
<212> PRT
<213> Homo Sapiens

<400> 584

Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
35 40 45

Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly
145 150 155 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Thr Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Ala Cys Asn Ala
195 200 205

```
Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
    210                 215                 220

Asn Ala Ala Arg Ala Ala Tyr Ala Cys Asn Met Thr Asn Thr Ala Tyr
225                 230                 235                 240

Met Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Met
                245                 250                 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Ala Cys
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Thr Asn Met Thr Asn Met Thr Asn Thr Gly Gly Thr Thr Tyr Gly
    290                 295                 300

Gly Asn Gly Ala Arg Ala Cys Asn Thr Thr Tyr Gly Ala Tyr Thr Ala
305                 310                 315                 320

Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Trp Ser Asn
                325                 330                 335

Met Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Cys
            340                 345                 350

Cys Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly
        355                 360                 365

Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn
    370                 375                 380

Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met
385                 390                 395                 400

Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser
                405                 410                 415

Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn
            420                 425                 430

Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr
        435                 440                 445

Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr
```

450 455 460

Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr
465 470 475 480

Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp
485 490 495

Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr
500 505 510

Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg
515 520 525

Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp
530 535 540

Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr
545 550 555 560

Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn
565 570 575

Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala
580 585 590

Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr
595 600 605

Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn
610 615 620

Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala
625 630 635 640

Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala
645 650 655

Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr
660 665 670

Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys
675 680 685

Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys
690 695 700

Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr
705 710 715 720

Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly
725 730 735

Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser
740 745 750

Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn
755 760 765

Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly
770 775 780

Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala
785 790 795 800

Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr
805 810 815

Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly
820 825 830

Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala
835 840 845

Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn
850 855 860

Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala
865 870 875 880

Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr
885 890 895

Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn
900 905 910

Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr
915 920 925

Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala
930 935 940

Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn

945 950 955 960

Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys
965 970 975

Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala
980 985 990

Arg Ala Cys Asn Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn
995 1000 1005

Ala Ala Arg Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn
1010 1015 1020

Gly Ala Arg Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr
1025 1030 1035

Ala Cys Asn Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn
1040 1045 1050

Met Gly Asn Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn
1055 1060 1065

Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn
1070 1075 1080

Met Thr Asn Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn
1085 1090 1095

Ala Ala Arg Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn
1100 1105 1110

Trp Ser Asn Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn
1115 1120 1125

Gly Ala Arg Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr
1130 1135 1140

Gly Gly Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr
1145 1150 1155

Ala Ala Tyr Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn
1160 1165 1170

Cys Cys Asn Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr
1175 1180 1185

Trp Ser Asn Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr
1190 1195 1200

Thr Thr Tyr Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg
1205 1210 1215

Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg
1220 1225 1230

Trp Ser Asn Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg
1235 1240 1245

Gly Gly Asn Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn
1250 1255 1260

Thr Gly Tyr Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr
1265 1270 1275

Gly Ala Arg Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr
1280 1285 1290

Cys Ala Tyr Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg
1295 1300 1305

Trp Ser Asn Met Thr Asn Trp Ser Asn Met Thr Asn Trp Ser Asn
1310 1315 1320

Cys Cys Asn Gly Gly Asn Ala Ala Arg
1325 1330

<210> 585
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<212> PRT
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<400> 585

Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
35 40 45

Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Trp Ser Asn Gly
145 150 155 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Thr Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Ala Cys Asn Ala
195 200 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
210 215 220

Asn Ala Ala Arg Ala Ala Tyr Ala Cys Asn Met Thr Asn Thr Ala Tyr
225 230 235 240

Met Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Met
245 250 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Ala Cys
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Ala Ala Tyr Met Thr Asn Cys Cys Asn Thr
290 295 300

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Thr Tyr Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala
305                 310                 315                 320

Arg Gly Gly Asn Ala Cys Asn Met Thr Asn Gly Thr Asn Ala Cys Asn
                325                 330                 335

Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala
            340                 345                 350

Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr
        355                 360                 365

Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn
    370                 375                 380

Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp
385                 390                 395                 400

Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys
                405                 410                 415

Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn
            420                 425                 430

Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly
        435                 440                 445

Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser
    450                 455                 460

Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn
465                 470                 475                 480

Met Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys
                485                 490                 495

Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr
            500                 505                 510

Asn Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn
        515                 520                 525

Met Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp
    530                 535                 540

Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys
545                 550                 555                 560
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Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn
                565                 570                 575

Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr
            580                 585                 590

Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala
        595                 600                 605

Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg
    610                 615                 620

Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly
625                 630                 635                 640

Ala Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr
                645                 650                 655

Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr
            660                 665                 670

Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly
        675                 680                 685

Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr
    690                 695                 700

Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg
705                 710                 715                 720

Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala
                725                 730                 735

Thr Gly Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys
            740                 745                 750

Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn
        755                 760                 765

Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys
    770                 775                 780

Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr
785                 790                 795                 800
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Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr
                805                 810                 815

Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly
            820                 825                 830

Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys
        835                 840                 845

Asn Ala Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg
    850                 855                 860

Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr
865                 870                 875                 880

Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr
                885                 890                 895

Asn Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr
            900                 905                 910

Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly
        915                 920                 925

Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly
    930                 935                 940

Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg
945                 950                 955                 960

Gly Gly Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala
                965                 970                 975

Thr His Gly Ala Arg Ala Ala Arg Ala Cys Asn Ala Thr His Trp Ser
            980                 985                 990

Asn Ala Ala Arg Ala Cys Asn Ala  Ala Arg Gly Gly Asn  Cys Ala Arg
        995                 1000                1005

Cys Cys  Asn Met Gly Asn Gly  Ala Arg Cys Cys Asn  Cys Ala Arg
    1010                1015                1020

Gly Thr  Asn Thr Ala Tyr Ala  Cys Asn Met Thr Asn  Cys Cys Asn
    1025                1030                1035

Cys Cys  Asn Trp Ser Asn Met  Gly Asn Gly Ala Arg  Gly Ala Arg
    1040                1045                1050
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Ala Thr Gly Ala Cys Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg
1055 1060 1065

Gly Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr Gly Tyr
1070 1075 1080

Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Gly Asn Thr Thr Tyr
1085 1090 1095

Thr Ala Tyr Cys Cys Asn Trp Ser Asn Gly Ala Tyr Ala Thr His
1100 1105 1110

Gly Cys Asn Gly Thr Asn Gly Ala Arg Thr Gly Gly Gly Ala Arg
1115 1120 1125

Trp Ser Asn Ala Ala Tyr Gly Gly Asn Cys Ala Arg Cys Cys Asn
1130 1135 1140

Gly Ala Arg Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr Ala Ala Arg
1145 1150 1155

Ala Cys Asn Ala Cys Asn Cys Cys Asn Cys Cys Asn Ala Thr Gly
1160 1165 1170

Met Thr Asn Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Gly Asn
1175 1180 1185

Trp Ser Asn Thr Thr Tyr Thr Thr Tyr Met Thr Asn Thr Ala Tyr
1190 1195 1200

Trp Ser Asn Ala Ala Arg Met Thr Asn Ala Cys Asn Gly Thr Asn
1205 1210 1215

Gly Ala Tyr Ala Ala Arg Trp Ser Asn Met Gly Asn Thr Gly Gly
1220 1225 1230

Cys Ala Arg Cys Ala Arg Gly Gly Asn Ala Ala Tyr Gly Thr Asn
1235 1240 1245

Thr Thr Tyr Trp Ser Asn Thr Gly Tyr Trp Ser Asn Gly Thr Asn
1250 1255 1260

Ala Thr Gly Cys Ala Tyr Gly Ala Arg Gly Cys Asn Met Thr Asn
1265 1270 1275

Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr Thr Ala Tyr Ala Cys Asn
1280 1285 1290

Cys Ala Arg Ala Ala Arg Trp Ser Asn Met Thr Asn Trp Ser Asn
1295 1300 1305

Met Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn Ala Ala Arg
1310 1315 1320

<210> 586
<211> 1347
<212> PRT
<213> Homo Sapiens

<400> 586

Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
35 40 45

Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Gly Ala Tyr Gly
145 150 155 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Ala Tyr Cys Ala Arg Thr Ala
165 170 175

```
Tyr Thr Ala Tyr Ala Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
            180                 185                 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Ala Cys Asn Gly
        195                 200                 205

Thr Asn Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
    210                 215                 220

Asn Ala Ala Arg Ala Ala Tyr Ala Cys Asn Met Thr Asn Thr Thr Tyr
225                 230                 235                 240

Met Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Met
                245                 250                 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Ala Cys
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Met Gly Asn Trp Ser Asn Cys Ala Tyr Thr Ala Tyr Gly
    290                 295                 300

Gly Asn Gly Gly Asn Gly Ala Tyr Thr Ala Tyr Gly Ala Tyr Thr Ala
305                 310                 315                 320

Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn
                325                 330                 335

Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Ala
            340                 345                 350

Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser
        355                 360                 365

Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn
    370                 375                 380

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met
385                 390                 395                 400

Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly
                405                 410                 415

Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn
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420 425 430

Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr
435 440 445

Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala
450 455 460

Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn
465 470 475 480

Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp
485 490 495

Ser Asn Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser
500 505 510

Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr
515 520 525

Cys Cys Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp
530 535 540

Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser
545 550 555 560

Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn
565 570 575

Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala
580 585 590

Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys
595 600 605

Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn
610 615 620

Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala
625 630 635 640

Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala
645 650 655

Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg
660 665 670

Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys
675 680 685

Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys
690 695 700

Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn
705 710 715 720

Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys
725 730 735

Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala
740 745 750

Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn
755 760 765

Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala
770 775 780

Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala
785 790 795 800

Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr
805 810 815

Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala
820 825 830

Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly
835 840 845

Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr
850 855 860

Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met
865 870 875 880

Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala
885 890 895

Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn
900 905 910

Gly Thr Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly

915 920 925

Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly
930 935 940

Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg
945 950 955 960

Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp
965 970 975

Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys Cys
980 985 990

Asn Gly Cys Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala Arg
995 1000 1005

Ala Cys Asn Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn
1010 1015 1020

Ala Ala Arg Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn
1025 1030 1035

Gly Ala Arg Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr
1040 1045 1050

Ala Cys Asn Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn
1055 1060 1065

Met Gly Asn Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn
1070 1075 1080

Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn
1085 1090 1095

Met Thr Asn Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn
1100 1105 1110

Ala Ala Arg Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn
1115 1120 1125

Trp Ser Asn Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn
1130 1135 1140

Gly Ala Arg Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr
1145 1150 1155

```
Gly Gly  Asn Cys Ala Arg Cys  Cys Asn Gly Ala Arg  Ala Ala Tyr
    1160                 1165                 1170

Ala Ala  Tyr Thr Ala Tyr Ala  Ala Arg Ala Cys Asn  Ala Cys Asn
    1175                 1180                 1185

Cys Cys  Asn Cys Cys Asn Ala  Thr Gly Met Thr Asn  Gly Ala Tyr
    1190                 1195                 1200

Trp Ser  Asn Gly Ala Tyr Gly  Gly Asn Trp Ser Asn  Thr Thr Tyr
    1205                 1210                 1215

Thr Thr  Tyr Met Thr Asn Thr  Ala Tyr Trp Ser Asn  Ala Ala Arg
    1220                 1225                 1230

Met Thr  Asn Ala Cys Asn Gly  Thr Asn Gly Ala Tyr  Ala Ala Arg
    1235                 1240                 1245

Trp Ser  Asn Met Gly Asn Thr  Gly Gly Cys Ala Arg  Cys Ala Arg
    1250                 1255                 1260

Gly Gly  Asn Ala Ala Tyr Gly  Thr Asn Thr Thr Tyr  Trp Ser Asn
    1265                 1270                 1275

Thr Gly  Tyr Trp Ser Asn Gly  Thr Asn Ala Thr Gly  Cys Ala Tyr
    1280                 1285                 1290

Gly Ala  Arg Gly Cys Asn Met  Thr Asn Cys Ala Tyr  Ala Ala Tyr
    1295                 1300                 1305

Cys Ala  Tyr Thr Ala Tyr Ala  Cys Asn Cys Ala Arg  Ala Ala Arg
    1310                 1315                 1320

Trp Ser  Asn Met Thr Asn Trp  Ser Asn Met Thr Asn  Trp Ser Asn
    1325                 1330                 1335

Cys Cys  Asn Gly Gly Asn Ala  Ala Arg
    1340                 1345
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<210> 587
<211> 1338
<212> PRT
<213> Homo Sapiens

<400> 587

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Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Gly Thr Asn Gly
1               5                  10                  15
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Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
            20                  25                  30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
        35                  40                  45

Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
    50                  55                  60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65                  70                  75                  80

Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
                85                  90                  95

Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
            100                 105                 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
        115                 120                 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
    130                 135                 140

Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly
145                 150                 155                 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Met Gly
                165                 170                 175

Asn Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
            180                 185                 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Ala Cys Asn Ala
        195                 200                 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
    210                 215                 220

Asn Ala Ala Arg Ala Ala Tyr Ala Cys Asn Met Thr Asn Thr Ala Tyr
225                 230                 235                 240

Met Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Met
                245                 250                 255
```

```
Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Ala Cys
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Met Gly Asn Gly Ala Tyr Gly Gly Asn Thr Gly Gly Cys
    290                 295                 300

Ala Arg Cys Ala Arg Cys Ala Arg Gly Cys Asn Cys Cys Asn Thr Thr
305                 310                 315                 320

Tyr Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg
                325                 330                 335

Gly Gly Asn Ala Cys Asn Met Thr Asn Gly Thr Asn Ala Cys Asn Gly
            340                 345                 350

Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys
        355                 360                 365

Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn
    370                 375                 380

Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr
385                 390                 395                 400

Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser
                405                 410                 415

Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn
            420                 425                 430

Met Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala
        435                 440                 445

Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala
    450                 455                 460

Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn
465                 470                 475                 480

Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met
                485                 490                 495

Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala
            500                 505                 510
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Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn
        515                 520                 525

Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met
    530                 535                 540

Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser
545                 550                 555                 560

Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn
                565                 570                 575

Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala
            580                 585                 590

Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly
        595                 600                 605

Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg
    610                 615                 620

Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly
625                 630                 635                 640

Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala
                645                 650                 655

Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn
            660                 665                 670

Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys
        675                 680                 685

Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys
    690                 695                 700

Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr
705                 710                 715                 720

Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys
                725                 730                 735

Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr
            740                 745                 750
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Gly Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn
755 760 765

Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly
770 775 780

Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala
785 790 795 800

Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn
805 810 815

Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly
820 825 830

Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr
835 840 845

Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn
850 855 860

Ala Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys
865 870 875 880

Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr
885 890 895

Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn
900 905 910

Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys
915 920 925

Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly
930 935 940

Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr
945 950 955 960

Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly
965 970 975

Gly Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr
980 985 990

His Gly Ala Arg Ala Ala Arg Ala Cys Asn Ala Thr His Trp Ser Asn
995 1000 1005

Ala Ala Arg Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Ala Arg
1010 1015 1020

Cys Cys Asn Met Gly Asn Gly Ala Arg Cys Cys Asn Cys Ala Arg
1025 1030 1035

Gly Thr Asn Thr Ala Tyr Ala Cys Asn Met Thr Asn Cys Cys Asn
1040 1045 1050

Cys Cys Asn Trp Ser Asn Met Gly Asn Gly Ala Arg Gly Ala Arg
1055 1060 1065

Ala Thr Gly Ala Cys Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg
1070 1075 1080

Gly Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr Gly Tyr
1085 1090 1095

Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Gly Asn Thr Thr Tyr
1100 1105 1110

Thr Ala Tyr Cys Cys Asn Trp Ser Asn Gly Ala Tyr Ala Thr His
1115 1120 1125

Gly Cys Asn Gly Thr Asn Gly Ala Arg Thr Gly Gly Gly Ala Arg
1130 1135 1140

Trp Ser Asn Ala Ala Tyr Gly Gly Asn Cys Ala Arg Cys Cys Asn
1145 1150 1155

Gly Ala Arg Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr Ala Ala Arg
1160 1165 1170

Ala Cys Asn Ala Cys Asn Cys Cys Asn Cys Cys Asn Ala Thr Gly
1175 1180 1185

Met Thr Asn Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Gly Asn
1190 1195 1200

Trp Ser Asn Thr Thr Tyr Thr Thr Tyr Met Thr Asn Thr Ala Tyr
1205 1210 1215

Trp Ser Asn Ala Ala Arg Met Thr Asn Ala Cys Asn Gly Thr Asn
1220 1225 1230

```
Gly Ala  Tyr Ala Ala Arg Trp  Ser Asn Met Gly Asn  Thr Gly Gly
    1235                 1240                 1245

Cys Ala  Arg Cys Ala Arg Gly  Gly Asn Ala Ala Tyr  Gly Thr Asn
    1250                 1255                 1260

Thr Thr  Tyr Trp Ser Asn Thr  Gly Tyr Trp Ser Asn  Gly Thr Asn
    1265                 1270                 1275

Ala Thr  Gly Cys Ala Tyr Gly  Ala Arg Gly Cys Asn  Met Thr Asn
    1280                 1285                 1290

Cys Ala  Tyr Ala Ala Tyr Cys  Ala Tyr Thr Ala Tyr  Ala Cys Asn
    1295                 1300                 1305

Cys Ala  Arg Ala Ala Arg Trp  Ser Asn Met Thr Asn  Trp Ser Asn
    1310                 1315                 1320

Met Thr  Asn Trp Ser Asn Cys  Cys Asn Gly Gly Asn  Ala Ala Arg
    1325                 1330                 1335
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<210> 588
<211> 1332
<212> PRT
<213> Homo Sapiens

<400> 588

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Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Gly Thr Asn Gly
1               5                  10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
            20                  25                  30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
        35                  40                  45

Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
    50                  55                  60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65                  70                  75                  80

Tyr Ala Cys Asn Thr Thr Tyr Met Gly Asn Trp Ser Asn Cys Ala Tyr
                85                  90                  95

Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
            100                 105                 110
```

```
Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
        115                 120                 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
    130                 135                 140

Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly
145                 150                 155                 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Ala Ala
                165                 170                 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
            180                 185                 190

Met Gly Asn Gly Gly Asn Met Gly Asn Thr Thr Tyr Ala Cys Asn Ala
        195                 200                 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
    210                 215                 220

Asn Ala Ala Arg Ala Ala Tyr Ala Cys Asn Met Thr Asn Gly Ala Tyr
225                 230                 235                 240

Met Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Met
                245                 250                 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Ala Cys
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Met Gly Asn Thr Gly Gly Gly Gly Asn Ala Thr His Trp
    290                 295                 300

Ser Asn Gly Cys Asn Cys Cys Asn Thr Thr Tyr Gly Ala Tyr Thr Gly
305                 310                 315                 320

Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn
                325                 330                 335

Met Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp
            340                 345                 350

Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly
```

355 360 365

Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn
370 375 380

Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met
385 390 395 400

Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser
405 410 415

Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn
420 425 430

Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr
435 440 445

Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr
450 455 460

Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr
465 470 475 480

Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp
485 490 495

Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr
500 505 510

Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg
515 520 525

Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp
530 535 540

Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr
545 550 555 560

Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn
565 570 575

Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala
580 585 590

Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr
595 600 605

Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn
610 615 620

Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala
625 630 635 640

Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala
645 650 655

Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr
660 665 670

Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys
675 680 685

Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys
690 695 700

Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr
705 710 715 720

Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly
725 730 735

Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser
740 745 750

Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn
755 760 765

Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly
770 775 780

Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala
785 790 795 800

Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr
805 810 815

Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly
820 825 830

Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala
835 840 845

Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn

```
    850                 855                 860

Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala
865                 870                 875                 880

Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr
                885                 890                 895

Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn
            900                 905                 910

Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr
        915                 920                 925

Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala
    930                 935                 940

Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn
945                 950                 955                 960

Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys
                965                 970                 975

Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala
            980                 985                 990

Arg Ala Cys Asn Ala Thr His Trp  Ser Asn Ala Ala Arg  Ala Cys Asn
        995                 1000                1005

Ala Ala  Arg Gly Gly Asn Cys  Ala Arg Cys Cys Asn  Met Gly Asn
    1010                1015                1020

Gly Ala  Arg Cys Cys Asn Cys  Ala Arg Gly Thr Asn  Thr Ala Tyr
    1025                1030                1035

Ala Cys  Asn Met Thr Asn Cys  Cys Asn Cys Cys Asn  Trp Ser Asn
    1040                1045                1050

Met Gly  Asn Gly Ala Arg Gly  Ala Arg Ala Thr Gly  Ala Cys Asn
    1055                1060                1065

Ala Ala  Arg Ala Ala Tyr Cys  Ala Arg Gly Thr Asn  Trp Ser Asn
    1070                1075                1080

Met Thr  Asn Ala Cys Asn Thr  Gly Tyr Met Thr Asn  Gly Thr Asn
    1085                1090                1095
```

Ala Ala Arg Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn
1100 1105 1110

Trp Ser Asn Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn
1115 1120 1125

Gly Ala Arg Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr
1130 1135 1140

Gly Gly Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr
1145 1150 1155

Ala Ala Tyr Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn
1160 1165 1170

Cys Cys Asn Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr
1175 1180 1185

Trp Ser Asn Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr
1190 1195 1200

Thr Thr Tyr Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg
1205 1210 1215

Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg
1220 1225 1230

Trp Ser Asn Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg
1235 1240 1245

Gly Gly Asn Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn
1250 1255 1260

Thr Gly Tyr Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr
1265 1270 1275

Gly Ala Arg Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr
1280 1285 1290

Cys Ala Tyr Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg
1295 1300 1305

Trp Ser Asn Met Thr Asn Trp Ser Asn Met Thr Asn Trp Ser Asn
1310 1315 1320

Cys Cys Asn Gly Gly Asn Ala Ala Arg

1325 1330

<210> 589
<211> 1323
<212> PRT
<213> Homo Sapiens

<400> 589

Gly Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Met Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
35 40 45

Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Gly Cys Asn Thr Ala Tyr
85 90 95

Trp Ser Asn Ala Thr Gly Ala Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Trp Ser Asn Thr Ala Tyr Ala Thr His Trp Ser Asn Trp Ser Asn Trp
145 150 155 160

Ser Asn Gly Gly Asn Met Gly Asn Ala Cys Asn Ala Thr His Thr Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Ala Cys Asn Ala
195 200 205

```
Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Gly Cys
    210                 215                 220

Asn Ala Ala Arg Ala Ala Tyr Trp Ser Asn Met Thr Asn Thr Thr Tyr
225                 230                 235                 240

Met Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Met
                245                 250                 255

Thr Asn Met Gly Asn Gly Ala Tyr Gly Ala Arg Gly Ala Tyr Ala Cys
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Met Thr Asn Thr Gly Gly Gly Cys Asn Cys Cys Asn Thr
    290                 295                 300

Thr Tyr Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala
305                 310                 315                 320

Arg Gly Gly Asn Ala Cys Asn Met Thr Asn Gly Thr Asn Ala Cys Asn
                325                 330                 335

Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala
            340                 345                 350

Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr
        355                 360                 365

Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn
    370                 375                 380

Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp
385                 390                 395                 400

Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys
                405                 410                 415

Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn
            420                 425                 430

Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly
        435                 440                 445

Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser
    450                 455                 460
```

Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn
465 470 475 480

Met Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys
485 490 495

Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr
500 505 510

Asn Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn
515 520 525

Met Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp
530 535 540

Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys
545 550 555 560

Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn
565 570 575

Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr
580 585 590

Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala
595 600 605

Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg
610 615 620

Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly
625 630 635 640

Ala Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr
645 650 655

Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr
660 665 670

Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly
675 680 685

Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr
690 695 700

```
Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg
705                 710                 715                 720

Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala
                725                 730                 735

Thr Gly Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys
            740                 745                 750

Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn
        755                 760                 765

Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys
    770                 775                 780

Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr
785                 790                 795                 800

Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr
                805                 810                 815

Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly
            820                 825                 830

Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys
        835                 840                 845

Asn Ala Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg
    850                 855                 860

Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr
865                 870                 875                 880

Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr
                885                 890                 895

Asn Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr
            900                 905                 910

Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly
        915                 920                 925

Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly
    930                 935                 940

Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg
945                 950                 955                 960
```

```
Gly Gly Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala
                965                 970                 975

Thr His Gly Ala Arg Ala Ala Arg Ala Cys Asn Ala Thr His Trp Ser
            980                 985                 990

Asn Ala Ala Arg Ala Cys Asn Ala  Ala Arg Gly Gly Asn  Cys Ala Arg
        995                 1000                1005

Cys Cys  Asn Met Gly Asn Gly  Ala Arg Cys Cys Asn  Cys Ala Arg
    1010                1015                1020

Gly Thr  Asn Thr Ala Tyr Ala  Cys Asn Met Thr Asn  Cys Cys Asn
    1025                1030                1035

Cys Cys  Asn Trp Ser Asn Met  Gly Asn Gly Ala Arg  Gly Ala Arg
    1040                1045                1050

Ala Thr  Gly Ala Cys Asn Ala  Ala Arg Ala Ala Tyr  Cys Ala Arg
    1055                1060                1065

Gly Thr  Asn Trp Ser Asn Met  Thr Asn Ala Cys Asn  Thr Gly Tyr
    1070                1075                1080

Met Thr  Asn Gly Thr Asn Ala  Ala Arg Gly Gly Asn  Thr Thr Tyr
    1085                1090                1095

Thr Ala  Tyr Cys Cys Asn Trp  Ser Asn Gly Ala Tyr  Ala Thr His
    1100                1105                1110

Gly Cys  Asn Gly Thr Asn Gly  Ala Arg Thr Gly Gly  Gly Ala Arg
    1115                1120                1125

Trp Ser  Asn Ala Ala Tyr Gly  Gly Asn Cys Ala Arg  Cys Cys Asn
    1130                1135                1140

Gly Ala  Arg Ala Ala Tyr Ala  Ala Tyr Thr Ala Tyr  Ala Ala Arg
    1145                1150                1155

Ala Cys  Asn Ala Cys Asn Cys  Cys Asn Cys Cys Asn  Ala Thr Gly
    1160                1165                1170

Met Thr  Asn Gly Ala Tyr Trp  Ser Asn Gly Ala Tyr  Gly Gly Asn
    1175                1180                1185
```

Trp Ser Asn Thr Thr Tyr Thr Thr Tyr Met Thr Asn Thr Ala Tyr
1190 1195 1200

Trp Ser Asn Ala Ala Arg Met Thr Asn Ala Cys Asn Gly Thr Asn
1205 1210 1215

Gly Ala Tyr Ala Ala Arg Trp Ser Asn Met Gly Asn Thr Gly Gly
1220 1225 1230

Cys Ala Arg Cys Ala Arg Gly Gly Asn Ala Ala Tyr Gly Thr Asn
1235 1240 1245

Thr Thr Tyr Trp Ser Asn Thr Gly Tyr Trp Ser Asn Gly Thr Asn
1250 1255 1260

Ala Thr Gly Cys Ala Tyr Gly Ala Arg Gly Cys Asn Met Thr Asn
1265 1270 1275

Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr Thr Ala Tyr Ala Cys Asn
1280 1285 1290

Cys Ala Arg Ala Ala Arg Trp Ser Asn Met Thr Asn Trp Ser Asn
1295 1300 1305

Met Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn Ala Ala Arg
1310 1315 1320

<210> 590
<211> 1353
<212> PRT
<213> Homo Sapiens

<400> 590

Gly Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Met Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
35 40 45

Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

```
Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
                85                  90                  95

Trp Ser Asn Ala Thr Gly Ala Ala Tyr Thr Gly Gly Gly Thr Asn Met
            100                 105                 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
        115                 120                 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
    130                 135                 140

Trp Ser Asn Cys Ala Tyr Ala Thr His Trp Ser Asn Trp Ser Asn Trp
145                 150                 155                 160

Ser Asn Trp Ser Asn Met Gly Asn Ala Cys Asn Ala Thr His Thr Ala
                165                 170                 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
            180                 185                 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Ala Cys Asn Ala
        195                 200                 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Gly Cys
    210                 215                 220

Asn Ala Ala Arg Ala Ala Tyr Trp Ser Asn Gly Thr Asn Thr Ala Tyr
225                 230                 235                 240

Met Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Met
                245                 250                 255

Thr Asn Met Gly Asn Gly Ala Tyr Gly Ala Arg Gly Ala Tyr Ala Cys
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Met Gly Asn Gly Ala Tyr Gly Gly Asn Thr Ala Tyr Ala
    290                 295                 300

Ala Tyr Thr Gly Gly Ala Ala Tyr Gly Gly Asn Gly Gly Asn Gly Gly
305                 310                 315                 320

Asn Ala Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly
```

325 330 335

Gly Ala Tyr Gly Thr Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly
340 345 350

Gly Asn Ala Cys Asn Ala Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr
355 360 365

Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn
370 375 380

Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr
385 390 395 400

Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly
405 410 415

Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn
420 425 430

Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met
435 440 445

Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala
450 455 460

Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg
465 470 475 480

Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr
485 490 495

Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr
500 505 510

Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr
515 520 525

Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met
530 535 540

Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr
545 550 555 560

Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
565 570 575

```
Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp
            580                 585                 590

Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys
        595                 600                 605

Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr
    610                 615                 620

Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys
625                 630                 635                 640

Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr
                645                 650                 655

Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg
            660                 665                 670

Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly
        675                 680                 685

Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys
    690                 695                 700

Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn
705                 710                 715                 720

Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met
                725                 730                 735

Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys
            740                 745                 750

Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly
        755                 760                 765

Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly
    770                 775                 780

Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr
785                 790                 795                 800

Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr
                805                 810                 815

Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys
```

820 825 830

Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr
835 840 845

Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn
850 855 860

Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala
865 870 875 880

Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala
885 890 895

Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr
900 905 910

Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met
915 920 925

Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala
930 935 940

Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn
945 950 955 960

Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala
965 970 975

Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly
980 985 990

Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His
995 1000 1005

Gly Ala Arg Ala Ala Arg Ala Cys Asn Ala Thr His Trp Ser Asn
1010 1015 1020

Ala Ala Arg Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Ala Arg
1025 1030 1035

Cys Cys Asn Met Gly Asn Gly Ala Arg Cys Cys Asn Cys Ala Arg
1040 1045 1050

Gly Thr Asn Thr Ala Tyr Ala Cys Asn Met Thr Asn Cys Cys Asn
1055 1060 1065

Cys Cys Asn Trp Ser Asn Met Gly Asn Gly Ala Arg Gly Ala Arg
1070 1075 1080

Ala Thr Gly Ala Cys Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg
1085 1090 1095

Gly Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr Gly Tyr
1100 1105 1110

Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Gly Asn Thr Thr Tyr
1115 1120 1125

Thr Ala Tyr Cys Cys Asn Trp Ser Asn Gly Ala Tyr Ala Thr His
1130 1135 1140

Gly Cys Asn Gly Thr Asn Gly Ala Arg Thr Gly Gly Gly Ala Arg
1145 1150 1155

Trp Ser Asn Ala Ala Tyr Gly Gly Asn Cys Ala Arg Cys Cys Asn
1160 1165 1170

Gly Ala Arg Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr Ala Ala Arg
1175 1180 1185

Ala Cys Asn Ala Cys Asn Cys Cys Asn Cys Cys Asn Ala Thr Gly
1190 1195 1200

Met Thr Asn Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Gly Asn
1205 1210 1215

Trp Ser Asn Thr Thr Tyr Thr Thr Tyr Met Thr Asn Thr Ala Tyr
1220 1225 1230

Trp Ser Asn Ala Ala Arg Met Thr Asn Ala Cys Asn Gly Thr Asn
1235 1240 1245

Gly Ala Tyr Ala Ala Arg Trp Ser Asn Met Gly Asn Thr Gly Gly
1250 1255 1260

Cys Ala Arg Cys Ala Arg Gly Gly Asn Ala Ala Tyr Gly Thr Asn
1265 1270 1275

Thr Thr Tyr Trp Ser Asn Thr Gly Tyr Trp Ser Asn Gly Thr Asn
1280 1285 1290

Ala Thr Gly Cys Ala Tyr Gly Ala Arg Gly Cys Asn Met Thr Asn

1295 1300 1305

Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr Thr Ala Tyr Ala Cys Asn
1310 1315 1320

Cys Ala Arg Ala Ala Arg Trp Ser Asn Met Thr Asn Trp Ser Asn
1325 1330 1335

Met Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn Ala Ala Arg
1340 1345 1350

<210> 591
<211> 1353
<212> PRT
<213> Homo Sapiens

<400> 591

Gly Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Met Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
35 40 45

Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Trp Ser Asn Ala Thr Gly Ala Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Trp Ser Asn Cys Ala Tyr Ala Thr His Trp Ser Asn Met Gly Asn Trp
145 150 155 160

Ser Asn Trp Ser Asn Met Gly Asn Ala Cys Asn Ala Thr His Thr Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Ala Cys Asn Ala
195 200 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Gly Cys
210 215 220

Asn Ala Ala Arg Ala Ala Tyr Trp Ser Asn Met Thr Asn Thr Ala Tyr
225 230 235 240

Met Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Met
245 250 255

Thr Asn Met Gly Asn Gly Ala Tyr Gly Ala Arg Gly Ala Tyr Ala Cys
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Gly Ala Tyr Gly Gly Asn Thr Ala Tyr Ala
290 295 300

Ala Tyr Thr Gly Gly Ala Ala Tyr Ala Ala Tyr Gly Gly Asn Gly Gly
305 310 315 320

Asn Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly
325 330 335

Gly Ala Tyr Gly Thr Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly
340 345 350

Gly Asn Ala Cys Asn Ala Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr
355 360 365

Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn
370 375 380

Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr
385 390 395 400

Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly
405 410 415

```
Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn
            420                 425                 430

Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met
        435                 440                 445

Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala
    450                 455                 460

Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg
465                 470                 475                 480

Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr
                485                 490                 495

Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr
            500                 505                 510

Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr
        515                 520                 525

Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met
    530                 535                 540

Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr
545                 550                 555                 560

Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
                565                 570                 575

Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp
            580                 585                 590

Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys
        595                 600                 605

Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr
    610                 615                 620

Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys
625                 630                 635                 640

Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr
                645                 650                 655
```

```
Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg
            660                 665                 670

Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly
        675                 680                 685

Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys
    690                 695                 700

Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn
705                 710                 715                 720

Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met
                725                 730                 735

Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys
            740                 745                 750

Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly
        755                 760                 765

Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly
    770                 775                 780

Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr
785                 790                 795                 800

Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr
                805                 810                 815

Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys
            820                 825                 830

Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr
        835                 840                 845

Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn
    850                 855                 860

Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala
865                 870                 875                 880

Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala
                885                 890                 895

Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr
            900                 905                 910
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Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met
915 920 925

Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala
930 935 940

Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn
945 950 955 960

Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala
965 970 975

Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly
980 985 990

Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His
995 1000 1005

Gly Ala Arg Ala Ala Arg Ala Cys Asn Ala Thr His Trp Ser Asn
1010 1015 1020

Ala Ala Arg Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Ala Arg
1025 1030 1035

Cys Cys Asn Met Gly Asn Gly Ala Arg Cys Cys Asn Cys Ala Arg
1040 1045 1050

Gly Thr Asn Thr Ala Tyr Ala Cys Asn Met Thr Asn Cys Cys Asn
1055 1060 1065

Cys Cys Asn Trp Ser Asn Met Gly Asn Gly Ala Arg Gly Ala Arg
1070 1075 1080

Ala Thr Gly Ala Cys Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg
1085 1090 1095

Gly Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr Gly Tyr
1100 1105 1110

Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Gly Asn Thr Thr Tyr
1115 1120 1125

Thr Ala Tyr Cys Cys Asn Trp Ser Asn Gly Ala Tyr Ala Thr His
1130 1135 1140

```
Gly Cys  Asn Gly Thr Asn Gly  Ala Arg Thr Gly Gly  Gly Ala Arg
    1145                 1150                 1155

Trp Ser  Asn Ala Ala Tyr Gly  Gly Asn Cys Ala Arg  Cys Cys Asn
    1160                 1165                 1170

Gly Ala  Arg Ala Ala Tyr Ala  Ala Tyr Thr Ala Tyr  Ala Ala Arg
    1175                 1180                 1185

Ala Cys  Asn Ala Cys Asn Cys  Cys Asn Cys Cys Asn  Ala Thr Gly
    1190                 1195                 1200

Met Thr  Asn Gly Ala Tyr Trp  Ser Asn Gly Ala Tyr  Gly Gly Asn
    1205                 1210                 1215

Trp Ser  Asn Thr Thr Tyr Thr  Thr Tyr Met Thr Asn  Thr Ala Tyr
    1220                 1225                 1230

Trp Ser  Asn Ala Ala Arg Met  Thr Asn Ala Cys Asn  Gly Thr Asn
    1235                 1240                 1245

Gly Ala  Tyr Ala Ala Arg Trp  Ser Asn Met Gly Asn  Thr Gly Gly
    1250                 1255                 1260

Cys Ala  Arg Cys Ala Arg Gly  Gly Asn Ala Ala Tyr  Gly Thr Asn
    1265                 1270                 1275

Thr Thr  Tyr Trp Ser Asn Thr  Gly Tyr Trp Ser Asn  Gly Thr Asn
    1280                 1285                 1290

Ala Thr  Gly Cys Ala Tyr Gly  Ala Arg Gly Cys Asn  Met Thr Asn
    1295                 1300                 1305

Cys Ala  Tyr Ala Ala Tyr Cys  Ala Tyr Thr Ala Tyr  Ala Cys Asn
    1310                 1315                 1320

Cys Ala  Arg Ala Ala Arg Trp  Ser Asn Met Thr Asn  Trp Ser Asn
    1325                 1330                 1335

Met Thr  Asn Trp Ser Asn Cys  Cys Asn Gly Gly Asn  Ala Ala Arg
    1340                 1345                 1350
```

<210> 592
<211> 1332
<212> PRT
<213> Homo Sapiens

<400> 592

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Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Cys Ala Arg Gly
1               5                  10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Met Thr
            20                  25                  30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
        35                  40                  45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr
    50                  55                  60

Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65                  70                  75                  80

Asn Trp Ser Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Gly Asn
                85                  90                  95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
            100                 105                 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Met Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Cys
145                 150                 155                 160

Ala Tyr Trp Ser Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Ala Cys
                165                 170                 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
            180                 185                 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Ala
        195                 200                 205

Cys Asn Ala Thr His Trp Ser Asn Gly Thr Asn Gly Ala Tyr Ala Cys
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225                 230                 235                 240

Trp Ser Asn Met Thr Asn Ala Ala Tyr Met Thr Asn Trp Ser Asn Trp
```

245 250 255

Ser Asn Gly Thr Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala
260 265 270

Tyr Ala Cys Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Gly Gly Asn Cys Cys Asn Thr
290 295 300

Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr
305 310 315 320

Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn
325 330 335

Ala Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp
340 345 350

Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly
355 360 365

Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn
370 375 380

Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met
385 390 395 400

Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser
405 410 415

Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn
420 425 430

Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr
435 440 445

Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr
450 455 460

Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr
465 470 475 480

Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp
485 490 495

```
Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr
            500                 505                 510

Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg
        515                 520                 525

Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp
    530                 535                 540

Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr
545                 550                 555                 560

Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn
                565                 570                 575

Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala
            580                 585                 590

Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr
        595                 600                 605

Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn
    610                 615                 620

Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala
625                 630                 635                 640

Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala
                645                 650                 655

Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr
            660                 665                 670

Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys
        675                 680                 685

Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys
    690                 695                 700

Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr
705                 710                 715                 720

Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly
                725                 730                 735

Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser
```

740 745 750

Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn
755 760 765

Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly
770 775 780

Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala
785 790 795 800

Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr
805 810 815

Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly
820 825 830

Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala
835 840 845

Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn
850 855 860

Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala
865 870 875 880

Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr
885 890 895

Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn
900 905 910

Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr
915 920 925

Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala
930 935 940

Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn
945 950 955 960

Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys
965 970 975

Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala
980 985 990

```
Arg Ala Cys Asn Ala Thr His Trp  Ser Asn Ala Ala Arg  Ala Cys Asn
        995                 1000                1005

Ala Ala  Arg Gly Gly Asn Cys  Ala Arg Cys Cys Asn  Met Gly Asn
    1010                1015                1020

Gly Ala  Arg Cys Cys Asn Cys  Ala Arg Gly Thr Asn  Thr Ala Tyr
    1025                1030                1035

Ala Cys  Asn Met Thr Asn Cys  Cys Asn Cys Cys Asn  Trp Ser Asn
    1040                1045                1050

Met Gly  Asn Gly Ala Arg Gly  Ala Arg Ala Thr Gly  Ala Cys Asn
    1055                1060                1065

Ala Ala  Arg Ala Ala Tyr Cys  Ala Arg Gly Thr Asn  Trp Ser Asn
    1070                1075                1080

Met Thr  Asn Ala Cys Asn Thr  Gly Tyr Met Thr Asn  Gly Thr Asn
    1085                1090                1095

Ala Ala  Arg Gly Gly Asn Thr  Thr Tyr Thr Ala Tyr  Cys Cys Asn
    1100                1105                1110

Trp Ser  Asn Gly Ala Tyr Ala  Thr His Gly Cys Asn  Gly Thr Asn
    1115                1120                1125

Gly Ala  Arg Thr Gly Gly Gly  Ala Arg Trp Ser Asn  Ala Ala Tyr
    1130                1135                1140

Gly Gly  Asn Cys Ala Arg Cys  Cys Asn Gly Ala Arg  Ala Ala Tyr
    1145                1150                1155

Ala Ala  Tyr Thr Ala Tyr Ala  Ala Arg Ala Cys Asn  Ala Cys Asn
    1160                1165                1170

Cys Cys  Asn Cys Cys Asn Ala  Thr Gly Met Thr Asn  Gly Ala Tyr
    1175                1180                1185

Trp Ser  Asn Gly Ala Tyr Gly  Gly Asn Trp Ser Asn  Thr Thr Tyr
    1190                1195                1200

Thr Thr  Tyr Met Thr Asn Thr  Ala Tyr Trp Ser Asn  Ala Ala Arg
    1205                1210                1215

Met Thr  Asn Ala Cys Asn Gly  Thr Asn Gly Ala Tyr  Ala Ala Arg
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1220 1225 1230

Trp Ser Asn Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg
1235 1240 1245

Gly Gly Asn Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn
1250 1255 1260

Thr Gly Tyr Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr
1265 1270 1275

Gly Ala Arg Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr
1280 1285 1290

Cys Ala Tyr Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg
1295 1300 1305

Trp Ser Asn Met Thr Asn Trp Ser Asn Met Thr Asn Trp Ser Asn
1310 1315 1320

Cys Cys Asn Gly Gly Asn Ala Ala Arg
1325 1330

<210> 593
<211> 1359
<212> PRT
<213> Homo Sapiens

<400> 593

Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Met Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr
50 55 60

Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Met Gly Asn Gly Gly Asn
85 90 95

```
Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
            100                 105                 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Met Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Cys Ala Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Ala Cys
                165                 170                 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
            180                 185                 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Ala
        195                 200                 205

Ala Tyr Ala Thr Gly Trp Ser Asn Gly Thr Asn Gly Ala Tyr Ala Cys
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225                 230                 235                 240

Trp Ser Asn Met Thr Asn Ala Ala Arg Met Thr Asn Trp Ser Asn Trp
                245                 250                 255

Ser Asn Gly Thr Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala
            260                 265                 270

Tyr Ala Cys Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Gly Cys Asn Met Thr Asn Met
    290                 295                 300

Gly Asn Gly Gly Asn Ala Thr His Gly Thr Asn Met Thr Asn Ala Thr
305                 310                 315                 320

Gly Gly Thr Asn Thr Ala Tyr Gly Thr Asn Met Thr Asn Gly Gly Asn
                325                 330                 335

Gly Cys Asn Met Thr Asn Gly Ala Tyr Ala Thr His Thr Gly Gly Gly
            340                 345                 350
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Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Ala Ala Arg Gly Thr
355 360 365

Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn
370 375 380

Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp
385 390 395 400

Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys
405 410 415

Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn
420 425 430

Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly
435 440 445

Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr
450 455 460

Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr
465 470 475 480

Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly
485 490 495

Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly
500 505 510

Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn
515 520 525

Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly
530 535 540

Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser
545 550 555 560

Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn
565 570 575

Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly
580 585 590

```
Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr
        595                 600                 605

Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr
    610                 615                 620

Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys
625                 630                 635                 640

Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys
                645                 650                 655

Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn
            660                 665                 670

Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr
        675                 680                 685

Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys
    690                 695                 700

Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn
705                 710                 715                 720

Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly
                725                 730                 735

Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys
            740                 745                 750

Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn
        755                 760                 765

Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn Met Gly Asn Ala
    770                 775                 780

Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly
785                 790                 795                 800

Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn
                805                 810                 815

Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly
            820                 825                 830

Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly
        835                 840                 845
```

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Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn
    850                 855                 860

Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala
865                 870                 875                 880

Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met Gly Asn Gly Ala
                885                 890                 895

Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn
            900                 905                 910

Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn Trp
        915                 920                 925

Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr
    930                 935                 940

Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn
945                 950                 955                 960

Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala
                965                 970                 975

Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala
            980                 985                 990

Tyr Ala Ala Arg Gly Gly Asn Met  Thr Asn Cys Cys Asn  Gly Cys Asn
        995                 1000                1005

Cys Cys  Asn Ala Thr His Gly  Ala Arg Ala Ala Arg  Ala Cys Asn
    1010                1015                1020

Ala Thr  His Trp Ser Asn Ala  Ala Arg Ala Cys Asn  Ala Ala Arg
    1025                1030                1035

Gly Gly  Asn Cys Ala Arg Cys  Cys Asn Met Gly Asn  Gly Ala Arg
    1040                1045                1050

Cys Cys  Asn Cys Ala Arg Gly  Thr Asn Thr Ala Tyr  Ala Cys Asn
    1055                1060                1065

Met Thr  Asn Cys Cys Asn Cys  Cys Asn Trp Ser Asn  Met Gly Asn
    1070                1075                1080
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```
Gly Ala  Arg Gly Ala Arg Ala  Thr Gly Ala Cys Asn  Ala Ala Arg
    1085                 1090                 1095

Ala Ala  Tyr Cys Ala Arg Gly  Thr Asn Trp Ser Asn  Met Thr Asn
    1100                 1105                 1110

Ala Cys  Asn Thr Gly Tyr Met  Thr Asn Gly Thr Asn  Ala Ala Arg
    1115                 1120                 1125

Gly Gly  Asn Thr Thr Tyr Thr  Ala Tyr Cys Cys Asn  Trp Ser Asn
    1130                 1135                 1140

Gly Ala  Tyr Ala Thr His Gly  Cys Asn Gly Thr Asn  Gly Ala Arg
    1145                 1150                 1155

Thr Gly  Gly Gly Ala Arg Trp  Ser Asn Ala Ala Tyr  Gly Gly Asn
    1160                 1165                 1170

Cys Ala  Arg Cys Cys Asn Gly  Ala Arg Ala Ala Tyr  Ala Ala Tyr
    1175                 1180                 1185

Thr Ala  Tyr Ala Ala Arg Ala  Cys Asn Ala Cys Asn  Cys Cys Asn
    1190                 1195                 1200

Cys Cys  Asn Ala Thr Gly Met  Thr Asn Gly Ala Tyr  Trp Ser Asn
    1205                 1210                 1215

Gly Ala  Tyr Gly Gly Asn Trp  Ser Asn Thr Thr Tyr  Thr Thr Tyr
    1220                 1225                 1230

Met Thr  Asn Thr Ala Tyr Trp  Ser Asn Ala Ala Arg  Met Thr Asn
    1235                 1240                 1245

Ala Cys  Asn Gly Thr Asn Gly  Ala Tyr Ala Ala Arg  Trp Ser Asn
    1250                 1255                 1260

Met Gly  Asn Thr Gly Gly Cys  Ala Arg Cys Ala Arg  Gly Gly Asn
    1265                 1270                 1275

Ala Ala  Tyr Gly Thr Asn Thr  Thr Tyr Trp Ser Asn  Thr Gly Tyr
    1280                 1285                 1290

Trp Ser  Asn Gly Thr Asn Ala  Thr Gly Cys Ala Tyr  Gly Ala Arg
    1295                 1300                 1305

Gly Cys  Asn Met Thr Asn Cys  Ala Tyr Ala Ala Tyr  Cys Ala Tyr
    1310                 1315                 1320
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Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg Trp Ser Asn
1325 1330 1335

Met Thr Asn Trp Ser Asn Met Thr Asn Trp Ser Asn Cys Cys Asn
1340 1345 1350

Gly Gly Asn Ala Ala Arg
1355

<210> 594
<211> 1359
<212> PRT
<213> Homo Sapiens

<400> 594

Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Met Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr
50 55 60

Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
85 90 95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Met Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Thr
145 150 155 160

Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Ala Cys

```
                165                 170                 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
            180                 185                 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Ala
        195                 200                 205

Cys Asn Ala Thr His Trp Ser Asn Gly Thr Asn Gly Ala Tyr Ala Cys
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225                 230                 235                 240

Trp Ser Asn Met Thr Asn Ala Ala Arg Met Thr Asn Trp Ser Asn Trp
                245                 250                 255

Ser Asn Gly Thr Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala
            260                 265                 270

Tyr Ala Cys Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Gly Ala Tyr Gly Ala Arg Ala
    290                 295                 300

Cys Asn Gly Thr Asn Gly Thr Asn Met Gly Asn Gly Gly Asn Met Thr
305                 310                 315                 320

Asn Ala Thr His Met Gly Asn Thr Ala Tyr Thr Gly Tyr Thr Ala Tyr
                325                 330                 335

Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr Gly Gly Gly
            340                 345                 350

Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Ala Cys Asn Gly Thr
        355                 360                 365

Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn
    370                 375                 380

Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp
385                 390                 395                 400

Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys
                405                 410                 415
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Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn
            420                 425                 430

Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly
        435                 440                 445

Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr
    450                 455                 460

Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr
465                 470                 475                 480

Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly
                485                 490                 495

Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly
            500                 505                 510

Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn
        515                 520                 525

Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly
    530                 535                 540

Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser
545                 550                 555                 560

Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn
                565                 570                 575

Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly
            580                 585                 590

Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr
        595                 600                 605

Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr
    610                 615                 620

Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys
625                 630                 635                 640

Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys
                645                 650                 655

Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn
```

660 665 670

Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr
675 680 685

Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys
690 695 700

Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn
705 710 715 720

Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly
725 730 735

Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys
740 745 750

Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn
755 760 765

Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn Met Gly Asn Ala
770 775 780

Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly
785 790 795 800

Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn
805 810 815

Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly
820 825 830

Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly
835 840 845

Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn
850 855 860

Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala
865 870 875 880

Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met Gly Asn Gly Ala
885 890 895

Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn
900 905 910

Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn Trp
915 920 925

Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr
930 935 940

Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn
945 950 955 960

Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala
965 970 975

Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala
980 985 990

Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys Cys Asn Gly Cys Asn
995 1000 1005

Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala Arg Ala Cys Asn
1010 1015 1020

Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg
1025 1030 1035

Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg
1040 1045 1050

Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr Ala Cys Asn
1055 1060 1065

Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn Met Gly Asn
1070 1075 1080

Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn Ala Ala Arg
1085 1090 1095

Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn Met Thr Asn
1100 1105 1110

Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg
1115 1120 1125

Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Trp Ser Asn
1130 1135 1140

Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn Gly Ala Arg

1145 1150 1155

Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr Gly Gly Asn
1160 1165 1170

Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr Ala Ala Tyr
1175 1180 1185

Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn Cys Cys Asn
1190 1195 1200

Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr Trp Ser Asn
1205 1210 1215

Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr Thr Thr Tyr
1220 1225 1230

Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg Met Thr Asn
1235 1240 1245

Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg Trp Ser Asn
1250 1255 1260

Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg Gly Gly Asn
1265 1270 1275

Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn Thr Gly Tyr
1280 1285 1290

Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr Gly Ala Arg
1295 1300 1305

Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr
1310 1315 1320

Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg Trp Ser Asn
1325 1330 1335

Met Thr Asn Trp Ser Asn Met Thr Asn Trp Ser Asn Cys Cys Asn
1340 1345 1350

Gly Gly Asn Ala Ala Arg
1355

<210> 595
<211> 1344
<212> PRT

<213> Homo Sapiens

<400> 595

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Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Cys Ala Arg Gly
1               5                  10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Met Thr
            20                  25                  30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
        35                  40                  45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Ala Tyr Thr
    50                  55                  60

Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65                  70                  75                  80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
                85                  90                  95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
            100                 105                 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Met Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Cys
145                 150                 155                 160

Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Ala Cys
                165                 170                 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
            180                 185                 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Ala Thr His Ala
        195                 200                 205

Cys Asn Ala Thr His Trp Ser Asn Gly Cys Asn Gly Ala Tyr Ala Cys
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225                 230                 235                 240
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```
Trp Ser Asn Met Thr Asn Ala Ala Arg Met Thr Asn Ala Ala Tyr Trp
                245                 250                 255

Ser Asn Gly Thr Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala
            260                 265                 270

Tyr Ala Cys Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Gly Ala Tyr Met Gly Asn Gly
    290                 295                 300

Gly Asn Gly Gly Asn Gly Gly Asn Gly Ala Tyr Thr Ala Tyr Gly Gly
305                 310                 315                 320

Asn Met Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr Gly Gly
                325                 330                 335

Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Ala Cys Asn Gly
            340                 345                 350

Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys
        355                 360                 365

Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn
    370                 375                 380

Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly
385                 390                 395                 400

Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser
                405                 410                 415

Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn
            420                 425                 430

Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr Met
        435                 440                 445

Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr
    450                 455                 460

Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn
465                 470                 475                 480
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Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly
                485                 490                 495

Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly
            500                 505                 510

Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn
        515                 520                 525

Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp Ser Asn Trp
    530                 535                 540

Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr
545                 550                 555                 560

Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn
                565                 570                 575

Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr
            580                 585                 590

Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala
        595                 600                 605

Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr
    610                 615                 620

Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala
625                 630                 635                 640

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys
                645                 650                 655

Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr
            660                 665                 670

Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys
        675                 680                 685

Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys
    690                 695                 700

Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn
705                 710                 715                 720

Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys
                725                 730                 735
```

```
Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys
            740                 745                 750

Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn Met Gly Asn
        755                 760                 765

Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr
    770                 775                 780

Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr
785                 790                 795                 800

Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn
                805                 810                 815

Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr
            820                 825                 830

Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr
        835                 840                 845

Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn
    850                 855                 860

Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met Gly Asn Gly
865                 870                 875                 880

Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser
                885                 890                 895

Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn
            900                 905                 910

Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly Thr Asn Gly
        915                 920                 925

Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr
    930                 935                 940

Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr
945                 950                 955                 960

Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala
                965                 970                 975
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```
Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys Cys Asn Gly Cys
            980                 985                 990

Asn Cys Cys Asn Ala Thr His Gly  Ala Arg Ala Ala Arg  Ala Cys Asn
        995                 1000                1005

Ala Thr  His Trp Ser Asn Ala  Ala Arg Ala Cys Asn  Ala Ala Arg
    1010                1015                1020

Gly Gly  Asn Cys Ala Arg Cys  Cys Asn Met Gly Asn  Gly Ala Arg
    1025                1030                1035

Cys Cys  Asn Cys Ala Arg Gly  Thr Asn Thr Ala Tyr  Ala Cys Asn
    1040                1045                1050

Met Thr  Asn Cys Cys Asn Cys  Cys Asn Trp Ser Asn  Met Gly Asn
    1055                1060                1065

Gly Ala  Arg Gly Ala Arg Ala  Thr Gly Ala Cys Asn  Ala Ala Arg
    1070                1075                1080

Ala Ala  Tyr Cys Ala Arg Gly  Thr Asn Trp Ser Asn  Met Thr Asn
    1085                1090                1095

Ala Cys  Asn Thr Gly Tyr Met  Thr Asn Gly Thr Asn  Ala Ala Arg
    1100                1105                1110

Gly Gly  Asn Thr Thr Tyr Thr  Ala Tyr Cys Cys Asn  Trp Ser Asn
    1115                1120                1125

Gly Ala  Tyr Ala Thr His Gly  Cys Asn Gly Thr Asn  Gly Ala Arg
    1130                1135                1140

Thr Gly  Gly Gly Ala Arg Trp  Ser Asn Ala Ala Tyr  Gly Gly Asn
    1145                1150                1155

Cys Ala  Arg Cys Cys Asn Gly  Ala Arg Ala Ala Tyr  Ala Ala Tyr
    1160                1165                1170

Thr Ala  Tyr Ala Ala Arg Ala  Cys Asn Ala Cys Asn  Cys Cys Asn
    1175                1180                1185

Cys Cys  Asn Ala Thr Gly Met  Thr Asn Gly Ala Tyr  Trp Ser Asn
    1190                1195                1200

Gly Ala  Tyr Gly Gly Asn Trp  Ser Asn Thr Thr Tyr  Thr Thr Tyr
    1205                1210                1215
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Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg Met Thr Asn
1220 1225 1230

Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg Trp Ser Asn
1235 1240 1245

Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg Gly Gly Asn
1250 1255 1260

Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn Thr Gly Tyr
1265 1270 1275

Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr Gly Ala Arg
1280 1285 1290

Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr
1295 1300 1305

Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg Trp Ser Asn
1310 1315 1320

Met Thr Asn Trp Ser Asn Met Thr Asn Trp Ser Asn Cys Cys Asn
1325 1330 1335

Gly Gly Asn Ala Ala Arg
1340

<210> 596
<211> 1344
<212> PRT
<213> Homo Sapiens

<400> 596

Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Met Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Ala Tyr Thr
50 55 60

Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly

65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
85 90 95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Met Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Cys
145 150 155 160

Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Ala Cys
165 170 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
180 185 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Ala Thr His Ala
195 200 205

Cys Asn Ala Thr His Trp Ser Asn Gly Cys Asn Gly Ala Tyr Ala Cys
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225 230 235 240

Trp Ser Asn Met Thr Asn Ala Ala Arg Met Thr Asn Ala Ala Tyr Trp
245 250 255

Ser Asn Gly Thr Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala
260 265 270

Tyr Ala Cys Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Gly Ala Tyr Met Gly Asn Gly
290 295 300

Gly Asn Gly Gly Asn Gly Gly Asn Gly Ala Tyr Thr Ala Tyr Gly Gly
305 310 315 320

Asn Met Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr Gly Gly
325 330 335

Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Ala Cys Asn Gly
340 345 350

Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys
355 360 365

Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn
370 375 380

Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly
385 390 395 400

Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser
405 410 415

Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn
420 425 430

Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr Met
435 440 445

Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr
450 455 460

Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn
465 470 475 480

Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly
485 490 495

Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly
500 505 510

Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn
515 520 525

Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp Ser Asn Trp
530 535 540

Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr
545 550 555 560

Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn

565 570 575

Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr
580 585 590

Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala
595 600 605

Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr
610 615 620

Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala
625 630 635 640

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys
645 650 655

Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr
660 665 670

Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys
675 680 685

Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys
690 695 700

Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn
705 710 715 720

Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys
725 730 735

Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys
740 745 750

Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn Met Gly Asn
755 760 765

Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr
770 775 780

Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr
785 790 795 800

Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn
805 810 815

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Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr
            820                 825                 830

Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr
        835                 840                 845

Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn
    850                 855                 860

Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met Gly Asn Gly
865                 870                 875                 880

Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser
                885                 890                 895

Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn
            900                 905                 910

Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly Thr Asn Gly
        915                 920                 925

Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr
    930                 935                 940

Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr
945                 950                 955                 960

Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala
                965                 970                 975

Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys Cys Asn Gly Cys
            980                 985                 990

Asn Cys Cys Asn Ala Thr His Gly  Ala Arg Ala Ala Arg  Ala Cys Asn
        995                 1000                1005

Ala Thr  His Trp Ser Asn Ala  Ala Arg Ala Cys Asn  Ala Ala Arg
    1010                1015                1020

Gly Gly  Asn Cys Ala Arg Cys  Cys Asn Met Gly Asn  Gly Ala Arg
    1025                1030                1035

Cys Cys  Asn Cys Ala Arg Gly  Thr Asn Thr Ala Tyr  Ala Cys Asn
    1040                1045                1050

Met Thr  Asn Cys Cys Asn Cys  Cys Asn Trp Ser Asn  Met Gly Asn
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1055 1060 1065

Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn Ala Ala Arg
1070 1075 1080

Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn Met Thr Asn
1085 1090 1095

Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg
1100 1105 1110

Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Trp Ser Asn
1115 1120 1125

Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn Gly Ala Arg
1130 1135 1140

Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr Gly Gly Asn
1145 1150 1155

Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr Ala Ala Tyr
1160 1165 1170

Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn Cys Cys Asn
1175 1180 1185

Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr Trp Ser Asn
1190 1195 1200

Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr Thr Thr Tyr
1205 1210 1215

Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg Met Thr Asn
1220 1225 1230

Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg Trp Ser Asn
1235 1240 1245

Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg Gly Gly Asn
1250 1255 1260

Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn Thr Gly Tyr
1265 1270 1275

Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr Gly Ala Arg
1280 1285 1290

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Gly Cys  Asn Met Thr Asn Cys  Ala Tyr Ala Ala Tyr  Cys Ala Tyr
    1295                1300                1305

Thr Ala  Tyr Ala Cys Asn Cys  Ala Arg Ala Ala Arg  Trp Ser Asn
    1310                1315                1320

Met Thr  Asn Trp Ser Asn Met  Thr Asn Trp Ser Asn  Cys Cys Asn
    1325                1330                1335

Gly Gly  Asn Ala Ala Arg
    1340
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<210> 597
<211> 1335
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<400> 597

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Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Cys Ala Arg Gly
1               5                  10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Met Thr
            20                  25                  30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
        35                  40                  45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr
    50                  55                  60

Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65                  70                  75                  80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
                85                  90                  95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
            100                 105                 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Met Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Cys
145                 150                 155                 160
```

```
Ala Tyr Trp Ser Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Ala Cys
                165                 170                 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
            180                 185                 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Ala Thr His Ala
        195                 200                 205

Cys Asn Ala Ala Arg Trp Ser Asn Gly Thr Asn Gly Ala Tyr Ala Cys
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225                 230                 235                 240

Trp Ser Asn Met Thr Asn Ala Ala Arg Met Thr Asn Trp Ser Asn Trp
                245                 250                 255

Ser Asn Gly Thr Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala
            260                 265                 270

Tyr Ala Cys Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Trp Ser Asn Ala Ala Tyr Ala
    290                 295                 300

Ala Tyr Thr Ala Tyr Gly Gly Asn Thr Gly Tyr Thr Thr Tyr Gly Cys
305                 310                 315                 320

Asn Met Thr Asn Thr Gly Gly Gly Gly Asn Met Gly Asn Gly Gly Asn
                325                 330                 335

Ala Cys Asn Met Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp
            340                 345                 350

Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala
        355                 360                 365

Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr
    370                 375                 380

Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp
385                 390                 395                 400
```

Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala
405 410 415

Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn
420 425 430

Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly
435 440 445

Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys
450 455 460

Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly
465 470 475 480

Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr Asn Ala
485 490 495

Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys
500 505 510

Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met Thr Asn
515 520 525

Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr
530 535 540

Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr
545 550 555 560

Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn
565 570 575

Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys
580 585 590

Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala
595 600 605

Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn
610 615 620

Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly
625 630 635 640

Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg Met Gly
645 650 655

```
Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg
            660                 665                 670

Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly
        675                 680                 685

Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly
    690                 695                 700

Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn
705                 710                 715                 720

Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala
                725                 730                 735

Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr
            740                 745                 750

His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg
        755                 760                 765

Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly
    770                 775                 780

Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala
785                 790                 795                 800

Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg
                805                 810                 815

Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly
            820                 825                 830

Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala
        835                 840                 845

Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg
    850                 855                 860

Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr
865                 870                 875                 880

Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly
                885                 890                 895
```

```
Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met Thr Asn
            900                 905                 910

Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly
        915                 920                 925

Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala
    930                 935                 940

Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg
945                 950                 955                 960

Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met
                965                 970                 975

Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His Gly Ala
            980                 985                 990

Arg Ala Ala Arg Ala Cys Asn Ala  Thr His Trp Ser Asn  Ala Ala Arg
        995                 1000                1005

Ala Cys  Asn Ala Ala Arg Gly  Gly Asn Cys Ala Arg  Cys Cys Asn
    1010                1015                1020

Met Gly  Asn Gly Ala Arg Cys  Cys Asn Cys Ala Arg  Gly Thr Asn
    1025                1030                1035

Thr Ala  Tyr Ala Cys Asn Met  Thr Asn Cys Cys Asn  Cys Cys Asn
    1040                1045                1050

Trp Ser  Asn Met Gly Asn Gly  Ala Arg Gly Ala Arg  Ala Thr Gly
    1055                1060                1065

Ala Cys  Asn Ala Ala Arg Ala  Ala Tyr Cys Ala Arg  Gly Thr Asn
    1070                1075                1080

Trp Ser  Asn Met Thr Asn Ala  Cys Asn Thr Gly Tyr  Met Thr Asn
    1085                1090                1095

Gly Thr  Asn Ala Ala Arg Gly  Gly Asn Thr Thr Tyr  Thr Ala Tyr
    1100                1105                1110

Cys Cys  Asn Trp Ser Asn Gly  Ala Tyr Ala Thr His  Gly Cys Asn
    1115                1120                1125

Gly Thr  Asn Gly Ala Arg Thr  Gly Gly Gly Ala Arg  Trp Ser Asn
    1130                1135                1140
```

```
Ala Ala  Tyr Gly Gly Asn Cys  Ala Arg Cys Cys Asn  Gly Ala Arg
    1145                 1150                 1155

Ala Ala  Tyr Ala Ala Tyr Thr  Ala Tyr Ala Ala Arg  Ala Cys Asn
    1160                 1165                 1170

Ala Cys  Asn Cys Cys Asn Cys  Cys Asn Ala Thr Gly  Met Thr Asn
    1175                 1180                 1185

Gly Ala  Tyr Trp Ser Asn Gly  Ala Tyr Gly Gly Asn  Trp Ser Asn
    1190                 1195                 1200

Thr Thr  Tyr Thr Thr Tyr Met  Thr Asn Thr Ala Tyr  Trp Ser Asn
    1205                 1210                 1215

Ala Ala  Arg Met Thr Asn Ala  Cys Asn Gly Thr Asn  Gly Ala Tyr
    1220                 1225                 1230

Ala Ala  Arg Trp Ser Asn Met  Gly Asn Thr Gly Gly  Cys Ala Arg
    1235                 1240                 1245

Cys Ala  Arg Gly Gly Asn Ala  Ala Tyr Gly Thr Asn  Thr Thr Tyr
    1250                 1255                 1260

Trp Ser  Asn Thr Gly Tyr Trp  Ser Asn Gly Thr Asn  Ala Thr Gly
    1265                 1270                 1275

Cys Ala  Tyr Gly Ala Arg Gly  Cys Asn Met Thr Asn  Cys Ala Tyr
    1280                 1285                 1290

Ala Ala  Tyr Cys Ala Tyr Thr  Ala Tyr Ala Cys Asn  Cys Ala Arg
    1295                 1300                 1305

Ala Ala  Arg Trp Ser Asn Met  Thr Asn Trp Ser Asn  Met Thr Asn
    1310                 1315                 1320

Trp Ser  Asn Cys Cys Asn Gly  Gly Asn Ala Ala Arg
    1325                 1330                 1335
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<210> 598
<211> 1335
<212> PRT
<213> Homo Sapiens

<400> 598

Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Cys Ala Arg Gly

1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Met Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr
50 55 60

Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
85 90 95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Met Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Cys
145 150 155 160

Ala Tyr Trp Ser Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Ala Cys
165 170 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
180 185 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Ala Thr His Ala
195 200 205

Cys Asn Ala Ala Arg Trp Ser Asn Gly Thr Asn Gly Ala Tyr Ala Cys
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225 230 235 240

Trp Ser Asn Met Thr Asn Ala Ala Arg Met Thr Asn Trp Ser Asn Trp
245 250 255

```
Ser Asn Gly Thr Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala
            260                 265                 270

Tyr Ala Cys Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Trp Ser Asn Ala Ala Tyr Ala
    290                 295                 300

Ala Tyr Thr Ala Tyr Gly Gly Asn Thr Gly Tyr Thr Thr Tyr Gly Cys
305                 310                 315                 320

Asn Met Thr Asn Thr Gly Gly Gly Gly Asn Met Gly Asn Gly Gly Asn
                325                 330                 335

Ala Cys Asn Met Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp
            340                 345                 350

Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala
        355                 360                 365

Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr
    370                 375                 380

Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp
385                 390                 395                 400

Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala
                405                 410                 415

Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn
            420                 425                 430

Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly
        435                 440                 445

Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys
    450                 455                 460

Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly
465                 470                 475                 480

Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr Asn Ala
                485                 490                 495

Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys
```

500 505 510

Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met Thr Asn
515 520 525

Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr
530 535 540

Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr
545 550 555 560

Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn
565 570 575

Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys
580 585 590

Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala
595 600 605

Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn
610 615 620

Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly
625 630 635 640

Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg Met Gly
645 650 655

Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg
660 665 670

Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly
675 680 685

Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly
690 695 700

Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn
705 710 715 720

Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala
725 730 735

Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr
740 745 750

His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg
755 760 765

Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly
770 775 780

Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala
785 790 795 800

Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg
805 810 815

Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly
820 825 830

Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala
835 840 845

Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg
850 855 860

Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr
865 870 875 880

Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly
885 890 895

Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met Thr Asn
900 905 910

Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly
915 920 925

Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala
930 935 940

Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg
945 950 955 960

Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met
965 970 975

Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His Gly Ala
980 985 990

Arg Ala Ala Arg Ala Cys Asn Ala Thr His Trp Ser Asn Ala Ala Arg

995 1000 1005

Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Ala Arg Cys Cys Asn
1010 1015 1020

Met Gly Asn Gly Ala Arg Cys Cys Asn Cys Ala Arg Gly Thr Asn
1025 1030 1035

Thr Ala Tyr Ala Cys Asn Met Thr Asn Cys Cys Asn Cys Cys Asn
1040 1045 1050

Trp Ser Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Ala Thr Gly
1055 1060 1065

Ala Cys Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn
1070 1075 1080

Trp Ser Asn Met Thr Asn Ala Cys Asn Thr Gly Tyr Met Thr Asn
1085 1090 1095

Gly Thr Asn Ala Ala Arg Gly Gly Asn Thr Thr Tyr Thr Ala Tyr
1100 1105 1110

Cys Cys Asn Trp Ser Asn Gly Ala Tyr Ala Thr His Gly Cys Asn
1115 1120 1125

Gly Thr Asn Gly Ala Arg Thr Gly Gly Gly Ala Arg Trp Ser Asn
1130 1135 1140

Ala Ala Tyr Gly Gly Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg
1145 1150 1155

Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr Ala Ala Arg Ala Cys Asn
1160 1165 1170

Ala Cys Asn Cys Cys Asn Cys Cys Asn Ala Thr Gly Met Thr Asn
1175 1180 1185

Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Gly Asn Trp Ser Asn
1190 1195 1200

Thr Thr Tyr Thr Thr Tyr Met Thr Asn Thr Ala Tyr Trp Ser Asn
1205 1210 1215

Ala Ala Arg Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Ala Tyr
1220 1225 1230

```
Ala Ala  Arg Trp Ser Asn Met  Gly Asn Thr Gly Gly  Cys Ala Arg
    1235                 1240                 1245

Cys Ala  Arg Gly Gly Asn Ala  Ala Tyr Gly Thr Asn  Thr Thr Tyr
    1250                 1255                 1260

Trp Ser  Asn Thr Gly Tyr Trp  Ser Asn Gly Thr Asn  Ala Thr Gly
    1265                 1270                 1275

Cys Ala  Tyr Gly Ala Arg Gly  Cys Asn Met Thr Asn  Cys Ala Tyr
    1280                 1285                 1290

Ala Ala  Tyr Cys Ala Tyr Thr  Ala Tyr Ala Cys Asn  Cys Ala Arg
    1295                 1300                 1305

Ala Ala  Arg Trp Ser Asn Met  Thr Asn Trp Ser Asn  Met Thr Asn
    1310                 1315                 1320

Trp Ser  Asn Cys Cys Asn Gly  Gly Asn Ala Ala Arg
    1325                 1330                 1335
```

<210> 599
<211> 1377
<212> PRT
<213> Homo Sapiens

<400> 599

```
Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Cys Ala Arg Gly
1               5                  10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Met Thr
            20                  25                  30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
        35                  40                  45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr
    50                  55                  60

Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65                  70                  75                  80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
                85                  90                  95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
            100                 105                 110
```

```
Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Met Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Cys
145                 150                 155                 160

Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Ala Cys
                165                 170                 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
            180                 185                 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Ala
        195                 200                 205

Cys Asn Ala Thr His Trp Ser Asn Gly Thr Asn Gly Ala Tyr Ala Cys
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225                 230                 235                 240

Trp Ser Asn Met Thr Asn Ala Ala Arg Met Thr Asn Trp Ser Asn Trp
                245                 250                 255

Ser Asn Gly Thr Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala
            260                 265                 270

Tyr Ala Cys Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Ala Tyr Ala
    290                 295                 300

Ala Tyr Thr Ala Tyr Gly Gly Asn Met Thr Asn Thr Ala Tyr Thr Ala
305                 310                 315                 320

Tyr Thr Ala Tyr Gly Ala Tyr Trp Ser Asn Trp Ser Asn Gly Gly Asn
                325                 330                 335

Thr Ala Tyr Cys Cys Asn Trp Ser Asn Thr Ala Tyr Thr Ala Tyr Thr
            340                 345                 350
```

```
Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr Gly
        355                 360                 365

Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Ala Cys Asn
    370                 375                 380

Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly
385                 390                 395                 400

Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys
                405                 410                 415

Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn
            420                 425                 430

Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp
        435                 440                 445

Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys
    450                 455                 460

Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr
465                 470                 475                 480

Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr
                485                 490                 495

Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys
            500                 505                 510

Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn
        515                 520                 525

Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser Asn Gly
    530                 535                 540

Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys
545                 550                 555                 560

Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp Ser Asn
                565                 570                 575

Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn Met
            580                 585                 590

Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys
        595                 600                 605
```

Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr
610 615 620

Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr
625 630 635 640

Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala
645 650 655

Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr
660 665 670

Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala
675 680 685

Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg Thr Gly
690 695 700

Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn
705 710 715 720

Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys
725 730 735

Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser
740 745 750

Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn
755 760 765

Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala
770 775 780

Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn Met Gly
785 790 795 800

Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn
805 810 815

Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly
820 825 830

Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys
835 840 845

```
Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr
    850                 855                 860

Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly
865                 870                 875                 880

Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys
                885                 890                 895

Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met Gly Asn
            900                 905                 910

Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp
        915                 920                 925

Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr
    930                 935                 940

Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly Thr Asn
945                 950                 955                 960

Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met
                965                 970                 975

Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala
            980                 985                 990

Tyr Ala Ala Arg Thr Gly Tyr Ala  Ala Arg Gly Thr Asn  Trp Ser Asn
        995                 1000                1005

Ala Ala  Tyr Ala Ala Arg Gly  Gly Asn Met Thr Asn  Cys Cys Asn
    1010                1015                1020

Gly Cys  Asn Cys Cys Asn Ala  Thr His Gly Ala Arg  Ala Ala Arg
    1025                1030                1035

Ala Cys  Asn Ala Thr His Trp  Ser Asn Ala Ala Arg  Ala Cys Asn
    1040                1045                1050

Ala Ala  Arg Gly Gly Asn Cys  Ala Arg Cys Cys Asn  Met Gly Asn
    1055                1060                1065

Gly Ala  Arg Cys Cys Asn Cys  Ala Arg Gly Thr Asn  Thr Ala Tyr
    1070                1075                1080

Ala Cys  Asn Met Thr Asn Cys  Cys Asn Cys Cys Asn  Trp Ser Asn
    1085                1090                1095
```

Met Gly Asn Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn
1100 1105 1110

Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn
1115 1120 1125

Met Thr Asn Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn
1130 1135 1140

Ala Ala Arg Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn
1145 1150 1155

Trp Ser Asn Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn
1160 1165 1170

Gly Ala Arg Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr
1175 1180 1185

Gly Gly Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr
1190 1195 1200

Ala Ala Tyr Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn
1205 1210 1215

Cys Cys Asn Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr
1220 1225 1230

Trp Ser Asn Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr
1235 1240 1245

Thr Thr Tyr Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg
1250 1255 1260

Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg
1265 1270 1275

Trp Ser Asn Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg
1280 1285 1290

Gly Gly Asn Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn
1295 1300 1305

Thr Gly Tyr Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr
1310 1315 1320

```
Gly Ala  Arg Gly Cys Asn Met  Thr Asn Cys Ala Tyr  Ala Ala Tyr
    1325                1330                1335

Cys Ala  Tyr Thr Ala Tyr Ala  Cys Asn Cys Ala Arg  Ala Ala Arg
    1340                1345                1350

Trp Ser  Asn Met Thr Asn Trp  Ser Asn Met Thr Asn  Trp Ser Asn
    1355                1360                1365

Cys Cys  Asn Gly Gly Asn Ala  Ala Arg
    1370                1375
```

<210> 600
<211> 1353
<212> PRT
<213> Homo Sapiens

<400> 600

```
Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Cys Ala Arg Gly
1               5                   10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Met Thr
            20                  25                  30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
        35                  40                  45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr
    50                  55                  60

Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65                  70                  75                  80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
                85                  90                  95

Gly Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Ala Ala Tyr Thr
            100                 105                 110

Gly Gly Gly Thr Asn Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Met Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Thr
145                 150                 155                 160
```

```
Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Gly Gly Asn Ala Cys
                  165                 170                 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
            180                 185                 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Ala
        195                 200                 205

Cys Asn Ala Thr His Trp Ser Asn Gly Thr Asn Gly Ala Tyr Ala Cys
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225                 230                 235                 240

Trp Ser Asn Met Thr Asn Ala Ala Arg Met Thr Asn Thr Thr Tyr Trp
                  245                 250                 255

Ser Asn Gly Thr Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala
            260                 265                 270

Tyr Ala Cys Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Thr Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Ala Cys Asn Thr Ala Tyr Thr
    290                 295                 300

Ala Tyr Gly Ala Tyr Ala Thr His Met Thr Asn Ala Cys Asn Gly Gly
305                 310                 315                 320

Asn Thr Ala Tyr Cys Cys Asn Thr Thr Tyr Thr Ala Tyr Thr Thr Tyr
                  325                 330                 335

Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly
            340                 345                 350

Gly Asn Ala Cys Asn Met Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr
        355                 360                 365

Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn
    370                 375                 380

Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr
385                 390                 395                 400

Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly
```

405 410 415

Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn
420 425 430

Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met
435 440 445

Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala
450 455 460

Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg
465 470 475 480

Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr
485 490 495

Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr
500 505 510

Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr
515 520 525

Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met
530 535 540

Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr
545 550 555 560

Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
565 570 575

Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp
580 585 590

Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys
595 600 605

Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr
610 615 620

Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys
625 630 635 640

Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr
645 650 655

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Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg
            660                 665                 670

Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly
        675                 680                 685

Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys
    690                 695                 700

Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn
705                 710                 715                 720

Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met
                725                 730                 735

Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys
            740                 745                 750

Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly
        755                 760                 765

Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly
    770                 775                 780

Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr
785                 790                 795                 800

Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr
                805                 810                 815

Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys
            820                 825                 830

Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr
        835                 840                 845

Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn
    850                 855                 860

Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala
865                 870                 875                 880

Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala
                885                 890                 895

Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr
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900 905 910

Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met
915 920 925

Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala
930 935 940

Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn
945 950 955 960

Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala
965 970 975

Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly
980 985 990

Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His
995 1000 1005

Gly Ala Arg Ala Ala Arg Ala Cys Asn Ala Thr His Trp Ser Asn
1010 1015 1020

Ala Ala Arg Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Ala Arg
1025 1030 1035

Cys Cys Asn Met Gly Asn Gly Ala Arg Cys Cys Asn Cys Ala Arg
1040 1045 1050

Gly Thr Asn Thr Ala Tyr Ala Cys Asn Met Thr Asn Cys Cys Asn
1055 1060 1065

Cys Cys Asn Trp Ser Asn Met Gly Asn Gly Ala Arg Gly Ala Arg
1070 1075 1080

Ala Thr Gly Ala Cys Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg
1085 1090 1095

Gly Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr Gly Tyr
1100 1105 1110

Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Gly Asn Thr Thr Tyr
1115 1120 1125

Thr Ala Tyr Cys Cys Asn Trp Ser Asn Gly Ala Tyr Ala Thr His
1130 1135 1140

```
Gly Cys  Asn Gly Thr Asn Gly  Ala Arg Thr Gly Gly  Gly Ala Arg
    1145                 1150                 1155

Trp Ser  Asn Ala Ala Tyr Gly  Gly Asn Cys Ala Arg  Cys Cys Asn
    1160                 1165                 1170

Gly Ala  Arg Ala Ala Tyr Ala  Ala Tyr Thr Ala Tyr  Ala Ala Arg
    1175                 1180                 1185

Ala Cys  Asn Ala Cys Asn Cys  Cys Asn Cys Cys Asn  Ala Thr Gly
    1190                 1195                 1200

Met Thr  Asn Gly Ala Tyr Trp  Ser Asn Gly Ala Tyr  Gly Gly Asn
    1205                 1210                 1215

Trp Ser  Asn Thr Thr Tyr Thr  Thr Tyr Met Thr Asn  Thr Ala Tyr
    1220                 1225                 1230

Trp Ser  Asn Ala Ala Arg Met  Thr Asn Ala Cys Asn  Gly Thr Asn
    1235                 1240                 1245

Gly Ala  Tyr Ala Ala Arg Trp  Ser Asn Met Gly Asn  Thr Gly Gly
    1250                 1255                 1260

Cys Ala  Arg Cys Ala Arg Gly  Gly Asn Ala Ala Tyr  Gly Thr Asn
    1265                 1270                 1275

Thr Thr  Tyr Trp Ser Asn Thr  Gly Tyr Trp Ser Asn  Gly Thr Asn
    1280                 1285                 1290

Ala Thr  Gly Cys Ala Tyr Gly  Ala Arg Gly Cys Asn  Met Thr Asn
    1295                 1300                 1305

Cys Ala  Tyr Ala Ala Tyr Cys  Ala Tyr Thr Ala Tyr  Ala Cys Asn
    1310                 1315                 1320

Cys Ala  Arg Ala Ala Arg Trp  Ser Asn Met Thr Asn  Trp Ser Asn
    1325                 1330                 1335

Met Thr  Asn Trp Ser Asn Cys  Cys Asn Gly Gly Asn  Ala Ala Arg
    1340                 1345                 1350
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<210> 601
<211> 1353
<212> PRT
<213> Homo Sapiens

<400> 601

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Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Cys Ala Arg Gly
1               5                  10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Met Thr
            20                  25                  30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
        35                  40                  45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr
    50                  55                  60

Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65                  70                  75                  80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
                85                  90                  95

Gly Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Ala Ala Tyr Thr
            100                 105                 110

Gly Gly Gly Thr Asn Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Met Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Gly Gly Asn Ala Cys
                165                 170                 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
            180                 185                 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Ala
        195                 200                 205

Cys Asn Ala Thr His Trp Ser Asn Gly Thr Asn Gly Ala Tyr Ala Cys
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225                 230                 235                 240
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```
Trp Ser Asn Met Thr Asn Ala Ala Arg Met Thr Asn Thr Thr Tyr Trp
                245                 250                 255

Ser Asn Gly Thr Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala
            260                 265                 270

Tyr Ala Cys Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Thr Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Ala Cys Asn Thr Ala Tyr Thr
    290                 295                 300

Ala Tyr Gly Ala Tyr Ala Thr His Met Thr Asn Ala Cys Asn Gly Gly
305                 310                 315                 320

Asn Thr Ala Tyr Cys Cys Asn Thr Thr Tyr Thr Ala Tyr Thr Thr Tyr
                325                 330                 335

Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly
            340                 345                 350

Gly Asn Ala Cys Asn Met Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr
        355                 360                 365

Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn
    370                 375                 380

Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr
385                 390                 395                 400

Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly
                405                 410                 415

Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn
            420                 425                 430

Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met
        435                 440                 445

Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala
    450                 455                 460

Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg
465                 470                 475                 480

Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr
                485                 490                 495
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```
Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr
            500                 505                 510

Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr
        515                 520                 525

Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met
    530                 535                 540

Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr
545                 550                 555                 560

Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
                565                 570                 575

Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp
            580                 585                 590

Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys
        595                 600                 605

Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr
    610                 615                 620

Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys
625                 630                 635                 640

Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr
                645                 650                 655

Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg
            660                 665                 670

Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly
        675                 680                 685

Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys
    690                 695                 700

Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn
705                 710                 715                 720

Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met
                725                 730                 735
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Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys
            740                 745                 750

Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly
        755                 760                 765

Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly
    770                 775                 780

Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr
785                 790                 795                 800

Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr
                805                 810                 815

Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys
            820                 825                 830

Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr
        835                 840                 845

Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn
    850                 855                 860

Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala
865                 870                 875                 880

Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala
                885                 890                 895

Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr
            900                 905                 910

Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met
        915                 920                 925

Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala
    930                 935                 940

Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn
945                 950                 955                 960

Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala
                965                 970                 975

Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly
            980                 985                 990
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Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His
995 1000 1005

Gly Ala Arg Ala Ala Arg Ala Cys Asn Ala Thr His Trp Ser Asn
1010 1015 1020

Ala Ala Arg Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Ala Arg
1025 1030 1035

Cys Cys Asn Met Gly Asn Gly Ala Arg Cys Cys Asn Cys Ala Arg
1040 1045 1050

Gly Thr Asn Thr Ala Tyr Ala Cys Asn Met Thr Asn Cys Cys Asn
1055 1060 1065

Cys Cys Asn Trp Ser Asn Met Gly Asn Gly Ala Arg Gly Ala Arg
1070 1075 1080

Ala Thr Gly Ala Cys Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg
1085 1090 1095

Gly Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr Gly Tyr
1100 1105 1110

Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Gly Asn Thr Thr Tyr
1115 1120 1125

Thr Ala Tyr Cys Cys Asn Trp Ser Asn Gly Ala Tyr Ala Thr His
1130 1135 1140

Gly Cys Asn Gly Thr Asn Gly Ala Arg Thr Gly Gly Gly Ala Arg
1145 1150 1155

Trp Ser Asn Ala Ala Tyr Gly Gly Asn Cys Ala Arg Cys Cys Asn
1160 1165 1170

Gly Ala Arg Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr Ala Ala Arg
1175 1180 1185

Ala Cys Asn Ala Cys Asn Cys Cys Asn Cys Cys Asn Ala Thr Gly
1190 1195 1200

Met Thr Asn Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Gly Asn
1205 1210 1215

Trp Ser Asn Thr Thr Tyr Thr Thr Tyr Met Thr Asn Thr Ala Tyr
1220 1225 1230

Trp Ser Asn Ala Ala Arg Met Thr Asn Ala Cys Asn Gly Thr Asn
1235 1240 1245

Gly Ala Tyr Ala Ala Arg Trp Ser Asn Met Gly Asn Thr Gly Gly
1250 1255 1260

Cys Ala Arg Cys Ala Arg Gly Gly Asn Ala Ala Tyr Gly Thr Asn
1265 1270 1275

Thr Thr Tyr Trp Ser Asn Thr Gly Tyr Trp Ser Asn Gly Thr Asn
1280 1285 1290

Ala Thr Gly Cys Ala Tyr Gly Ala Arg Gly Cys Asn Met Thr Asn
1295 1300 1305

Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr Thr Ala Tyr Ala Cys Asn
1310 1315 1320

Cys Ala Arg Ala Ala Arg Trp Ser Asn Met Thr Asn Trp Ser Asn
1325 1330 1335

Met Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn Ala Ala Arg
1340 1345 1350

<210> 602
<211> 1338
<212> PRT
<213> Homo Sapiens

<400> 602

Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Cys Ala Arg Cys
1 5 10 15

Ala Arg Thr Gly Gly Gly Gly Asn Gly Cys Asn Gly Gly Asn Met Thr
20 25 30

Asn Met Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Gly Ala Arg
35 40 45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Thr Asn Thr Ala Tyr Gly Gly Asn Gly Gly
65 70 75 80

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Asn Trp Ser Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Ala Tyr
                85                  90                  95

Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr Gly Gly Ala Thr His Met
            100                 105                 110

Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
        115                 120                 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr His
    130                 135                 140

Gly Gly Asn Gly Ala Arg Ala Thr His Ala Ala Tyr Cys Ala Tyr Trp
145                 150                 155                 160

Ser Asn Gly Gly Asn Trp Ser Asn Ala Cys Asn Ala Ala Tyr Thr Ala
                165                 170                 175

Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn Met Thr Asn Ala Ala Arg
            180                 185                 190

Trp Ser Asn Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Trp
        195                 200                 205

Ser Asn Gly Thr Asn Gly Ala Tyr Ala Cys Asn Trp Ser Asn Ala Ala
    210                 215                 220

Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Met Thr Asn
225                 230                 235                 240

Ala Ala Arg Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Ala
                245                 250                 255

Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala Tyr Ala Cys Asn Gly Cys
            260                 265                 270

Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn
        275                 280                 285

Met Gly Asn Gly Gly Asn Gly Gly Asn Thr Ala Tyr Trp Ser Asn Trp
    290                 295                 300

Ser Asn Trp Ser Asn Thr Gly Gly Thr Ala Tyr Thr Gly Gly Thr Thr
305                 310                 315                 320

Tyr Gly Ala Tyr Cys Cys Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg
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325 330 335

Gly Gly Asn Ala Cys Asn Met Thr Asn Gly Thr Asn Ala Cys Asn Gly
340 345 350

Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys
355 360 365

Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn
370 375 380

Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr
385 390 395 400

Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser
405 410 415

Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn
420 425 430

Met Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala
435 440 445

Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala
450 455 460

Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn
465 470 475 480

Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met
485 490 495

Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala
500 505 510

Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn
515 520 525

Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met
530 535 540

Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser
545 550 555 560

Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn
565 570 575

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Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala
            580                 585                 590

Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly
        595                 600                 605

Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg
    610                 615                 620

Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly
625                 630                 635                 640

Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala
                645                 650                 655

Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn
            660                 665                 670

Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys
        675                 680                 685

Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys
    690                 695                 700

Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr
705                 710                 715                 720

Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys
                725                 730                 735

Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr
            740                 745                 750

Gly Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn
        755                 760                 765

Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly
    770                 775                 780

Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala
785                 790                 795                 800

Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn
                805                 810                 815

Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly
```

820 825 830

Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr
835 840 845

Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn
850 855 860

Ala Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys
865 870 875 880

Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr
885 890 895

Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn
900 905 910

Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys
915 920 925

Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly
930 935 940

Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr
945 950 955 960

Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly
965 970 975

Gly Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr
980 985 990

His Gly Ala Arg Ala Ala Arg Ala Cys Asn Ala Thr His Trp Ser Asn
995 1000 1005

Ala Ala Arg Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Ala Arg
1010 1015 1020

Cys Cys Asn Met Gly Asn Gly Ala Arg Cys Cys Asn Cys Ala Arg
1025 1030 1035

Gly Thr Asn Thr Ala Tyr Ala Cys Asn Met Thr Asn Cys Cys Asn
1040 1045 1050

Cys Cys Asn Trp Ser Asn Met Gly Asn Gly Ala Arg Gly Ala Arg
1055 1060 1065

Ala Thr Gly Ala Cys Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg
1070 1075 1080

Gly Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr Gly Tyr
1085 1090 1095

Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Gly Asn Thr Thr Tyr
1100 1105 1110

Thr Ala Tyr Cys Cys Asn Trp Ser Asn Gly Ala Tyr Ala Thr His
1115 1120 1125

Gly Cys Asn Gly Thr Asn Gly Ala Arg Thr Gly Gly Gly Ala Arg
1130 1135 1140

Trp Ser Asn Ala Ala Tyr Gly Gly Asn Cys Ala Arg Cys Cys Asn
1145 1150 1155

Gly Ala Arg Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr Ala Ala Arg
1160 1165 1170

Ala Cys Asn Ala Cys Asn Cys Cys Asn Cys Cys Asn Ala Thr Gly
1175 1180 1185

Met Thr Asn Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Gly Asn
1190 1195 1200

Trp Ser Asn Thr Thr Tyr Thr Thr Tyr Met Thr Asn Thr Ala Tyr
1205 1210 1215

Trp Ser Asn Ala Ala Arg Met Thr Asn Ala Cys Asn Gly Thr Asn
1220 1225 1230

Gly Ala Tyr Ala Ala Arg Trp Ser Asn Met Gly Asn Thr Gly Gly
1235 1240 1245

Cys Ala Arg Cys Ala Arg Gly Gly Asn Ala Ala Tyr Gly Thr Asn
1250 1255 1260

Thr Thr Tyr Trp Ser Asn Thr Gly Tyr Trp Ser Asn Gly Thr Asn
1265 1270 1275

Ala Thr Gly Cys Ala Tyr Gly Ala Arg Gly Cys Asn Met Thr Asn
1280 1285 1290

Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr Thr Ala Tyr Ala Cys Asn

1295 1300 1305

Cys Ala Arg Ala Ala Arg Trp Ser Asn Met Thr Asn Trp Ser Asn
1310 1315 1320

Met Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn Ala Ala Arg
1325 1330 1335

<210> 603
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<212> PRT
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<400> 603

Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Cys Ala Arg Cys
1 5 10 15

Ala Arg Thr Gly Gly Gly Gly Asn Gly Cys Asn Gly Gly Asn Met Thr
20 25 30

Asn Met Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Gly Ala Arg
35 40 45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Thr Asn Thr Ala Tyr Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Ala Tyr
85 90 95

Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr Gly Gly Ala Thr His Met
100 105 110

Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr His
130 135 140

Gly Gly Asn Gly Ala Arg Ala Thr His Ala Ala Tyr Cys Ala Tyr Trp
145 150 155 160

Ser Asn Gly Gly Asn Trp Ser Asn Ala Cys Asn Ala Ala Tyr Thr Ala
165 170 175

Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn Met Thr Asn Ala Ala Arg
180 185 190

Trp Ser Asn Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Trp
195 200 205

Ser Asn Gly Thr Asn Gly Ala Tyr Ala Cys Asn Trp Ser Asn Ala Ala
210 215 220

Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Met Thr Asn
225 230 235 240

Ala Ala Arg Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Ala
245 250 255

Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala Tyr Ala Cys Asn Gly Cys
260 265 270

Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn
275 280 285

Met Gly Asn Gly Gly Asn Gly Gly Asn Thr Ala Tyr Trp Ser Asn Trp
290 295 300

Ser Asn Trp Ser Asn Thr Gly Gly Thr Thr Tyr Thr Gly Gly Thr Thr
305 310 315 320

Tyr Gly Ala Tyr Cys Cys Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg
325 330 335

Gly Gly Asn Ala Cys Asn Met Thr Asn Gly Thr Asn Ala Cys Asn Gly
340 345 350

Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys
355 360 365

Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn
370 375 380

Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr
385 390 395 400

Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser
405 410 415

Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn
420 425 430

Met Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala
435 440 445

Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala
450 455 460

Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn
465 470 475 480

Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met
485 490 495

Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala
500 505 510

Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn
515 520 525

Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met
530 535 540

Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser
545 550 555 560

Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn
565 570 575

Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala
580 585 590

Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly
595 600 605

Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg
610 615 620

Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly
625 630 635 640

Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala
645 650 655

Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn
660 665 670

Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys
675 680 685

Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys
690 695 700

Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr
705 710 715 720

Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys
725 730 735

Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr
740 745 750

Gly Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn
755 760 765

Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly
770 775 780

Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala
785 790 795 800

Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn
805 810 815

Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly
820 825 830

Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr
835 840 845

Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn
850 855 860

Ala Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys
865 870 875 880

Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr
885 890 895

Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn
900 905 910

Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys
915 920 925

Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly
930 935 940

Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr
945 950 955 960

Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly
965 970 975

Gly Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr
980 985 990

His Gly Ala Arg Ala Ala Arg Ala Cys Asn Ala Thr His Trp Ser Asn
995 1000 1005

Ala Ala Arg Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Ala Arg
1010 1015 1020

Cys Cys Asn Met Gly Asn Gly Ala Arg Cys Cys Asn Cys Ala Arg
1025 1030 1035

Gly Thr Asn Thr Ala Tyr Ala Cys Asn Met Thr Asn Cys Cys Asn
1040 1045 1050

Cys Cys Asn Trp Ser Asn Met Gly Asn Gly Ala Arg Gly Ala Arg
1055 1060 1065

Ala Thr Gly Ala Cys Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg
1070 1075 1080

Gly Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr Gly Tyr
1085 1090 1095

Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Gly Asn Thr Thr Tyr
1100 1105 1110

Thr Ala Tyr Cys Cys Asn Trp Ser Asn Gly Ala Tyr Ala Thr His
1115 1120 1125

Gly Cys Asn Gly Thr Asn Gly Ala Arg Thr Gly Gly Gly Ala Arg
1130 1135 1140

Trp Ser Asn Ala Ala Tyr Gly Gly Asn Cys Ala Arg Cys Cys Asn
1145 1150 1155

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Gly Ala  Arg Ala Ala Tyr Ala  Ala Tyr Thr Ala Tyr  Ala Ala Arg
    1160                 1165                 1170

Ala Cys  Asn Ala Cys Asn Cys  Cys Asn Cys Cys Asn  Ala Thr Gly
    1175                 1180                 1185

Met Thr  Asn Gly Ala Tyr Trp  Ser Asn Gly Ala Tyr  Gly Gly Asn
    1190                 1195                 1200

Trp Ser  Asn Thr Thr Tyr Thr  Thr Tyr Met Thr Asn  Thr Ala Tyr
    1205                 1210                 1215

Trp Ser  Asn Ala Ala Arg Met  Thr Asn Ala Cys Asn  Gly Thr Asn
    1220                 1225                 1230

Gly Ala  Tyr Ala Ala Arg Trp  Ser Asn Met Gly Asn  Thr Gly Gly
    1235                 1240                 1245

Cys Ala  Arg Cys Ala Arg Gly  Gly Asn Ala Ala Tyr  Gly Thr Asn
    1250                 1255                 1260

Thr Thr  Tyr Trp Ser Asn Thr  Gly Tyr Trp Ser Asn  Gly Thr Asn
    1265                 1270                 1275

Ala Thr  Gly Cys Ala Tyr Gly  Ala Arg Gly Cys Asn  Met Thr Asn
    1280                 1285                 1290

Cys Ala  Tyr Ala Ala Tyr Cys  Ala Tyr Thr Ala Tyr  Ala Cys Asn
    1295                 1300                 1305

Cys Ala  Arg Ala Ala Arg Trp  Ser Asn Met Thr Asn  Trp Ser Asn
    1310                 1315                 1320

Met Thr  Asn Trp Ser Asn Cys  Cys Asn Gly Gly Asn  Ala Ala Arg
    1325                 1330                 1335
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<210> 604
<211> 1347
<212> PRT
<213> Homo Sapiens

<400> 604

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Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Met Thr
            20                  25                  30
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Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Gly Ala Arg
35 40 45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr
50 55 60

Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr Gly Gly Ala Thr His Met
100 105 110

Gly Asn Cys Ala Arg Cys Cys Asn Gly Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr His
130 135 140

Gly Gly Asn Met Gly Asn Ala Thr His Thr Ala Tyr Ala Cys Asn Trp
145 150 155 160

Ser Asn Gly Gly Asn Ala Cys Asn Ala Cys Asn Ala Ala Tyr Thr Ala
165 170 175

Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn Met Thr Asn Ala Ala Arg
180 185 190

Trp Ser Asn Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr Gly Trp
195 200 205

Ser Asn Gly Thr Asn Gly Ala Tyr Ala Cys Asn Trp Ser Asn Ala Ala
210 215 220

Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Met Thr Asn
225 230 235 240

Ala Ala Arg Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Ala
245 250 255

Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala Tyr Ala Cys Asn Gly Cys
260 265 270

Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn

275 280 285

Met Gly Asn Gly Ala Tyr Gly Gly Asn Thr Ala Tyr Trp Ser Asn Thr
290 295 300

Ala Tyr Gly Gly Asn Cys Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala
305 310 315 320

Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn
325 330 335

Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Ala
340 345 350

Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser
355 360 365

Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn
370 375 380

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met
385 390 395 400

Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly
405 410 415

Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn
420 425 430

Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr
435 440 445

Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala
450 455 460

Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn
465 470 475 480

Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp
485 490 495

Ser Asn Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser
500 505 510

Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr
515 520 525

Cys Cys Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp
530 535 540

Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser
545 550 555 560

Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn
565 570 575

Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala
580 585 590

Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys
595 600 605

Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn
610 615 620

Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala
625 630 635 640

Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala
645 650 655

Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg
660 665 670

Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys
675 680 685

Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys
690 695 700

Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn
705 710 715 720

Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys
725 730 735

Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala
740 745 750

Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn
755 760 765

Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala

770 775 780

Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala
785 790 795 800

Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr
805 810 815

Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala
820 825 830

Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly
835 840 845

Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr
850 855 860

Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met
865 870 875 880

Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala
885 890 895

Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn
900 905 910

Gly Thr Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly
915 920 925

Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly
930 935 940

Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg
945 950 955 960

Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp
965 970 975

Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys Cys
980 985 990

Asn Gly Cys Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala Arg
995 1000 1005

Ala Cys Asn Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn
1010 1015 1020

Ala Ala Arg Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn
1025 1030 1035

Gly Ala Arg Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr
1040 1045 1050

Ala Cys Asn Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn
1055 1060 1065

Met Gly Asn Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn
1070 1075 1080

Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn
1085 1090 1095

Met Thr Asn Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn
1100 1105 1110

Ala Ala Arg Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn
1115 1120 1125

Trp Ser Asn Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn
1130 1135 1140

Gly Ala Arg Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr
1145 1150 1155

Gly Gly Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr
1160 1165 1170

Ala Ala Tyr Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn
1175 1180 1185

Cys Cys Asn Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr
1190 1195 1200

Trp Ser Asn Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr
1205 1210 1215

Thr Thr Tyr Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg
1220 1225 1230

Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg
1235 1240 1245

Trp Ser Asn Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg

1250 1255 1260

Gly Gly Asn Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn
1265 1270 1275

Thr Gly Tyr Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr
1280 1285 1290

Gly Ala Arg Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr
1295 1300 1305

Cys Ala Tyr Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg
1310 1315 1320

Trp Ser Asn Met Thr Asn Trp Ser Asn Met Thr Asn Trp Ser Asn
1325 1330 1335

Cys Cys Asn Gly Gly Asn Ala Ala Arg
1340 1345

<210> 605
<211> 1356
<212> PRT
<213> Homo Sapiens

<400> 605

Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Met Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Gly Ala Arg
35 40 45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr
50 55 60

Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Gly Asn
85 90 95

Gly Gly Asn Trp Ser Asn Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
100 105 110

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Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Met Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Ala Cys
                165                 170                 175

Asn Ala Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
            180                 185                 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Ala
        195                 200                 205

Cys Asn Ala Thr His Trp Ser Asn Ala Thr His Gly Thr Asn Ala Cys
    210                 215                 220

Asn Trp Ser Asn Met Gly Asn Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225                 230                 235                 240

Trp Ser Asn Met Thr Asn Ala Ala Arg Met Thr Asn Trp Ser Asn Trp
                245                 250                 255

Ser Asn Gly Thr Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala
            260                 265                 270

Tyr Ala Cys Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Trp Ser Asn Gly Cys Asn Met
    290                 295                 300

Thr Asn Met Gly Asn Thr Ala Tyr Thr Thr Tyr Gly Ala Tyr Thr Gly
305                 310                 315                 320

Gly Met Thr Asn Thr Thr Tyr Trp Ser Asn Gly Ala Tyr Gly Thr Asn
                325                 330                 335

Trp Ser Asn Gly Ala Tyr Ala Thr His Thr Gly Gly Gly Gly Asn Cys
            340                 345                 350

Ala Arg Gly Gly Asn Ala Cys Asn Ala Thr Gly Gly Thr Asn Ala Cys
        355                 360                 365
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Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn
    370                 375                 380

Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly
385                 390                 395                 400

Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys
                405                 410                 415

Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn
            420                 425                 430

Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly
        435                 440                 445

Cys Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr
    450                 455                 460

Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn
465                 470                 475                 480

Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp
                485                 490                 495

Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys
            500                 505                 510

Asn Met Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn
        515                 520                 525

Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly
    530                 535                 540

Thr Asn Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly
545                 550                 555                 560

Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
                565                 570                 575

Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys
            580                 585                 590

Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly
        595                 600                 605
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Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn
    610                 615                 620

Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala
625                 630                 635                 640

Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala
                645                 650                 655

Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn
            660                 665                 670

Gly Ala Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly
        675                 680                 685

Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly
    690                 695                 700

Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn
705                 710                 715                 720

Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr
                725                 730                 735

Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala
            740                 745                 750

Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn
        755                 760                 765

Ala Thr Gly Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys
    770                 775                 780

Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr
785                 790                 795                 800

Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn
                805                 810                 815

Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly
            820                 825                 830

Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala
        835                 840                 845

Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg
    850                 855                 860
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Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala
865                 870                 875                 880

Cys Asn Ala Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala
                885                 890                 895

Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn
            900                 905                 910

Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly
        915                 920                 925

Thr Asn Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala
    930                 935                 940

Tyr Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr
945                 950                 955                 960

Gly Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr
                965                 970                 975

Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala
            980                 985                 990

Arg Gly Gly Asn Met Thr Asn Cys  Cys Asn Gly Cys Asn  Cys Cys Asn
        995                 1000                1005

Ala Thr  His Gly Ala Arg Ala  Ala Arg Ala Cys Asn  Ala Thr His
    1010                1015                1020

Trp Ser  Asn Ala Ala Arg Ala  Cys Asn Ala Ala Arg  Gly Gly Asn
    1025                1030                1035

Cys Ala  Arg Cys Cys Asn Met  Gly Asn Gly Ala Arg  Cys Cys Asn
    1040                1045                1050

Cys Ala  Arg Gly Thr Asn Thr  Ala Tyr Ala Cys Asn  Met Thr Asn
    1055                1060                1065

Cys Cys  Asn Cys Cys Asn Trp  Ser Asn Met Gly Asn  Gly Ala Arg
    1070                1075                1080

Gly Ala  Arg Ala Thr Gly Ala  Cys Asn Ala Ala Arg  Ala Ala Tyr
    1085                1090                1095
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Cys Ala  Arg Gly Thr Asn Trp  Ser Asn Met Thr Asn  Ala Cys Asn
    1100                 1105                 1110

Thr Gly  Tyr Met Thr Asn Gly  Thr Asn Ala Ala Arg  Gly Gly Asn
    1115                 1120                 1125

Thr Thr  Tyr Thr Ala Tyr Cys  Cys Asn Trp Ser Asn  Gly Ala Tyr
    1130                 1135                 1140

Ala Thr  His Gly Cys Asn Gly  Thr Asn Gly Ala Arg  Thr Gly Gly
    1145                 1150                 1155

Gly Ala  Arg Trp Ser Asn Ala  Ala Tyr Gly Gly Asn  Cys Ala Arg
    1160                 1165                 1170

Cys Cys  Asn Gly Ala Arg Ala  Ala Tyr Ala Ala Tyr  Thr Ala Tyr
    1175                 1180                 1185

Ala Ala  Arg Ala Cys Asn Ala  Cys Asn Cys Cys Asn  Cys Cys Asn
    1190                 1195                 1200

Ala Thr  Gly Met Thr Asn Gly  Ala Tyr Trp Ser Asn  Gly Ala Tyr
    1205                 1210                 1215

Gly Gly  Asn Trp Ser Asn Thr  Thr Tyr Thr Thr Tyr  Met Thr Asn
    1220                 1225                 1230

Thr Ala  Tyr Trp Ser Asn Ala  Ala Arg Met Thr Asn  Ala Cys Asn
    1235                 1240                 1245

Gly Thr  Asn Gly Ala Tyr Ala  Ala Arg Trp Ser Asn  Met Gly Asn
    1250                 1255                 1260

Thr Gly  Gly Cys Ala Arg Cys  Ala Arg Gly Gly Asn  Ala Ala Tyr
    1265                 1270                 1275

Gly Thr  Asn Thr Thr Tyr Trp  Ser Asn Thr Gly Tyr  Trp Ser Asn
    1280                 1285                 1290

Gly Thr  Asn Ala Thr Gly Cys  Ala Tyr Gly Ala Arg  Gly Cys Asn
    1295                 1300                 1305

Met Thr  Asn Cys Ala Tyr Ala  Ala Tyr Cys Ala Tyr  Thr Ala Tyr
    1310                 1315                 1320

Ala Cys  Asn Cys Ala Arg Ala  Ala Arg Trp Ser Asn  Met Thr Asn
    1325                 1330                 1335
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Trp Ser Asn Met Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn
1340 1345 1350

Ala Ala Arg
1355

<210> 606
<211> 1338
<212> PRT
<213> Homo Sapiens

<400> 606

Gly Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Met Thr
20 25 30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Ala Arg
35 40 45

Trp Ser Asn Met Thr Asn Ala Ala Arg Ala Thr His Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Gly Asn Trp Ser Asn Gly Gly Asn Thr Ala
65 70 75 80

Tyr Met Gly Asn Thr Thr Tyr Ala Cys Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Ala Thr Gly Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
130 135 140

Gly Gly Asn Ala Thr His Ala Thr His Thr Ala Tyr Cys Cys Asn Gly
145 150 155 160

Ala Tyr Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Ala Cys Asn Met Gly
165 170 175

Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn Thr Thr Tyr

180 185 190

Cys Ala Arg Gly Gly Asn Cys Ala Arg Gly Thr Asn Ala Cys Asn Ala
195 200 205

Thr His Trp Ser Asn Gly Cys Asn Gly Ala Tyr Ala Ala Arg Trp Ser
210 215 220

Asn Ala Thr His Trp Ser Asn Ala Cys Asn Gly Cys Asn Thr Ala Tyr
225 230 235 240

Met Thr Asn Cys Ala Arg Thr Gly Gly Trp Ser Asn Trp Ser Asn Met
245 250 255

Thr Asn Ala Ala Arg Gly Cys Asn Trp Ser Asn Gly Ala Tyr Ala Cys
260 265 270

Asn Gly Cys Asn Ala Thr Gly Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Cys Ala Arg Ala Ala Arg Trp Ser Asn Thr
290 295 300

Ala Tyr Gly Gly Asn Thr Ala Tyr Trp Ser Asn Thr Ala Tyr Thr Thr
305 310 315 320

Tyr Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg
325 330 335

Gly Gly Asn Ala Cys Asn Met Thr Asn Gly Thr Asn Ala Cys Asn Gly
340 345 350

Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys
355 360 365

Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn
370 375 380

Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr
385 390 395 400

Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser
405 410 415

Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn
420 425 430

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Met Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala
        435                 440                 445

Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala
    450                 455                 460

Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn
465                 470                 475                 480

Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met
                485                 490                 495

Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala
            500                 505                 510

Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn
        515                 520                 525

Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met
    530                 535                 540

Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser
545                 550                 555                 560

Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn
                565                 570                 575

Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala
            580                 585                 590

Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly
        595                 600                 605

Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg
    610                 615                 620

Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly
625                 630                 635                 640

Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala
                645                 650                 655

Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn
            660                 665                 670

Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys
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675 680 685

Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys
690 695 700

Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr
705 710 715 720

Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys
725 730 735

Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr
740 745 750

Gly Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn
755 760 765

Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly
770 775 780

Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala
785 790 795 800

Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn
805 810 815

Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly
820 825 830

Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr
835 840 845

Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn
850 855 860

Ala Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys
865 870 875 880

Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr
885 890 895

Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn
900 905 910

Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys
915 920 925

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Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly
    930                 935                 940

Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr
945                 950                 955                 960

Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly
                965                 970                 975

Gly Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr
            980                 985                 990

His Gly Ala Arg Ala Ala Arg Ala  Cys Asn Ala Thr His  Trp Ser Asn
        995                 1000                1005

Ala Ala  Arg Ala Cys Asn Ala  Ala Arg Gly Gly Asn  Cys Ala Arg
    1010                1015                1020

Cys Cys  Asn Met Gly Asn Gly  Ala Arg Cys Cys Asn  Cys Ala Arg
    1025                1030                1035

Gly Thr  Asn Thr Ala Tyr Ala  Cys Asn Met Thr Asn  Cys Cys Asn
    1040                1045                1050

Cys Cys  Asn Trp Ser Asn Met  Gly Asn Gly Ala Arg  Gly Ala Arg
    1055                1060                1065

Ala Thr  Gly Ala Cys Asn Ala  Ala Arg Ala Ala Tyr  Cys Ala Arg
    1070                1075                1080

Gly Thr  Asn Trp Ser Asn Met  Thr Asn Ala Cys Asn  Thr Gly Tyr
    1085                1090                1095

Met Thr  Asn Gly Thr Asn Ala  Ala Arg Gly Gly Asn  Thr Thr Tyr
    1100                1105                1110

Thr Ala  Tyr Cys Cys Asn Trp  Ser Asn Gly Ala Tyr  Ala Thr His
    1115                1120                1125

Gly Cys  Asn Gly Thr Asn Gly  Ala Arg Thr Gly Gly  Gly Ala Arg
    1130                1135                1140

Trp Ser  Asn Ala Ala Tyr Gly  Gly Asn Cys Ala Arg  Cys Cys Asn
    1145                1150                1155

Gly Ala  Arg Ala Ala Tyr Ala  Ala Tyr Thr Ala Tyr  Ala Ala Arg
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1160 1165 1170

Ala Cys Asn Ala Cys Asn Cys Cys Asn Cys Cys Asn Ala Thr Gly
1175 1180 1185

Met Thr Asn Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Gly Asn
1190 1195 1200

Trp Ser Asn Thr Thr Tyr Thr Thr Tyr Met Thr Asn Thr Ala Tyr
1205 1210 1215

Trp Ser Asn Ala Ala Arg Met Thr Asn Ala Cys Asn Gly Thr Asn
1220 1225 1230

Gly Ala Tyr Ala Ala Arg Trp Ser Asn Met Gly Asn Thr Gly Gly
1235 1240 1245

Cys Ala Arg Cys Ala Arg Gly Gly Asn Ala Ala Tyr Gly Thr Asn
1250 1255 1260

Thr Thr Tyr Trp Ser Asn Thr Gly Tyr Trp Ser Asn Gly Thr Asn
1265 1270 1275

Ala Thr Gly Cys Ala Tyr Gly Ala Arg Gly Cys Asn Met Thr Asn
1280 1285 1290

Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr Thr Ala Tyr Ala Cys Asn
1295 1300 1305

Cys Ala Arg Ala Ala Arg Trp Ser Asn Met Thr Asn Trp Ser Asn
1310 1315 1320

Met Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn Ala Ala Arg
1325 1330 1335

<210> 607
<211> 1341
<212> PRT
<213> Homo Sapiens

<400> 607

Gly Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
20 25 30

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Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Ala Arg
        35                  40                  45

Trp Ser Asn Met Thr Asn Ala Ala Arg Ala Thr His Trp Ser Asn Thr
    50                  55                  60

Gly Tyr Ala Ala Arg Gly Gly Asn Trp Ser Asn Gly Gly Asn Thr Ala
65                  70                  75                  80

Tyr Trp Ser Asn Thr Thr Tyr Ala Cys Asn Trp Ser Asn Thr Ala Tyr
                85                  90                  95

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Gly Gly Gly Thr Asn Met
            100                 105                 110

Gly Asn Cys Ala Arg Ala Thr Gly Cys Cys Asn Gly Gly Asn Ala Ala
        115                 120                 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
    130                 135                 140

Gly Gly Asn Ala Thr His Ala Thr His Thr Ala Tyr Cys Cys Asn Gly
145                 150                 155                 160

Ala Tyr Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Cys Asn Met Gly
                165                 170                 175

Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn Thr Thr Tyr
            180                 185                 190

Cys Ala Arg Gly Gly Asn Cys Ala Arg Gly Thr Asn Ala Cys Asn Ala
        195                 200                 205

Thr His Trp Ser Asn Gly Cys Asn Gly Ala Tyr Ala Ala Arg Trp Ser
    210                 215                 220

Asn Ala Thr His Ala Ala Tyr Ala Cys Asn Gly Cys Asn Thr Ala Tyr
225                 230                 235                 240

Met Thr Asn Cys Ala Arg Thr Gly Gly Trp Ser Asn Trp Ser Asn Met
                245                 250                 255

Thr Asn Ala Ala Arg Gly Cys Asn Trp Ser Asn Gly Ala Tyr Ala Cys
            260                 265                 270

Asn Gly Cys Asn Ala Thr Gly Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285
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Gly Cys Asn Met Gly Asn Cys Ala Arg Gly Gly Asn Thr Ala Tyr Gly
    290                 295                 300

Gly Asn Trp Ser Asn Gly Gly Asn Thr Gly Gly Gly Gly Asn Thr Ala
305                 310                 315                 320

Tyr Thr Thr Tyr Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn
                325                 330                 335

Cys Ala Arg Gly Gly Asn Ala Cys Asn Met Thr Asn Gly Thr Asn Ala
            340                 345                 350

Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser
        355                 360                 365

Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn
    370                 375                 380

Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys
385                 390                 395                 400

Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys
                405                 410                 415

Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn
            420                 425                 430

Gly Cys Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly
        435                 440                 445

Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys
    450                 455                 460

Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn
465                 470                 475                 480

Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly
                485                 490                 495

Cys Asn Met Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr
            500                 505                 510

Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn
        515                 520                 525
```

```
Gly Thr Asn Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly
    530                 535                 540

Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser
545                 550                 555                 560

Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn
                565                 570                 575

Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly
            580                 585                 590

Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys
        595                 600                 605

Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr
    610                 615                 620

Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala
625                 630                 635                 640

Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr
                645                 650                 655

Asn Gly Ala Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr
            660                 665                 670

Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr
        675                 680                 685

Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr
    690                 695                 700

Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn
705                 710                 715                 720

Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala
                725                 730                 735

Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr
            740                 745                 750

Asn Ala Thr Gly Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn
        755                 760                 765

Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly
    770                 775                 780
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Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser
785                 790                 795                 800

Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg
                805                 810                 815

Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr
            820                 825                 830

Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala
        835                 840                 845

Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg
    850                 855                 860

Ala Cys Asn Ala Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly
865                 870                 875                 880

Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys
                885                 890                 895

Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn
            900                 905                 910

Gly Thr Asn Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys
        915                 920                 925

Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala
    930                 935                 940

Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg
945                 950                 955                 960

Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala
                965                 970                 975

Ala Arg Gly Gly Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys
            980                 985                 990

Asn Ala Thr His Gly Ala Arg Ala  Ala Arg Ala Cys Asn  Ala Thr His
        995                 1000                1005

Trp Ser  Asn Ala Ala Arg Ala  Cys Asn Ala Ala Arg  Gly Gly Asn
    1010                1015                1020
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Cys Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Cys Cys Asn
1025 1030 1035

Cys Ala Arg Gly Thr Asn Thr Ala Tyr Ala Cys Asn Met Thr Asn
1040 1045 1050

Cys Cys Asn Cys Cys Asn Trp Ser Asn Met Gly Asn Gly Ala Arg
1055 1060 1065

Gly Ala Arg Ala Thr Gly Ala Cys Asn Ala Ala Arg Ala Ala Tyr
1070 1075 1080

Cys Ala Arg Gly Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn
1085 1090 1095

Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Gly Asn
1100 1105 1110

Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Trp Ser Asn Gly Ala Tyr
1115 1120 1125

Ala Thr His Gly Cys Asn Gly Thr Asn Gly Ala Arg Thr Gly Gly
1130 1135 1140

Gly Ala Arg Trp Ser Asn Ala Ala Tyr Gly Gly Asn Cys Ala Arg
1145 1150 1155

Cys Cys Asn Gly Ala Arg Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr
1160 1165 1170

Ala Ala Arg Ala Cys Asn Ala Cys Asn Cys Cys Asn Cys Cys Asn
1175 1180 1185

Ala Thr Gly Met Thr Asn Gly Ala Tyr Trp Ser Asn Gly Ala Tyr
1190 1195 1200

Gly Gly Asn Trp Ser Asn Thr Thr Tyr Thr Thr Tyr Met Thr Asn
1205 1210 1215

Thr Ala Tyr Trp Ser Asn Ala Ala Arg Met Thr Asn Ala Cys Asn
1220 1225 1230

Gly Thr Asn Gly Ala Tyr Ala Ala Arg Trp Ser Asn Met Gly Asn
1235 1240 1245

Thr Gly Gly Cys Ala Arg Cys Ala Arg Gly Gly Asn Ala Ala Tyr
1250 1255 1260

Gly Thr Asn Thr Thr Tyr Trp Ser Asn Thr Gly Tyr Trp Ser Asn
1265 1270 1275

Gly Thr Asn Ala Thr Gly Cys Ala Tyr Gly Ala Arg Gly Cys Asn
1280 1285 1290

Met Thr Asn Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr Thr Ala Tyr
1295 1300 1305

Ala Cys Asn Cys Ala Arg Ala Ala Arg Trp Ser Asn Met Thr Asn
1310 1315 1320

Trp Ser Asn Met Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn
1325 1330 1335

Ala Ala Arg
1340

<210> 608
<211> 1359
<212> PRT
<213> Homo Sapiens

<400> 608

Gly Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
20 25 30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Ala Arg
35 40 45

Trp Ser Asn Met Thr Asn Ala Ala Arg Ala Thr His Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Gly Asn Trp Ser Asn Gly Gly Asn Thr Ala
65 70 75 80

Tyr Trp Ser Asn Thr Thr Tyr Ala Cys Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Ala Thr Gly Cys Cys Asn Gly Gly Asn Ala Ala

115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
130 135 140

Gly Gly Asn Ala Thr His Ala Thr His Thr Ala Tyr Cys Cys Asn Gly
145 150 155 160

Gly Asn Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Ala Thr His Met Gly
165 170 175

Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn Thr Thr Tyr
180 185 190

Cys Ala Arg Gly Gly Asn Cys Ala Arg Gly Thr Asn Ala Cys Asn Ala
195 200 205

Thr His Trp Ser Asn Gly Cys Asn Gly Ala Tyr Ala Ala Arg Trp Ser
210 215 220

Asn Ala Thr His Trp Ser Asn Ala Cys Asn Gly Cys Asn Thr Ala Tyr
225 230 235 240

Met Thr Asn Cys Ala Arg Thr Gly Gly Trp Ser Asn Trp Ser Asn Met
245 250 255

Thr Asn Ala Ala Arg Gly Cys Asn Trp Ser Asn Gly Ala Tyr Ala Cys
260 265 270

Asn Gly Cys Asn Ala Thr Gly Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Cys Ala Arg Gly Gly Asn Met Thr Asn Gly
290 295 300

Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Ala Cys Asn Trp Ser
305 310 315 320

Asn Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr
325 330 335

Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr Gly Gly Gly
340 345 350

Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Ala Cys Asn Gly Thr
355 360 365

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Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn
    370                 375                 380

Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp
385                 390                 395                 400

Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys
                405                 410                 415

Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn
            420                 425                 430

Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly
        435                 440                 445

Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr
    450                 455                 460

Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr
465                 470                 475                 480

Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly
                485                 490                 495

Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly
            500                 505                 510

Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn
        515                 520                 525

Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly
    530                 535                 540

Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser
545                 550                 555                 560

Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn
                565                 570                 575

Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly
            580                 585                 590

Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr
        595                 600                 605

Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr
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610 615 620

Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys
625 630 635 640

Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys
645 650 655

Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn
660 665 670

Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr
675 680 685

Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys
690 695 700

Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn
705 710 715 720

Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly
725 730 735

Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys
740 745 750

Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn
755 760 765

Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn Met Gly Asn Ala
770 775 780

Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly
785 790 795 800

Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn
805 810 815

Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly
820 825 830

Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly
835 840 845

Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn
850 855 860

Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala
865 870 875 880

Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met Gly Asn Gly Ala
885 890 895

Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn
900 905 910

Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn Trp
915 920 925

Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr
930 935 940

Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn
945 950 955 960

Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala
965 970 975

Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala
980 985 990

Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys Cys Asn Gly Cys Asn
995 1000 1005

Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala Arg Ala Cys Asn
1010 1015 1020

Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg
1025 1030 1035

Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg
1040 1045 1050

Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr Ala Cys Asn
1055 1060 1065

Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn Met Gly Asn
1070 1075 1080

Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn Ala Ala Arg
1085 1090 1095

Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn Met Thr Asn

1100 1105 1110

Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg
1115 1120 1125

Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Trp Ser Asn
1130 1135 1140

Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn Gly Ala Arg
1145 1150 1155

Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr Gly Gly Asn
1160 1165 1170

Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr Ala Ala Tyr
1175 1180 1185

Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn Cys Cys Asn
1190 1195 1200

Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr Trp Ser Asn
1205 1210 1215

Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr Thr Thr Tyr
1220 1225 1230

Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg Met Thr Asn
1235 1240 1245

Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg Trp Ser Asn
1250 1255 1260

Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg Gly Gly Asn
1265 1270 1275

Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn Thr Gly Tyr
1280 1285 1290

Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr Gly Ala Arg
1295 1300 1305

Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr
1310 1315 1320

Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg Trp Ser Asn
1325 1330 1335

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Met Thr  Asn Trp Ser Asn Met  Thr Asn Trp Ser Asn  Cys Cys Asn
    1340                1345                1350

Gly Gly  Asn Ala Ala Arg
    1355
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<210> 609
<211> 1353
<212> PRT
<213> Homo Sapiens

<400> 609

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Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Cys Ala Arg Cys
1               5                  10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Met Thr
            20                  25                  30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
        35                  40                  45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr
    50                  55                  60

Gly Tyr Gly Cys Asn Ala Thr His Trp Ser Asn Gly Gly Asn Gly Ala
65                  70                  75                  80

Tyr Trp Ser Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Thr Ala Tyr
                85                  90                  95

Trp Ser Asn Gly Cys Asn Gly Cys Asn Thr Gly Gly Ala Ala Tyr Thr
            100                 105                 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Trp Ser Asn Cys Cys
        115                 120                 125

Asn Trp Ser Asn Met Gly Asn Gly Gly Asn Met Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Met Thr Asn Gly Gly Asn Met Gly Asn Ala Cys Asn Thr
145                 150                 155                 160

Ala Tyr Thr Gly Tyr Met Gly Asn Trp Ser Asn Ala Ala Arg Thr Gly
                165                 170                 175

Gly Thr Ala Tyr Ala Ala Tyr Gly Ala Tyr Thr Ala Tyr Gly Cys Asn
            180                 185                 190
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Gly Thr Asn Trp Ser Asn Gly Thr Asn Ala Ala Arg Trp Ser Asn Met
        195                 200                 205

Gly Asn Ala Thr His Ala Cys Asn Ala Thr His Ala Ala Tyr Cys Cys
    210                 215                 220

Asn Gly Ala Tyr Ala Cys Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr
225                 230                 235                 240

Cys Ala Arg Thr Thr Tyr Trp Ser Asn Met Thr Asn Cys Ala Arg Met
                245                 250                 255

Thr Asn Ala Ala Tyr Trp Ser Asn Gly Thr Asn Ala Cys Asn Cys Cys
            260                 265                 270

Asn Gly Ala Arg Gly Ala Tyr Ala Cys Asn Gly Cys Asn Gly Thr Asn
        275                 280                 285

Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn Gly
    290                 295                 300

Ala Tyr Met Gly Asn Gly Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly
305                 310                 315                 320

Asn Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly
                325                 330                 335

Gly Ala Tyr Gly Thr Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly
            340                 345                 350

Gly Asn Ala Cys Asn Ala Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr
        355                 360                 365

Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn
    370                 375                 380

Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr
385                 390                 395                 400

Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly
                405                 410                 415

Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn
            420                 425                 430
```

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Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met
        435                 440                 445

Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala
    450                 455                 460

Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg
465                 470                 475                 480

Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr
                485                 490                 495

Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr
            500                 505                 510

Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr
        515                 520                 525

Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met
    530                 535                 540

Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr
545                 550                 555                 560

Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
                565                 570                 575

Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp
            580                 585                 590

Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys
        595                 600                 605

Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr
    610                 615                 620

Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys
625                 630                 635                 640

Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr
                645                 650                 655

Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg
            660                 665                 670

Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly
        675                 680                 685
```

Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys
690 695 700

Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn
705 710 715 720

Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met
725 730 735

Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys
740 745 750

Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly
755 760 765

Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly
770 775 780

Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr
785 790 795 800

Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr
805 810 815

Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys
820 825 830

Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr
835 840 845

Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn
850 855 860

Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala
865 870 875 880

Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala
885 890 895

Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr
900 905 910

Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met
915 920 925

Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala
930 935 940

Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn
945 950 955 960

Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala
965 970 975

Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly
980 985 990

Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His
995 1000 1005

Gly Ala Arg Ala Ala Arg Ala Cys Asn Ala Thr His Trp Ser Asn
1010 1015 1020

Ala Ala Arg Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Ala Arg
1025 1030 1035

Cys Cys Asn Met Gly Asn Gly Ala Arg Cys Cys Asn Cys Ala Arg
1040 1045 1050

Gly Thr Asn Thr Ala Tyr Ala Cys Asn Met Thr Asn Cys Cys Asn
1055 1060 1065

Cys Cys Asn Trp Ser Asn Met Gly Asn Gly Ala Arg Gly Ala Arg
1070 1075 1080

Ala Thr Gly Ala Cys Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg
1085 1090 1095

Gly Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr Gly Tyr
1100 1105 1110

Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Gly Asn Thr Thr Tyr
1115 1120 1125

Thr Ala Tyr Cys Cys Asn Trp Ser Asn Gly Ala Tyr Ala Thr His
1130 1135 1140

Gly Cys Asn Gly Thr Asn Gly Ala Arg Thr Gly Gly Gly Ala Arg
1145 1150 1155

Trp Ser Asn Ala Ala Tyr Gly Gly Asn Cys Ala Arg Cys Cys Asn
1160 1165 1170

Gly Ala Arg Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr Ala Ala Arg
1175 1180 1185

Ala Cys Asn Ala Cys Asn Cys Cys Asn Cys Cys Asn Ala Thr Gly
1190 1195 1200

Met Thr Asn Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Gly Asn
1205 1210 1215

Trp Ser Asn Thr Thr Tyr Thr Thr Tyr Met Thr Asn Thr Ala Tyr
1220 1225 1230

Trp Ser Asn Ala Ala Arg Met Thr Asn Ala Cys Asn Gly Thr Asn
1235 1240 1245

Gly Ala Tyr Ala Ala Arg Trp Ser Asn Met Gly Asn Thr Gly Gly
1250 1255 1260

Cys Ala Arg Cys Ala Arg Gly Gly Asn Ala Ala Tyr Gly Thr Asn
1265 1270 1275

Thr Thr Tyr Trp Ser Asn Thr Gly Tyr Trp Ser Asn Gly Thr Asn
1280 1285 1290

Ala Thr Gly Cys Ala Tyr Gly Ala Arg Gly Cys Asn Met Thr Asn
1295 1300 1305

Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr Thr Ala Tyr Ala Cys Asn
1310 1315 1320

Cys Ala Arg Ala Ala Arg Trp Ser Asn Met Thr Asn Trp Ser Asn
1325 1330 1335

Met Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn Ala Ala Arg
1340 1345 1350

<210> 610
<211> 336
<212> PRT
<213> Homo Sapiens

<400> 610

Gly Ala Tyr Gly Thr Asn Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Tyr Thr Asn Trp Ser Asn Tyr Thr

20 25 30

Asn Cys Cys Asn Gly Thr Asn Cys Ala Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr Met Gly Asn Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Tyr Thr Asn Gly Thr Asn Thr Ala Tyr Trp Ser Asn
85 90 95

Gly Ala Tyr Gly Gly Asn Ala Ala Tyr Cys Ala Asn Thr Ala Tyr Tyr
100 105 110

Thr Asn Ala Ala Tyr Thr Gly Gly Thr Thr Tyr Cys Ala Arg Cys Ala
115 120 125

Arg Met Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala Arg Trp Ser Asn
130 135 140

Cys Cys Asn Met Gly Asn Met Gly Asn Tyr Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Thr Gly
165 170 175

Gly Gly Ala Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
180 185 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Ala Ala Tyr Gly Gly Asn Trp
195 200 205

Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly Ala
210 215 220

Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Ala Ala Arg Ala Thr His
225 230 235 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
245 250 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
260 265 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Trp Ser Asn
275 280 285

Cys Ala Asn Cys Ala Tyr Thr Gly Gly Cys Cys Asn Ala Thr His Cys
290 295 300

Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala
305 310 315 320

Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
325 330 335

<210> 611
<211> 336
<212> PRT
<213> Homo Sapiens

<400> 611

Gly Ala Tyr Gly Thr Asn Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Tyr Thr Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Cys Cys Asn Gly Thr Asn Cys Ala Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr Met Gly Asn Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Tyr Thr Asn Gly Thr Asn Thr Ala Tyr Trp Ser Asn
85 90 95

Gly Ala Tyr Gly Gly Asn Ala Ala Tyr Cys Ala Asn Thr Ala Tyr Tyr
100 105 110

Thr Asn Ala Ala Tyr Thr Gly Gly Thr Thr Tyr Cys Ala Arg Cys Ala
115 120 125

Arg Met Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala Arg Trp Ser Asn
130 135 140

Cys Cys Asn Met Gly Asn Met Gly Asn Tyr Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Thr Gly
165 170 175

Gly Gly Ala Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
180 185 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp
195 200 205

Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly Ala
210 215 220

Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Ala Ala Arg Ala Thr His
225 230 235 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
245 250 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
260 265 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr His Cys Ala Arg Gly Gly Asn
275 280 285

Cys Ala Asn Cys Ala Tyr Thr Gly Gly Cys Cys Asn Cys Ala Asn Cys
290 295 300

Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala
305 310 315 320

Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
325 330 335

<210> 612
<211> 336
<212> PRT
<213> Homo Sapiens

<400> 612

Gly Ala Tyr Gly Thr Asn Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Tyr Thr Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Cys Cys Asn Gly Thr Asn Cys Ala Asn Tyr Thr Asn Gly Gly Asn

35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr Met Gly Asn Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Tyr Thr Asn Gly Thr Asn Thr Ala Tyr Trp Ser Asn
85 90 95

Gly Ala Tyr Gly Gly Asn Ala Ala Tyr Cys Ala Asn Thr Ala Tyr Tyr
100 105 110

Thr Asn Ala Ala Tyr Thr Gly Gly Tyr Thr Asn Cys Ala Arg Cys Ala
115 120 125

Arg Met Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala Arg Trp Ser Asn
130 135 140

Cys Cys Asn Met Gly Asn Met Gly Asn Tyr Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Thr Gly
165 170 175

Gly Gly Ala Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
180 185 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp
195 200 205

Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly Ala
210 215 220

Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Ala Ala Arg Ala Thr His
225 230 235 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
245 250 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
260 265 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Gly Gly Asn
275 280 285

Cys Ala Asn Cys Ala Tyr Thr Gly Gly Cys Cys Asn Ala Thr His Cys
290 295 300

Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala
305 310 315 320

Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
325 330 335

<210> 613
<211> 336
<212> PRT
<213> Homo Sapiens

<400> 613

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Cys Ala Asn Cys Cys Asn Tyr Thr Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Thr Asn Cys Ala Asn Cys Cys Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Tyr Thr Asn Tyr Thr Asn Cys Ala Tyr Trp Ser Asn
85 90 95

Gly Ala Tyr Gly Gly Asn Ala Ala Arg Cys Ala Asn Thr Ala Tyr Tyr
100 105 110

Thr Asn Thr Ala Tyr Thr Gly Gly Thr Ala Tyr Tyr Thr Asn Cys Ala
115 120 125

Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn
130 135 140

Cys Cys Asn Cys Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Gly Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Met Gly
165 170 175

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Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
            180                 185                 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp
        195                 200                 205

Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly Ala
    210                 215                 220

Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Ala Ala Arg Ala Thr His
225                 230                 235                 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
                245                 250                 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
            260                 265                 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Gly Gly Asn
        275                 280                 285

Ala Thr His Cys Ala Arg Tyr Thr Asn Cys Cys Asn Thr Gly Tyr Trp
    290                 295                 300

Ser Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala
305                 310                 315                 320

Asn Ala Ala Arg Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
                325                 330                 335
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<210> 614
<211> 336
<212> PRT
<213> Homo Sapiens

<400> 614

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Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1               5                   10                  15

Ala Arg Cys Ala Asn Cys Cys Asn Tyr Thr Asn Trp Ser Asn Tyr Thr
            20                  25                  30

Asn Trp Ser Asn Gly Thr Asn Cys Ala Asn Cys Cys Asn Gly Gly Asn
        35                  40                  45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
```

```
    50                  55                  60

Ser Asn Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Trp Ser Asn Tyr Thr Asn Tyr Thr Asn Cys Ala Tyr Trp Ser Asn
                85                  90                  95

Gly Ala Tyr Gly Gly Asn Ala Ala Arg Cys Ala Asn Thr Ala Tyr Tyr
            100                 105                 110

Thr Asn Thr Ala Tyr Thr Gly Gly Thr Ala Tyr Tyr Thr Asn Cys Ala
        115                 120                 125

Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn
    130                 135                 140

Cys Cys Asn Cys Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Gly Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Met Gly
                165                 170                 175

Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
            180                 185                 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp
        195                 200                 205

Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly Ala
    210                 215                 220

Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Ala Ala Arg Ala Thr His
225                 230                 235                 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
                245                 250                 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
            260                 265                 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Trp Ser Asn
        275                 280                 285

Ala Thr His Cys Ala Arg Tyr Thr Asn Cys Cys Asn Tyr Thr Asn Cys
    290                 295                 300
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Ala Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Cys Ala
305 310 315 320

Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
325 330 335

<210> 615
<211> 336
<212> PRT
<213> Homo Sapiens

<400> 615

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Cys Ala Asn Cys Cys Asn Tyr Thr Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Thr Asn Cys Ala Asn Cys Cys Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Tyr Thr Asn Tyr Thr Asn Cys Ala Tyr Trp Ser Asn
85 90 95

Gly Ala Tyr Gly Gly Asn Ala Ala Arg Cys Ala Asn Thr Ala Tyr Tyr
100 105 110

Thr Asn Thr Ala Tyr Thr Gly Gly Thr Thr Tyr Tyr Thr Asn Cys Ala
115 120 125

Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn
130 135 140

Cys Cys Asn Cys Ala Arg Cys Cys Asn Tyr Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Gly Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Met Gly
165 170 175

Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
180 185 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp
195 200 205

Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly Ala
210 215 220

Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Ala Ala Arg Ala Thr His
225 230 235 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
245 250 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
260 265 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Trp Ser Asn
275 280 285

Ala Thr His Cys Ala Arg Tyr Thr Asn Cys Cys Asn Ala Thr His Cys
290 295 300

Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Tyr Gly Gly Asn Cys Ala
305 310 315 320

Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
325 330 335

<210> 616
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 616

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala

65 70 75 80

Arg Gly Gly Asn Ala Thr His Gly Cys Asn Ala Ala Tyr Thr Ala Tyr
85 90 95

Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Thr
115 120 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Thr Asn Gly Cys Asn Trp Ser Asn Cys Ala Asn Tyr
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Ala Ala Tyr Thr Ala
260 265 270

Tyr Ala Ala Tyr Trp Ser Asn Gly Cys Asn Cys Cys Asn Thr Thr Tyr
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Cys
290 295 300

Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 617
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 617

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Ala
50 55 60

Thr His Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Gly Asn Ala Thr His Trp Ser Asn Ala Ala Tyr Gly Ala Tyr
85 90 95

Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Thr
115 120 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Cys Ala Asn Tyr
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

```
Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Cys Ala Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Ala Ala Arg Thr Ala
            260                 265                 270

Tyr Ala Ala Tyr Trp Ser Asn Gly Thr Asn Cys Cys Asn Tyr Thr Asn
        275                 280                 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Cys
    290                 295                 300

Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305                 310                 315                 320

Arg
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<210> 618
<211> 336
<212> PRT
<213> Homo Sapiens

<400> 618

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Ala Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1               5                   10                  15

Ala Arg Cys Ala Asn Cys Cys Asn Tyr Thr Asn Trp Ser Asn Trp Ser
            20                  25                  30

Asn Cys Cys Asn Gly Thr Asn Cys Ala Asn Tyr Thr Asn Gly Gly Asn
        35                  40                  45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
    50                  55                  60

Ser Asn Thr Gly Tyr Met Gly Asn Trp Ser Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Trp Ser Asn Tyr Thr Asn Gly Thr Asn Cys Ala Tyr Trp Ser Asn
```

85 90 95

Gly Ala Tyr Gly Gly Asn Ala Ala Tyr Cys Ala Asn Thr Ala Tyr Tyr
100 105 110

Thr Asn Trp Ser Asn Thr Gly Gly Tyr Thr Asn Cys Ala Arg Cys Ala
115 120 125

Arg Met Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn
130 135 140

Cys Cys Asn Met Gly Asn Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Ala Ala Arg Ala Thr His Trp Ser Asn Ala Ala Tyr Met Gly
165 170 175

Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
180 185 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp
195 200 205

Ser Asn Gly Gly Asn Gly Cys Asn Gly Gly Asn Cys Ala Asn Gly Ala
210 215 220

Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Ala Ala Arg Ala Thr His
225 230 235 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
245 250 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
260 265 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Gly Cys Asn
275 280 285

Cys Ala Asn Cys Ala Arg Thr Thr Tyr Cys Cys Asn Cys Ala Tyr Cys
290 295 300

Ala Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala
305 310 315 320

Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Thr His Ala Ala Arg
325 330 335

<210> 619
<211> 336
<212> PRT
<213> Homo Sapiens

<400> 619

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Gly Ala Arg Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1               5                  10                  15

Ala Arg Cys Ala Asn Cys Cys Asn Tyr Thr Asn Trp Ser Asn Trp Ser
            20                  25                  30

Asn Cys Cys Asn Gly Thr Asn Cys Ala Asn Tyr Thr Asn Gly Gly Asn
        35                  40                  45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
    50                  55                  60

Ser Asn Thr Gly Tyr Met Gly Asn Trp Ser Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Trp Ser Asn Tyr Thr Asn Gly Thr Asn Cys Ala Tyr Trp Ser Asn
                85                  90                  95

Gly Ala Tyr Gly Gly Asn Ala Ala Tyr Cys Ala Asn Thr Ala Tyr Tyr
            100                 105                 110

Thr Asn Trp Ser Asn Thr Gly Gly Tyr Thr Asn Cys Ala Arg Cys Ala
        115                 120                 125

Arg Met Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn
    130                 135                 140

Cys Cys Asn Met Gly Asn Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Ala Ala Arg Ala Thr His Trp Ser Asn Ala Ala Tyr Met Gly
                165                 170                 175

Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
            180                 185                 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Cys
        195                 200                 205

Ala Asn Gly Gly Asn Gly Cys Asn Gly Gly Asn Cys Ala Asn Gly Ala
    210                 215                 220
```

Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Ala Ala Arg Ala Thr His
225 230 235 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
245 250 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
260 265 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Gly Cys Asn
275 280 285

Cys Ala Asn Cys Ala Arg Thr Thr Tyr Cys Cys Asn Cys Ala Tyr Cys
290 295 300

Ala Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Cys Ala
305 310 315 320

Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
325 330 335

<210> 620
<211> 324
<212> PRT
<213> Homo Sapiens

<400> 620

Gly Ala Arg Ala Thr His Gly Thr Asn Tyr Thr Asn Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Gly Asn Cys Ala Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Tyr Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Tyr Thr Asn Trp
50 55 60

Ser Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Cys Ala Asn Gly Thr Asn Ala Thr His Trp Ser Asn Trp Ser Asn
85 90 95

Thr Ala Tyr Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys

```
            100                 105                 110

Ala Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala
        115                 120                 125

Arg Gly Cys Asn Cys Cys Asn Met Gly Asn Tyr Thr Asn Tyr Thr Asn
    130                 135                 140

Ala Thr His Trp Ser Asn Gly Gly Asn Gly Cys Asn Trp Ser Asn Trp
145                 150                 155                 160

Ser Asn Met Gly Asn Gly Cys Asn Cys Ala Asn Gly Gly Asn Ala Thr
                165                 170                 175

His Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn
            180                 185                 190

Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys
        195                 200                 205

Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala
    210                 215                 220

Asn Ala Thr His Trp Ser Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg
225                 230                 235                 240

Cys Cys Asn Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Gly
                245                 250                 255

Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala
            260                 265                 270

Arg Thr Ala Tyr Gly Gly Asn Trp Ser Asn Trp Ser Asn Cys Cys Asn
        275                 280                 285

Met Gly Asn Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly
    290                 295                 300

Gly Asn Cys Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr
305                 310                 315                 320

His Ala Ala Arg
```

<210> 621
<211> 318
<212> PRT

1069

<213> Homo Sapiens

<400> 621

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Gly Ala Arg Ala Thr His Gly Thr Asn Tyr Thr Asn Cys Ala Asn Cys
1               5                  10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Gly Asn Cys Ala Asn Tyr Thr
            20                  25                  30

Asn Trp Ser Asn Tyr Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn
        35                  40                  45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Tyr Thr Asn Trp
    50                  55                  60

Ser Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Trp Ser Asn Gly Thr Asn Trp Ser Asn Met Gly Asn Tyr Thr Asn
                85                  90                  95

Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala
            100                 105                 110

Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys
        115                 120                 125

Asn Met Gly Asn Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
    130                 135                 140

Gly Gly Asn Gly Cys Asn Trp Ser Asn Met Gly Asn Met Gly Asn Gly
145                 150                 155                 160

Cys Asn Cys Ala Asn Gly Gly Asn Ala Thr His Cys Cys Asn Gly Ala
                165                 170                 175

Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn
            180                 185                 190

Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr
        195                 200                 205

Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser
    210                 215                 220

Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Cys Cys Asn Gly Ala Arg
225                 230                 235                 240
```

Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr
245 250 255

Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala Tyr Gly Gly
260 265 270

Asn Trp Ser Asn Trp Ser Asn Cys Cys Asn Met Gly Asn Trp Ser Asn
275 280 285

Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Ala
290 295 300

Ala Arg Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
305 310 315

<210> 622
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 622

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Gly Asn Ala Thr His Met Gly Asn Ala Ala Tyr Gly Ala Tyr
85 90 95

Tyr Thr Asn Gly Gly Asn Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Met Gly Asn Tyr Thr Asn Ala Thr His

130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Arg Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Tyr Thr Asn Cys Ala Arg Cys Ala
260 265 270

Tyr Ala Ala Tyr Trp Ser Asn Thr Ala Tyr Cys Cys Asn Cys Cys Asn
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
290 295 300

Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 623
<211> 339
<212> PRT
<213> Homo Sapiens

<400> 623

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

```
Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Tyr Thr
            20                  25                  30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
    50                  55                  60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Trp Ser Asn Gly Thr Asn Tyr Thr Asn Thr Ala Tyr Trp Ser Asn
                85                  90                  95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
            100                 105                 110

Ala Tyr Tyr Thr Asn Gly Thr Asn Thr Gly Gly Thr Ala Tyr Cys Ala
        115                 120                 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
    130                 135                 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Thr Thr Tyr Ala
145                 150                 155                 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Cys Ala
                165                 170                 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
            180                 185                 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Cys Ala Asn Gly
        195                 200                 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala
    210                 215                 220

Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn
225                 230                 235                 240

Ala Thr His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Gly
                245                 250                 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
            260                 265                 270
```

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
275 280 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Thr Thr Tyr Cys Cys Asn Thr
290 295 300

Gly Gly Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly
305 310 315 320

Asn Cys Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
325 330 335

Ala Ala Arg

<210> 624
<211> 339
<212> PRT
<213> Homo Sapiens

<400> 624

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Tyr Thr
20 25 30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Gly Thr Asn Tyr Thr Asn Thr Ala Tyr Trp Ser Asn
85 90 95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
100 105 110

Ala Tyr Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
115 120 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg

```
    130                 135                 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala
145                 150                 155                 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Cys Ala
                165                 170                 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
            180                 185                 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
        195                 200                 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala
    210                 215                 220

Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn
225                 230                 235                 240

Ala Thr His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Gly
                245                 250                 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
            260                 265                 270

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
        275                 280                 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Cys Ala Asn Cys Ala Asn Thr
    290                 295                 300

Gly Gly Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly
305                 310                 315                 320

Asn Cys Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
                325                 330                 335

Ala Ala Arg
```

<210> 625
<211> 339
<212> PRT
<213> Homo Sapiens

<400> 625

```
Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1               5                  10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Tyr Thr
            20                  25                  30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
    50                  55                  60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Ala Ala Tyr Gly Thr Asn Tyr Thr Asn Thr Ala Tyr Trp Ser Asn
                85                  90                  95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
            100                 105                 110

Ala Tyr Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
        115                 120                 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
    130                 135                 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala
145                 150                 155                 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Cys Ala
                165                 170                 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
            180                 185                 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
        195                 200                 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala
    210                 215                 220

Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn
225                 230                 235                 240

Ala Thr His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Gly
                245                 250                 255
```

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
260 265 270

Asn Thr Ala Tyr Thr Thr Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
275 280 285

Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Cys Ala Asn Cys Cys Asn Met
290 295 300

Gly Asn Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly
305 310 315 320

Asn Cys Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
325 330 335

Ala Ala Arg

<210> 626
<211> 339
<212> PRT
<213> Homo Sapiens

<400> 626

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Tyr Thr
20 25 30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Ala Ala Tyr Gly Thr Asn Tyr Thr Asn Thr Ala Tyr Trp Ser Asn
85 90 95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
100 105 110

Ala Tyr Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala

115 120 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
130 135 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala
145 150 155 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Cys Ala
165 170 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
180 185 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
195 200 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala
210 215 220

Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn
225 230 235 240

Ala Thr His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Gly
245 250 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
260 265 270

Asn Thr Ala Tyr Thr Thr Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
275 280 285

Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Cys Ala Asn Cys Cys Asn Met
290 295 300

Gly Asn Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly
305 310 315 320

Asn Cys Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
325 330 335

Ala Ala Arg

<210> 627
<211> 339
<212> PRT

<213> Homo Sapiens

<400> 627

```
Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1               5                  10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Tyr Thr
            20                  25                  30

Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
    50                  55                  60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Trp Ser Asn Gly Thr Asn Tyr Thr Asn Thr Ala Tyr Trp Ser Asn
                85                  90                  95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
            100                 105                 110

Ala Tyr Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
        115                 120                 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
    130                 135                 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala
145                 150                 155                 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Cys Ala
                165                 170                 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
            180                 185                 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Gly Gly Asn Gly
        195                 200                 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala
    210                 215                 220

Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn
225                 230                 235                 240
```

```
Ala Thr His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Gly
                245                 250                 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
            260                 265                 270

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
        275                 280                 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Ala Thr His Trp Ser Asn Met
    290                 295                 300

Gly Asn Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly
305                 310                 315                 320

Asn Cys Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
                325                 330                 335

Ala Ala Arg
```

<210> 628
<211> 339
<212> PRT
<213> Homo Sapiens

<400> 628

```
Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1               5                   10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Tyr Thr
            20                  25                  30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
    50                  55                  60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Trp Ser Asn Gly Thr Asn Tyr Thr Asn Thr Ala Tyr Ala Ala Tyr
                85                  90                  95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
```

```
                100                 105                 110

Ala Tyr Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
        115                 120                 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
    130                 135                 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala
145                 150                 155                 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Cys Ala
                165                 170                 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
            180                 185                 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
        195                 200                 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala
    210                 215                 220

Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn
225                 230                 235                 240

Ala Thr His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Gly
                245                 250                 255

Cys Asn Gly Ala Tyr Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
            260                 265                 270

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
        275                 280                 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Cys Ala Asn Cys Ala Asn Thr
    290                 295                 300

Gly Gly Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly
305                 310                 315                 320

Asn Cys Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
                325                 330                 335

Ala Ala Arg
```

<210> 629
<211> 339
<212> PRT
<213> Homo Sapiens

<400> 629

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Tyr Thr
20 25 30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Gly Thr Asn Tyr Thr Asn Thr Ala Tyr Ala Ala Tyr
85 90 95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
100 105 110

Ala Tyr Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
115 120 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
130 135 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala
145 150 155 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Cys Ala
165 170 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
180 185 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
195 200 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala
210 215 220

```
Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn
225                 230                 235                 240

Ala Thr His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Gly
                245                 250                 255

Cys Asn Gly Ala Tyr Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
            260                 265                 270

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
        275                 280                 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Cys Ala Asn Cys Ala Asn Thr
    290                 295                 300

Gly Gly Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly
305                 310                 315                 320

Asn Cys Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
                325                 330                 335

Ala Ala Arg
```

<210> 630
<211> 339
<212> PRT
<213> Homo Sapiens

<400> 630

```
Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1               5                   10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Tyr Thr
            20                  25                  30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
    50                  55                  60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Trp Ser Asn Gly Thr Asn Tyr Thr Asn Thr Ala Tyr Trp Ser Asn
```

```
                85                  90                  95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
            100                 105                 110

Ala Tyr Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
        115                 120                 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
    130                 135                 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Gly Thr Asn Tyr Thr Asn Ala
145                 150                 155                 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Cys Ala
                165                 170                 175

Asn Met Gly Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
            180                 185                 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
        195                 200                 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala
    210                 215                 220

Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn
225                 230                 235                 240

Ala Thr His Trp Ser Asn Gly Gly Asn Tyr Thr Asn Cys Ala Arg Gly
                245                 250                 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Tyr Thr
            260                 265                 270

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
        275                 280                 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Cys Ala Asn Ala Thr Gly Thr
    290                 295                 300

Thr Tyr Trp Ser Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly
305                 310                 315                 320

Asn Cys Ala Asn Ala Ala Arg Tyr Thr Asn Gly Ala Arg Ala Thr His
                325                 330                 335
```

Ala Ala Arg

<210> 631
<211> 339
<212> PRT
<213> Homo Sapiens

<400> 631

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Tyr Thr
20 25 30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Gly Thr Asn Tyr Thr Asn Gly Ala Tyr Trp Ser Asn
85 90 95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
100 105 110

Ala Tyr Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
115 120 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
130 135 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala
145 150 155 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Cys Ala
165 170 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
180 185 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
195 200 205

```
Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala
    210                 215                 220

Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn
225                 230                 235                 240

Ala Thr His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Gly
                245                 250                 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
            260                 265                 270

Asn Thr Thr Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Tyr Cys Ala Arg
        275                 280                 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Cys Ala Asn Cys Cys Asn Tyr
    290                 295                 300

Thr Asn Cys Ala Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly
305                 310                 315                 320

Asn Cys Ala Asn Ala Ala Arg Gly Thr Asn Gly Cys Asn Ala Thr His
                325                 330                 335

Ala Ala Arg
```

<210> 632
<211> 339
<212> PRT
<213> Homo Sapiens

<400> 632

```
Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1               5                   10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Tyr Thr
            20                  25                  30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
    50                  55                  60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
```

```
65                  70                  75                  80

Arg Trp Ser Asn Ala Thr His Tyr Thr Asn Thr Ala Tyr Met Gly Asn
                85                  90                  95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
            100                 105                 110

Ala Tyr Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
        115                 120                 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
    130                 135                 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala
145                 150                 155                 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Gly Cys
                165                 170                 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
            180                 185                 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
        195                 200                 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala
    210                 215                 220

Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn
225                 230                 235                 240

Ala Thr His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Gly
                245                 250                 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
            260                 265                 270

Asn Thr Ala Tyr Thr Thr Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
        275                 280                 285

Thr Ala Tyr Thr Thr Tyr Ala Thr His Cys Ala Asn Cys Cys Asn Tyr
    290                 295                 300

Thr Asn Cys Ala Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly
305                 310                 315                 320
```

Asn Cys Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
325 330 335

Ala Ala Arg

<210> 633
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 633

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Cys Ala Tyr Thr Ala Tyr
85 90 95

Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Thr Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Trp Ser Asn Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Ala Ala Arg Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala
260 265 270

Tyr Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr Cys Cys Asn Thr Thr Tyr
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Cys
290 295 300

Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 634
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 634

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Gly Cys Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala

65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Thr Ala Tyr
85 90 95

Tyr Thr Asn Gly Cys Asn Thr Gly Gly Tyr Thr Asn Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Trp Ser Asn Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala
260 265 270

Tyr Ala Ala Tyr Cys Ala Asn Thr Ala Tyr Cys Cys Asn Thr Thr Tyr
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Cys
290 295 300

Ala Asn Ala Ala Arg Ala Thr Gly Gly Ala Tyr Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 635
<211> 324
<212> PRT
<213> Homo Sapiens

<400> 635

```
Gly Ala Arg Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1               5                  10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Cys Asn Cys Ala Asn Tyr Thr
            20                  25                  30

Asn Trp Ser Asn Gly Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn
        35                  40                  45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Tyr Thr Asn Trp
    50                  55                  60

Ser Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Trp Ser Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr
                85                  90                  95

Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Gly Ala Tyr Cys Cys Asn Gly Gly Asn Cys Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Met Gly Asn Tyr Thr Asn Tyr Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Gly Asn Gly Cys Asn Trp Ser Asn Met Gly Asn Met
145                 150                 155                 160

Gly Asn Gly Cys Asn Cys Ala Asn Gly Gly Asn Ala Thr His Cys Cys
                165                 170                 175

Asn Gly Cys Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
        195                 200                 205
```

Ala Arg Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Trp Ser Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Gly Thr Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Cys Ala
260 265 270

Tyr Ala Ala Tyr Ala Ala Tyr Thr Gly Gly Cys Cys Asn Cys Cys Asn
275 280 285

Thr Gly Gly Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly
290 295 300

Gly Asn Cys Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr
305 310 315 320

His Ala Ala Arg

<210> 636
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 636

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Gly Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Met Gly Asn Thr Gly Gly

```
                85                  90                  95

Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr
145                 150                 155                 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Cys Ala Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Gly Cys
            260                 265                 270

Asn Ala Ala Tyr Trp Ser Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn
        275                 280                 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
    290                 295                 300

Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Thr Thr Tyr Ala Ala
305                 310                 315                 320

Arg
```

<210> 637
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 637

```
Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1               5                  10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
            20                  25                  30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
    50                  55                  60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Trp Ser Asn Ala Thr His Trp Ser Asn Cys Ala Asn Thr Ala Tyr
                85                  90                  95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Thr Thr Tyr Tyr Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr
145                 150                 155                 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
    210                 215                 220
```

```
His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Gly Cys Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
            260                 265                 270

Asn Cys Ala Tyr Trp Ser Asn Gly Cys Asn Cys Cys Asn Thr Thr Tyr
        275                 280                 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Cys
    290                 295                 300

Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Thr His Ala Ala
305                 310                 315                 320

Arg
```

<210> 638
<211> 318
<212> PRT
<213> Homo Sapiens

<400> 638

```
Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1               5                   10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
            20                  25                  30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
    50                  55                  60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Cys Ala Asn Ala Thr His Trp Ser Asn Ala Thr His Thr Ala Tyr
                85                  90                  95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
```

100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
260 265 270

Asn Thr Ala Tyr Trp Ser Asn Cys Ala Asn Tyr Thr Asn Cys Ala Asn
275 280 285

Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Cys Ala Asn Ala
290 295 300

Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
305 310 315

<210> 639
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 639

```
Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1               5                  10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
            20                  25                  30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
    50                  55                  60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Trp Ser Asn Ala Thr His Met Gly Asn Trp Ser Asn Thr Ala Tyr
                85                  90                  95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Met Gly Asn Cys Cys Asn Gly Gly Asn Ala Ala Tyr Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr
145                 150                 155                 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
    210                 215                 220

His Met Gly Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Cys Ala Asn Thr
                245                 250                 255
```

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
260 265 270

Asn Thr Ala Tyr Trp Ser Asn Ala Thr His Cys Cys Asn Tyr Thr Asn
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Cys
290 295 300

Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 640
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 640

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Gly
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Cys Ala Asn Ala Thr His Trp Ser Asn Met Gly Asn Thr Ala Tyr
85 90 95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His

130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Cys Ala Asn Tyr
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Tyr Thr
210 215 220

Asn Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Ala Thr
260 265 270

His Thr Ala Tyr Trp Ser Asn Cys Ala Asn Trp Ser Asn Ala Thr His
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
290 295 300

Ala Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 641
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 641

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

```
Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
            20                  25                  30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
    50                  55                  60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Met Gly Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr
                85                  90                  95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Gly Thr Asn Tyr Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Cys Asn Gly Ala Arg Trp Ser Asn Trp Ser Asn Tyr
145                 150                 155                 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Cys Ala Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
            260                 265                 270
```

1100.

Asn Thr Ala Tyr Ala Thr His Cys Ala Asn Cys Cys Asn Ala Thr His
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
290 295 300

Ala Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Thr
305 310 315 320

His

<210> 642
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 642

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Ala Thr His Trp Ser Asn Met Gly Asn Thr Ala Tyr
85 90 95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Cys Ala Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr

145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Ala Ala Tyr Thr Thr Tyr Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
260 265 270

Asn Thr Ala Tyr Thr Thr Tyr Cys Ala Asn Cys Cys Asn Ala Thr His
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
290 295 300

Ala Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 643
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 643

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

```
Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
    50                  55                  60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr
                85                  90                  95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Cys Ala Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr
145                 150                 155                 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Thr Thr
    210                 215                 220

Tyr Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Cys Ala Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
            260                 265                 270

Asn Thr Ala Tyr Thr Thr Tyr Trp Ser Asn Cys Cys Asn Ala Thr His
        275                 280                 285
```

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
290 295 300

Ala Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 644
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 644

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Cys Ala Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys

```
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Tyr Thr
    210                 215                 220

Asn Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Trp Ser Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
            260                 265                 270

Asn Thr Thr Tyr Thr Ala Tyr Cys Ala Asn Cys Cys Asn Ala Thr His
        275                 280                 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
    290                 295                 300

Ala Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305                 310                 315                 320

Arg
```

<210> 645
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 645

```
Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1               5                   10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
            20                  25                  30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
        35                  40                  45
```

```
Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
    50                  55                  60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr
                85                  90                  95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Tyr
145                 150                 155                 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Cys Ala Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
            260                 265                 270

Asn Thr Ala Tyr Thr Thr Tyr Cys Ala Asn Cys Cys Asn Ala Thr His
        275                 280                 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
    290                 295                 300
```

```
Ala Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305                 310                 315                 320

Arg
```

<210> 646
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 646

```
Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1               5                   10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
            20                  25                  30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
    50                  55                  60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr
                85                  90                  95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Cys Ala Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr
145                 150                 155                 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
```

180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Trp Ser Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
260 265 270

Asn Thr Thr Tyr Thr Ala Tyr Gly Cys Asn Cys Cys Asn Ala Thr His
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
290 295 300

Ala Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 647
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 647

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

```
Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr
                85                  90                  95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Cys Ala Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr
145                 150                 155                 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Cys Ala Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
            260                 265                 270

Asn Thr Ala Tyr Thr Thr Tyr Cys Ala Asn Cys Cys Asn Ala Thr His
        275                 280                 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
    290                 295                 300

Ala Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305                 310                 315                 320
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Arg

<210> 648
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 648

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Thr Ala Tyr
85 90 95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Tyr
145 150 155 160

Thr Asn Gly Ala Arg Cys Ala Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly

195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala
260 265 270

Tyr Gly Ala Tyr Thr Ala Tyr Tyr Thr Asn Cys Cys Asn Thr Thr Tyr
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Cys
290 295 300

Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 649
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 649

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

```
Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Trp Ser Asn
                85                  90                  95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Gly Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Tyr
145                 150                 155                 160

Thr Asn Gly Ala Arg Cys Ala Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Cys Ala Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Gly
            260                 265                 270

Tyr Gly Ala Tyr Gly Ala Tyr Tyr Thr Asn Cys Cys Asn Tyr Thr Asn
        275                 280                 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Cys
    290                 295                 300

Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305                 310                 315                 320

Arg
```

<210> 650
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 650

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Gly Ala Tyr Thr Ala Tyr
85 90 95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Tyr
145 150 155 160

Thr Asn Gly Ala Arg Cys Ala Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Ala Thr

210 215 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Tyr Thr Ala
260 265 270

Tyr Gly Ala Tyr Ala Ala Tyr Tyr Thr Asn Cys Cys Asn Tyr Thr Asn
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Cys
290 295 300

Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 651
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 651

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Gly Cys Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Thr Ala Tyr
85 90 95

```
Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Tyr
145                 150                 155                 160

Thr Asn Gly Ala Arg Cys Ala Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Cys Ala Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala
            260                 265                 270

Tyr Gly Ala Tyr Ala Ala Tyr Tyr Thr Asn Cys Cys Asn Tyr Thr Asn
        275                 280                 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Cys
    290                 295                 300

Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305                 310                 315                 320

Arg
```

<210> 652
<211> 321

<212> PRT
<213> Homo Sapiens

<400> 652

```
Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1               5                  10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
            20                  25                  30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
    50                  55                  60

Ala Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Trp Ser Asn
                85                  90                  95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Thr His Tyr
145                 150                 155                 160

Thr Asn Gly Ala Arg Cys Ala Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Ala Arg Cys Ala Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
```

225 230 235 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Gly
260 265 270

Tyr Gly Ala Tyr Ala Thr His Tyr Thr Asn Cys Cys Asn Tyr Thr Asn
275 280 285

Trp Ser Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Cys
290 295 300

Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 653
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 653

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Trp Ser Asn
85 90 95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Tyr
145 150 155 160

Thr Asn Gly Ala Arg Cys Ala Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala
260 265 270

Tyr Gly Ala Tyr Ala Ala Tyr Tyr Thr Asn Cys Cys Asn Tyr Thr Asn
275 280 285

Gly Cys Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Cys
290 295 300

Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Met Gly
305 310 315 320

Asn

<210> 654
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 654

```
Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1               5                  10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
            20                  25                  30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Tyr Gly Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
    50                  55                  60

Ala Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Gly Ala Tyr Ala Thr His Cys Ala Asn Ala Ala Tyr Thr Ala Tyr
                85                  90                  95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Tyr
145                 150                 155                 160

Thr Asn Gly Ala Arg Cys Ala Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Cys Ala Asn Thr
```

245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala
260 265 270

Tyr Gly Ala Tyr Trp Ser Asn Tyr Thr Asn Cys Cys Asn Ala Thr His
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
290 295 300

Ala Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 655
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 655

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Thr Ala Tyr
85 90 95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Tyr Thr Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
130 135 140

Cys Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Tyr
145 150 155 160

Thr Asn Gly Ala Arg Cys Ala Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala
260 265 270

Tyr Gly Ala Tyr Ala Ala Tyr Tyr Thr Asn Cys Cys Asn Ala Thr His
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
290 295 300

Ala Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 656
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 656

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

```
Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
            20                  25                  30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
    50                  55                  60

Ala Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Gly Ala Tyr Thr Ala Tyr
                85                  90                  95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Tyr
145                 150                 155                 160

Thr Asn Gly Ala Arg Cys Ala Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Cys Ala Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Tyr Thr Ala
```

260 265 270

Tyr Gly Ala Tyr Ala Ala Tyr Tyr Thr Asn Cys Cys Asn Ala Thr His
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
290 295 300

Ala Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 657
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 657

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Trp Ser Asn
85 90 95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Tyr
145 150 155 160

Thr Asn Gly Ala Arg Cys Ala Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Tyr Thr Ala
260 265 270

Tyr Gly Ala Tyr Ala Ala Tyr Tyr Thr Asn Cys Cys Asn Ala Thr His
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
290 295 300

Ala Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 658
<211> 360
<212> PRT
<213> Homo Sapiens

<400> 658

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
20 25 30

```
Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Cys Asn
        35                  40                  45

Trp Ser Asn Gly Thr Asn Ala Ala Arg Gly Thr Asn Trp Ser Asn Thr
    50                  55                  60

Gly Tyr Ala Ala Arg Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Ala
65                  70                  75                  80

Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Trp Ser Asn Thr Ala Tyr
                85                  90                  95

Gly Gly Asn Ala Thr His Trp Ser Asn Thr Gly Gly Gly Thr Asn Met
            100                 105                 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Cys Ala
        115                 120                 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
    130                 135                 140

Gly Gly Asn Thr Gly Gly Ala Thr His Trp Ser Asn Gly Cys Asn Trp
145                 150                 155                 160

Ser Asn Ala Ala Tyr Gly Gly Asn Ala Ala Tyr Cys Ala Asn Ala Ala
                165                 170                 175

Tyr Thr Ala Tyr Gly Cys Asn Cys Ala Arg Ala Ala Arg Tyr Thr Asn
            180                 185                 190

Cys Ala Arg Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala
        195                 200                 205

Thr Gly Cys Ala Asn Cys Ala Asn Gly Ala Tyr Cys Ala Asn Trp Ser
    210                 215                 220

Asn Cys Ala Asn Trp Ser Asn Cys Ala Asn Gly Cys Asn Thr Ala Tyr
225                 230                 235                 240

Ala Thr Gly Gly Ala Arg Tyr Thr Asn Met Gly Asn Trp Ser Asn Tyr
                245                 250                 255

Thr Asn Met Gly Asn Trp Ser Asn Gly Ala Tyr Gly Ala Tyr Cys Ala
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
```

275 280 285

Gly Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Tyr Ala Ala Tyr Thr
290 295 300

Gly Gly Ala Ala Tyr Thr Ala Tyr Gly Gly Asn Thr Thr Tyr Thr Thr
305 310 315 320

Tyr Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg
325 330 335

Gly Gly Asn Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly
340 345 350

Thr Asn Trp Ser Asn Trp Ser Asn
355 360

<210> 659
<211> 351
<212> PRT
<213> Homo Sapiens

<400> 659

Cys Ala Arg Gly Thr Asn Cys Ala Tyr Tyr Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
20 25 30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Cys Asn
35 40 45

Trp Ser Asn Gly Thr Asn Ala Ala Arg Gly Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Gly Gly Asn Thr Ala
65 70 75 80

Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Gly Gly Asn Cys Ala Tyr
85 90 95

Thr Ala Tyr Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Cys Ala
115 120 125

```
Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
    130                 135                 140

Gly Gly Asn Thr Gly Gly Ala Thr His Ala Ala Tyr Cys Cys Asn Ala
145                 150                 155                 160

Ala Tyr Trp Ser Asn Gly Gly Asn Gly Gly Asn Cys Ala Asn Ala Ala
                165                 170                 175

Tyr Thr Gly Tyr Gly Cys Asn Cys Ala Arg Ala Ala Arg Thr Thr Tyr
            180                 185                 190

Cys Ala Arg Gly Gly Asn Met Gly Asn Gly Thr Asn Cys Ala Asn Ala
        195                 200                 205

Thr Gly Cys Ala Asn Met Gly Asn Gly Ala Tyr Cys Ala Asn Trp Ser
    210                 215                 220

Asn Ala Thr His Trp Ser Asn Cys Ala Asn Gly Cys Asn Thr Ala Tyr
225                 230                 235                 240

Ala Thr Gly Gly Ala Arg Tyr Thr Asn Trp Ser Asn Met Gly Asn Tyr
                245                 250                 255

Thr Asn Met Gly Asn Trp Ser Asn Gly Ala Tyr Gly Ala Tyr Cys Ala
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Met Gly Asn Trp Ser Asn Ala Thr His Gly Cys Asn Gly
    290                 295                 300

Thr Asn Gly Cys Asn Tyr Thr Asn Gly Ala Tyr Thr Ala Tyr Thr Gly
305                 310                 315                 320

Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Tyr Thr Asn
                325                 330                 335

Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
            340                 345                 350
```

<210> 660
<211> 351
<212> PRT
<213> Homo Sapiens

<400> 660

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
20 25 30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Cys Asn
35 40 45

Trp Ser Asn Gly Thr Asn Ala Ala Arg Gly Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Ala
65 70 75 80

Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Gly Gly Asn Thr Ala Tyr
85 90 95

Thr Ala Tyr Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Cys Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
130 135 140

Gly Gly Asn Thr Gly Gly Ala Thr His Ala Ala Tyr Cys Cys Asn Ala
145 150 155 160

Ala Tyr Trp Ser Asn Gly Gly Asn Gly Gly Asn Cys Ala Asn Ala Ala
165 170 175

Tyr Cys Ala Tyr Cys Ala Asn Cys Ala Arg Ala Ala Arg Thr Thr Tyr
180 185 190

Cys Ala Arg Gly Gly Asn Met Gly Asn Gly Thr Asn Cys Ala Asn Ala
195 200 205

Thr Gly Cys Ala Asn Met Gly Asn Gly Ala Tyr Cys Ala Asn Trp Ser
210 215 220

Asn Ala Thr His Trp Ser Asn Cys Ala Asn Gly Cys Asn Thr Ala Tyr
225 230 235 240

Ala Thr Gly Gly Ala Arg Tyr Thr Asn Trp Ser Asn Met Gly Asn Tyr

245 250 255

Thr Asn Met Gly Asn Trp Ser Asn Gly Ala Tyr Gly Ala Tyr Cys Ala
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Trp Ser Asn Ala Thr His Gly Cys Asn Gly
290 295 300

Thr Asn Gly Cys Asn Tyr Thr Asn Gly Ala Tyr Thr Ala Tyr Thr Gly
305 310 315 320

Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Tyr Thr Asn
325 330 335

Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
340 345 350

<210> 661
<211> 366
<212> PRT
<213> Homo Sapiens

<400> 661

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
20 25 30

Asn Met Gly Asn Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Cys Asn
35 40 45

Trp Ser Asn Gly Thr Asn Ala Ala Arg Gly Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Gly Gly Asn Thr Ala
65 70 75 80

Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Gly Ala Arg Tyr Thr Asn
85 90 95

Trp Ser Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

```
Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
        115                 120                 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
    130                 135                 140

Gly Gly Asn Trp Ser Asn Thr Thr Tyr Gly Ala Tyr Cys Cys Asn Gly
145                 150                 155                 160

Ala Arg Gly Ala Tyr Gly Gly Asn Gly Ala Arg Cys Ala Asn Ala Thr
                165                 170                 175

His Thr Ala Tyr Gly Cys Asn Cys Ala Arg Ala Ala Arg Thr Thr Tyr
            180                 185                 190

Cys Ala Arg Gly Gly Asn Met Gly Asn Gly Thr Asn Cys Ala Asn Ala
        195                 200                 205

Thr Gly Tyr Thr Asn Gly Ala Arg Gly Ala Tyr Cys Ala Asn Trp Ser
    210                 215                 220

Asn Cys Ala Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Thr Ala Tyr
225                 230                 235                 240

Ala Thr Gly Gly Ala Arg Tyr Thr Asn Trp Ser Asn Trp Ser Asn Tyr
                245                 250                 255

Thr Asn Met Gly Asn Trp Ser Asn Gly Ala Arg Gly Ala Tyr Cys Ala
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Cys Ala Asn Gly Ala Arg Gly Gly Asn Gly Ala Tyr Gly
    290                 295                 300

Gly Asn Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala
305                 310                 315                 320

Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr Gly Gly
                325                 330                 335

Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Cys Ala Asn Gly
            340                 345                 350

Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
        355                 360                 365
```

<210> 662
<211> 366
<212> PRT
<213> Homo Sapiens

<400> 662

Cys Ala Arg Gly Thr Asn Cys Ala Asn Tyr Thr Asn Ala Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Thr Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Cys Ala Asn Gly Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Cys Ala Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Trp Ser Asn Tyr Thr Asn Trp Ser Asn Ala Ala Tyr Gly Cys Asn
85 90 95

Met Gly Asn Ala Thr Gly Gly Gly Asn Gly Thr Asn Trp Ser Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Tyr Thr Asn Gly Cys Asn Cys Ala Tyr Ala Thr His Thr
145 150 155 160

Thr Tyr Trp Ser Asn Ala Ala Tyr Gly Ala Tyr Gly Ala Arg Ala Ala
165 170 175

Arg Trp Ser Asn Thr Ala Tyr Trp Ser Asn Cys Ala Asn Trp Ser Asn
180 185 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Tyr Thr Asn Cys
195 200 205

Ala Asn Ala Thr His Trp Ser Asn Ala Ala Arg Gly Ala Tyr Cys Ala

210 215 220

Asn Trp Ser Asn Ala Ala Arg Trp Ser Asn Cys Ala Arg Gly Thr Asn
225 230 235 240

Gly Thr Asn Tyr Thr Asn Cys Ala Asn Ala Thr Gly Cys Ala Asn Ala
245 250 255

Ala Tyr Ala Thr Gly Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
260 265 270

Tyr Cys Ala Asn Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Ala Thr Gly Thr Ala Tyr Trp
290 295 300

Ser Asn Trp Ser Asn Gly Gly Asn Thr Gly Gly Thr Ala Tyr Gly Gly
305 310 315 320

Asn Gly Thr Asn Thr Thr Tyr Gly Ala Tyr Thr Ala Tyr Thr Gly Gly
325 330 335

Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Tyr Thr Asn Gly
340 345 350

Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
355 360 365

<210> 663
<211> 369
<212> PRT
<213> Homo Sapiens

<400> 663

Cys Ala Arg Gly Thr Asn Cys Ala Asn Tyr Thr Asn Ala Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Thr Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Cys Ala Asn Gly Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Cys Ala Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

```
Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Thr Thr
65                  70                  75                  80

Tyr Trp Ser Asn Tyr Thr Asn Trp Ser Asn Ala Ala Tyr Gly Cys Asn
                85                  90                  95

Met Gly Asn Ala Thr Gly Gly Gly Asn Gly Thr Asn Trp Ser Asn Thr
            100                 105                 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Tyr Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Tyr Thr Asn Gly Thr Asn Tyr Thr Asn Ala Thr His Thr
145                 150                 155                 160

Thr Tyr Trp Ser Asn Ala Ala Tyr Gly Ala Tyr Gly Ala Arg Ala Ala
                165                 170                 175

Arg Trp Ser Asn Thr Ala Tyr Trp Ser Asn Cys Ala Asn Trp Ser Asn
            180                 185                 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Tyr Thr Asn Cys
        195                 200                 205

Ala Asn Ala Thr His Trp Ser Asn Ala Ala Arg Gly Ala Tyr Cys Ala
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Trp Ser Asn Cys Ala Arg Gly Thr Asn
225                 230                 235                 240

Gly Thr Asn Tyr Thr Asn Cys Ala Asn Ala Thr Gly Cys Ala Asn Ala
                245                 250                 255

Ala Tyr Ala Thr Gly Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
            260                 265                 270

Tyr Cys Ala Asn Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Gly Thr Asn Thr Ala Tyr Trp
    290                 295                 300

Ser Asn Trp Ser Asn Gly Gly Asn Thr Gly Gly Trp Ser Asn Thr Thr
305                 310                 315                 320
```

Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn
325 330 335

Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Cys
340 345 350

Ala Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser
355 360 365

Asn

<210> 664
<211> 354
<212> PRT
<213> Homo Sapiens

<400> 664

Cys Ala Arg Ala Thr His Cys Ala Asn Tyr Thr Asn Ala Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Cys Ala Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Cys Ala Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Cys Ala Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Trp Ser Asn Tyr Thr Asn Trp Ser Asn Cys Ala Asn Gly Gly Asn
85 90 95

Gly Gly Asn Gly Thr Asn Gly Gly Asn Gly Thr Asn Gly Gly Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Tyr Thr Asn Gly Cys Asn Tyr Thr Asn Ala Thr His Thr

```
145                 150                 155                 160

Ala Tyr Thr Gly Gly Ala Ala Tyr Gly Ala Tyr Gly Ala Tyr Ala Ala
                165                 170                 175

Arg Met Gly Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn
            180                 185                 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Tyr Thr Asn Cys
        195                 200                 205

Ala Asn Ala Thr His Cys Ala Asn Ala Ala Arg Gly Ala Tyr Cys Ala
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn
225                 230                 235                 240

Gly Thr Asn Tyr Thr Asn Cys Ala Asn Ala Thr Gly Cys Ala Asn Ala
                245                 250                 255

Ala Tyr Ala Thr Gly Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
            260                 265                 270

Tyr Cys Ala Asn Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Cys Ala Tyr Met Gly Asn Met Gly Asn Gly
    290                 295                 300

Ala Arg Tyr Thr Asn Cys Cys Asn Thr Thr Tyr Gly Ala Tyr Thr Ala
305                 310                 315                 320

Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn
                325                 330                 335

Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp
            340                 345                 350

Ser Asn
```

<210> 665
<211> 354
<212> PRT
<213> Homo Sapiens

<400> 665

```
Cys Ala Arg Ala Thr His Cys Ala Asn Tyr Thr Asn Ala Ala Arg Gly
1               5                  10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Cys Ala Asn Tyr Thr
            20                  25                  30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Cys Ala Asn Cys Ala Arg
        35                  40                  45

Cys Ala Asn Tyr Thr Asn Cys Ala Asn Tyr Thr Asn Cys Ala Asn Thr
    50                  55                  60

Gly Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Thr
65                  70                  75                  80

Tyr Trp Ser Asn Tyr Thr Asn Trp Ser Asn Cys Ala Asn Gly Gly Asn
                85                  90                  95

Gly Gly Asn Gly Thr Asn Gly Gly Asn Gly Thr Asn Gly Gly Asn Thr
            100                 105                 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Tyr Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Tyr Thr Asn Gly Cys Asn Tyr Thr Asn Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Thr Gly Gly Ala Ala Tyr Gly Ala Tyr Gly Ala Tyr Ala Ala
                165                 170                 175

Arg Met Gly Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn
            180                 185                 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Tyr Thr Asn Cys
        195                 200                 205

Ala Asn Ala Thr His Cys Ala Asn Ala Ala Arg Gly Ala Tyr Cys Ala
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Cys Ala Asn Cys Ala Arg Gly Thr Asn
225                 230                 235                 240

Gly Thr Asn Tyr Thr Asn Cys Ala Asn Gly Thr Asn Cys Ala Asn Gly
                245                 250                 255
```

```
Ala Tyr Ala Thr Gly Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
            260                 265                 270

Tyr Cys Ala Asn Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Cys Ala Tyr Met Gly Asn Ala Ala Tyr Thr
    290                 295                 300

Gly Gly Cys Ala Asn Cys Cys Asn Thr Thr Tyr Gly Ala Tyr Thr Ala
305                 310                 315                 320

Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn
                325                 330                 335

Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp
            340                 345                 350

Ser Asn
```

<210> 666
<211> 354
<212> PRT
<213> Homo Sapiens

<400> 666

```
Cys Ala Arg Ala Thr His Cys Ala Asn Tyr Thr Asn Ala Ala Arg Gly
1               5                   10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Cys Ala Asn Tyr Thr
            20                  25                  30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Cys Ala Asn Cys Ala Arg
        35                  40                  45

Cys Ala Asn Tyr Thr Asn Cys Ala Asn Tyr Thr Asn Cys Ala Asn Thr
    50                  55                  60

Gly Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Thr
65                  70                  75                  80

Tyr Trp Ser Asn Tyr Thr Asn Ala Ala Tyr Cys Ala Asn Gly Gly Asn
                85                  90                  95

Gly Gly Asn Gly Thr Asn Gly Gly Asn Gly Thr Asn Gly Gly Asn Thr
```

```
            100                 105                 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Tyr Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Tyr Thr Asn Gly Cys Asn Tyr Thr Asn Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Thr Gly Gly Ala Ala Tyr Gly Ala Tyr Gly Ala Tyr Ala Ala
                165                 170                 175

Arg Met Gly Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn
            180                 185                 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Tyr Thr Asn Cys
        195                 200                 205

Ala Asn Ala Thr His Cys Ala Asn Ala Ala Arg Gly Ala Tyr Cys Ala
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn
225                 230                 235                 240

Gly Thr Asn Tyr Thr Asn Cys Ala Asn Ala Thr Gly Cys Ala Asn Ala
                245                 250                 255

Ala Tyr Ala Thr Gly Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
            260                 265                 270

Tyr Cys Ala Asn Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Cys Ala Tyr Met Gly Asn Tyr Thr Asn Gly
    290                 295                 300

Ala Arg Tyr Thr Asn Cys Cys Asn Thr Thr Tyr Gly Ala Tyr Thr Ala
305                 310                 315                 320

Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn
                325                 330                 335

Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp
            340                 345                 350
```

Ser Asn

<210> 667
<211> 354
<212> PRT
<213> Homo Sapiens

<400> 667

Cys Ala Arg Ala Thr His Cys Ala Asn Tyr Thr Asn Ala Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Cys Ala Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Cys Ala Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Cys Ala Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Trp Ser Asn Tyr Thr Asn Trp Ser Asn Cys Ala Asn Gly Gly Asn
85 90 95

Gly Gly Asn Gly Thr Asn Gly Gly Asn Gly Thr Asn Gly Gly Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Tyr Thr Asn Gly Cys Asn Tyr Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Thr Gly Gly Ala Ala Tyr Gly Ala Tyr Gly Ala Tyr Ala Ala
165 170 175

Arg Met Gly Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn
180 185 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Tyr Thr Asn Cys
195 200 205

Ala Asn Ala Thr His Cys Ala Asn Ala Ala Arg Gly Ala Tyr Cys Ala
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn
225 230 235 240

Gly Thr Asn Tyr Thr Asn Cys Ala Asn Ala Thr Gly Cys Ala Asn Ala
245 250 255

Ala Tyr Tyr Thr Asn Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
260 265 270

Tyr Cys Ala Asn Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Cys Ala Tyr Met Gly Asn Met Gly Asn Gly
290 295 300

Ala Arg Gly Thr Asn Cys Cys Asn Thr Thr Tyr Gly Ala Tyr Thr Ala
305 310 315 320

Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn
325 330 335

Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp
340 345 350

Ser Asn

<210> 668
<211> 354
<212> PRT
<213> Homo Sapiens

<400> 668

Cys Ala Arg Ala Thr His Cys Ala Asn Tyr Thr Asn Ala Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Cys Ala Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Cys Ala Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Cys Ala Asn Tyr Thr Asn Cys Ala Asn Thr

```
    50                  55                  60

Gly Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Thr
65                  70                  75                  80

Tyr Trp Ser Asn Tyr Thr Asn Trp Ser Asn Cys Ala Asn Gly Gly Asn
                85                  90                  95

Gly Gly Asn Gly Thr Asn Gly Gly Asn Gly Thr Asn Gly Gly Asn Thr
            100                 105                 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Tyr Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Tyr Thr Asn Gly Cys Asn Tyr Thr Asn Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Thr Gly Gly Ala Ala Tyr Gly Thr Asn Gly Ala Arg Ala Ala
                165                 170                 175

Arg Met Gly Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn
            180                 185                 190

Tyr Thr Asn Met Gly Asn Trp Ser Asn Met Gly Asn Tyr Thr Asn Cys
        195                 200                 205

Ala Asn Ala Thr His Cys Ala Asn Ala Ala Arg Gly Cys Asn Cys Ala
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn
225                 230                 235                 240

Gly Thr Asn Tyr Thr Asn Cys Ala Asn Ala Thr Gly Cys Ala Asn Ala
                245                 250                 255

Ala Tyr Ala Thr Gly Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
            260                 265                 270

Tyr Cys Ala Asn Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Cys Ala Tyr Met Gly Asn Cys Ala Tyr Cys
    290                 295                 300
```

Ala Asn Ala Ala Tyr Cys Cys Asn Thr Thr Tyr Gly Ala Arg Thr Ala
305 310 315 320

Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn
325 330 335

Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp
340 345 350

Ser Asn

<210> 669
<211> 354
<212> PRT
<213> Homo Sapiens

<400> 669

Cys Ala Arg Ala Thr His Cys Ala Asn Tyr Thr Asn Ala Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Cys Ala Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Cys Ala Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Cys Ala Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Trp Ser Asn Tyr Thr Asn Trp Ser Asn Cys Ala Asn Gly Gly Asn
85 90 95

Gly Gly Asn Gly Thr Asn Gly Gly Asn Gly Thr Asn Gly Gly Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Tyr Thr Asn Gly Cys Asn Tyr Thr Asn Ala Thr His Thr
145 150 155 160

```
Ala Tyr Thr Gly Gly Ala Ala Tyr Gly Ala Tyr Gly Ala Tyr Ala Ala
                165                 170                 175

Arg Met Gly Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn
            180                 185                 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Tyr Thr Asn Cys
        195                 200                 205

Ala Asn Ala Thr His Cys Ala Asn Ala Ala Arg Gly Ala Tyr Cys Ala
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn
225                 230                 235                 240

Gly Thr Asn Tyr Thr Asn Cys Ala Asn Ala Thr Gly Cys Ala Asn Ala
                245                 250                 255

Ala Tyr Ala Thr Gly Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
            260                 265                 270

Tyr Cys Ala Asn Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Cys Ala Tyr Met Gly Asn Gly Gly Asn Gly
    290                 295                 300

Ala Arg Tyr Thr Asn Cys Cys Asn Thr Thr Tyr Gly Ala Tyr Thr Ala
305                 310                 315                 320

Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn
                325                 330                 335

Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp
            340                 345                 350

Ser Asn
```

<210> 670
<211> 363
<212> PRT
<213> Homo Sapiens

<400> 670

```
Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
```

```
1               5                  10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Tyr Thr
            20                  25                  30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
        35                  40                  45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
    50                  55                  60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65                  70                  75                  80

Tyr Cys Cys Asn Thr Thr Tyr Trp Ser Asn Met Gly Asn Thr Ala Tyr
                85                  90                  95

Trp Ser Asn Ala Thr Gly Ala Ala Tyr Thr Gly Gly Gly Thr Asn Met
            100                 105                 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
        115                 120                 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
    130                 135                 140

Trp Ser Asn Gly Cys Asn Ala Thr His Trp Ser Asn Trp Ser Asn Trp
145                 150                 155                 160

Ser Asn Trp Ser Asn Trp Ser Asn Thr Ala Tyr Ala Thr His Thr Ala
                165                 170                 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
            180                 185                 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
        195                 200                 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Gly Cys
    210                 215                 220

Asn Ala Ala Arg Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Thr Ala Tyr
225                 230                 235                 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
                245                 250                 255
```

```
Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Met Gly Asn Gly Ala Tyr Met Gly Asn Gly Thr Asn Gly
    290                 295                 300

Gly Asn Gly Cys Asn Cys Ala Asn Cys Cys Asn Gly Ala Tyr Gly Cys
305                 310                 315                 320

Asn Thr Thr Tyr Gly Ala Tyr Ala Thr His Thr Gly Gly Gly Gly Asn
                325                 330                 335

Cys Ala Arg Gly Gly Asn Cys Ala Asn Ala Thr Gly Gly Thr Asn Cys
            340                 345                 350

Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
        355                 360
```

<210> 671
<211> 384
<212> PRT
<213> Homo Sapiens

<400> 671

```
Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Tyr Thr Asn Gly
1               5                   10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Tyr Thr
            20                  25                  30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
        35                  40                  45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
    50                  55                  60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65                  70                  75                  80

Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
                85                  90                  95

Gly Cys Asn Ala Thr Gly Ala Ala Tyr Thr Gly Gly Gly Thr Asn Met
            100                 105                 110
```

```
Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
        115                 120                 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
    130                 135                 140

Trp Ser Asn Gly Cys Asn Ala Thr His Trp Ser Asn Gly Gly Asn Trp
145                 150                 155                 160

Ser Asn Gly Gly Asn Gly Gly Asn Trp Ser Asn Cys Ala Asn Thr Ala
                165                 170                 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
            180                 185                 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
        195                 200                 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
    210                 215                 220

Asn Ala Ala Arg Ala Ala Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr
225                 230                 235                 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
                245                 250                 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Ala Ala Arg Gly Ala Arg Gly Gly Asn Ala Thr His Gly
    290                 295                 300

Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Ala Asn Gly Cys
305                 310                 315                 320

Asn Gly Ala Arg Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr
                325                 330                 335

Thr Ala Tyr Gly Cys Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr
            340                 345                 350
```

Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Cys Ala
355 360 365

Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
370 375 380

<210> 672
<211> 375
<212> PRT
<213> Homo Sapiens

<400> 672

Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Tyr Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Cys Asn Ala Thr Gly Trp Ser Asn Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Trp Ser Asn Gly Cys Asn Ala Thr His Trp Ser Asn Gly Gly Asn Trp
145 150 155 160

Ser Asn Gly Gly Asn Gly Gly Asn Trp Ser Asn Cys Ala Asn Thr Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

```
Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
        195                 200                 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
    210                 215                 220

Asn Ala Ala Arg Ala Ala Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr
225                 230                 235                 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
                245                 250                 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Ala Ala Arg Gly Ala Arg Gly Gly Asn Ala Thr His Gly
    290                 295                 300

Cys Asn Gly Cys Asn Met Gly Asn Gly Ala Tyr Trp Ser Asn Thr Ala
305                 310                 315                 320

Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Cys Asn Ala Thr Gly
                325                 330                 335

Gly Ala Tyr Gly Thr Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly
            340                 345                 350

Gly Asn Cys Ala Asn Cys Ala Asn Gly Thr Asn Cys Ala Asn Gly Thr
        355                 360                 365

Asn Trp Ser Asn Trp Ser Asn
    370                 375
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<210> 673
<211> 375
<212> PRT
<213> Homo Sapiens

<400> 673

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Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Tyr Thr Asn Gly
1               5                   10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Tyr Thr
            20                  25                  30
```

```
Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
        35                  40                  45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
    50                  55                  60

Gly Tyr Cys Ala Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65                  70                  75                  80

Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
                85                  90                  95

Gly Cys Asn Ala Thr Gly Trp Ser Asn Thr Gly Gly Gly Thr Asn Met
            100                 105                 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
        115                 120                 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
    130                 135                 140

Trp Ser Asn Gly Cys Asn Ala Thr His Trp Ser Asn Gly Gly Asn Trp
145                 150                 155                 160

Ser Asn Gly Gly Asn Gly Gly Asn Trp Ser Asn Cys Ala Asn Thr Ala
                165                 170                 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
            180                 185                 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
        195                 200                 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
    210                 215                 220

Asn Ala Ala Arg Ala Ala Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr
225                 230                 235                 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
                245                 250                 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala
            260                 265                 270
```

```
Asn Gly Cys Asn Gly Ala Arg Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Ala Ala Arg Gly Ala Arg Gly Gly Asn Ala Thr His Gly
    290                 295                 300

Cys Asn Gly Gly Asn Met Gly Asn Gly Ala Tyr Trp Ser Asn Thr Ala
305                 310                 315                 320

Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly
                325                 330                 335

Gly Ala Tyr Gly Thr Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly
            340                 345                 350

Gly Asn Cys Ala Asn Cys Ala Asn Gly Thr Asn Cys Ala Asn Gly Thr
        355                 360                 365

Asn Trp Ser Asn Trp Ser Asn
    370                 375
```

<210> 674
<211> 369
<212> PRT
<213> Homo Sapiens

<400> 674

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Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1               5                   10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
            20                  25                  30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
        35                  40                  45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
    50                  55                  60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65                  70                  75                  80

Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
                85                  90                  95

Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
            100                 105                 110
```

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Gly Cys Asn Thr Thr Tyr Ala Thr His Trp Ser Asn Gly Ala Tyr Gly
145 150 155 160

Ala Tyr Gly Gly Asn Trp Ser Asn Cys Ala Asn Ala Ala Arg Thr Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
195 200 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
210 215 220

Asn Ala Thr Gly Ala Ala Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr
225 230 235 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
245 250 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Trp Ser Asn Thr Ala Tyr Thr Ala Tyr Gly
290 295 300

Ala Tyr Trp Ser Asn Trp Ser Asn Gly Gly Asn Thr Ala Tyr Thr Ala
305 310 315 320

Tyr Thr Ala Tyr Gly Gly Asn Thr Thr Tyr Gly Ala Tyr Thr Ala Tyr
325 330 335

Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Tyr
340 345 350

Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser

355 360 365

Asn

<210> 675
<211> 342
<212> PRT
<213> Homo Sapiens

<400> 675

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly
145 150 155 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Thr Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
195 200 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
210 215 220

Asn Ala Ala Arg Ala Ala Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr
225 230 235 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
245 250 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Ala Ala Tyr Gly Thr Asn Ala Thr His Gly
290 295 300

Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly
305 310 315 320

Asn Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn
325 330 335

Trp Ser Asn Trp Ser Asn
340

<210> 676
<211> 360
<212> PRT
<213> Homo Sapiens

<400> 676

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Ala Tyr Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly
145 150 155 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Thr His Ala Ala Arg Thr Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
195 200 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
210 215 220

Asn Ala Ala Arg Ala Ala Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr
225 230 235 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
245 250 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Gly Gly Asn Gly Gly Asn Gly Cys Asn Cys
290 295 300

Ala Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Thr Ala Tyr Thr Thr

305 310 315 320

Tyr Cys Ala Arg Cys Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg
325 330 335

Gly Gly Asn Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly
340 345 350

Thr Asn Trp Ser Asn Trp Ser Asn
355 360

<210> 677
<211> 354
<212> PRT
<213> Homo Sapiens

<400> 677

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly
145 150 155 160

```
Ala Tyr Gly Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Thr Ala
                165                 170                 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
            180                 185                 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
        195                 200                 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
    210                 215                 220

Asn Ala Ala Arg Ala Ala Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr
225                 230                 235                 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
                245                 250                 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Thr Asn Tyr Thr Asn Tyr Thr Asn Thr Gly Gly Thr Thr Tyr Gly
    290                 295                 300

Gly Asn Gly Ala Arg Cys Ala Asn Thr Thr Tyr Gly Ala Tyr Thr Ala
305                 310                 315                 320

Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Trp Ser Asn
                325                 330                 335

Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Cys
            340                 345                 350

Cys Asn
```

<210> 678
<211> 345
<212> PRT
<213> Homo Sapiens

<400> 678

```
Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1               5                   10                  15
```

```
Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
            20                  25                  30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
        35                  40                  45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
    50                  55                  60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65                  70                  75                  80

Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
                85                  90                  95

Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
            100                 105                 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
        115                 120                 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
    130                 135                 140

Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Trp Ser Asn Gly
145                 150                 155                 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Thr Ala
                165                 170                 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
            180                 185                 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
        195                 200                 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
    210                 215                 220

Asn Ala Ala Arg Ala Ala Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr
225                 230                 235                 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
                245                 250                 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala
```

260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Ala Ala Tyr Tyr Thr Asn Cys Cys Asn Thr
290 295 300

Thr Tyr Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala
305 310 315 320

Arg Gly Gly Asn Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys Ala Asn
325 330 335

Gly Thr Asn Trp Ser Asn Trp Ser Asn
340 345

<210> 679
<211> 369
<212> PRT
<213> Homo Sapiens

<400> 679

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

```
Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
    130                 135                 140

Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Gly Ala Tyr Gly
145                 150                 155                 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Ala Tyr Cys Ala Arg Thr Ala
                165                 170                 175

Tyr Thr Ala Tyr Cys Ala Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
            180                 185                 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Gly
        195                 200                 205

Thr Asn Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
    210                 215                 220

Asn Ala Ala Arg Ala Ala Tyr Cys Ala Asn Tyr Thr Asn Thr Thr Tyr
225                 230                 235                 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
                245                 250                 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Met Gly Asn Trp Ser Asn Cys Ala Tyr Thr Ala Tyr Gly
    290                 295                 300

Gly Asn Gly Gly Asn Gly Ala Tyr Thr Ala Tyr Gly Ala Tyr Thr Ala
305                 310                 315                 320

Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn
                325                 330                 335

Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Cys
            340                 345                 350

Ala Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser
        355                 360                 365

Asn
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<210> 680
<211> 360
<212> PRT
<213> Homo Sapiens

<400> 680

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly
145 150 155 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Met Gly
165 170 175

Asn Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
195 200 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser

210 215 220

Asn Ala Ala Arg Ala Ala Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr
225 230 235 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
245 250 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Gly Ala Tyr Gly Gly Asn Thr Gly Gly Cys
290 295 300

Ala Arg Cys Ala Arg Cys Ala Arg Gly Cys Asn Cys Cys Asn Thr Thr
305 310 315 320

Tyr Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg
325 330 335

Gly Gly Asn Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly
340 345 350

Thr Asn Trp Ser Asn Trp Ser Asn
355 360

<210> 681
<211> 354
<212> PRT
<213> Homo Sapiens

<400> 681

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

```
Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65                  70                  75                  80

Tyr Cys Ala Asn Thr Thr Tyr Met Gly Asn Trp Ser Asn Cys Ala Tyr
                85                  90                  95

Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
            100                 105                 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
        115                 120                 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
    130                 135                 140

Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly
145                 150                 155                 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Ala Ala
                165                 170                 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
            180                 185                 190

Met Gly Asn Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
        195                 200                 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
    210                 215                 220

Asn Ala Ala Arg Ala Ala Tyr Cys Ala Asn Tyr Thr Asn Gly Ala Tyr
225                 230                 235                 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
                245                 250                 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Met Gly Asn Thr Gly Gly Gly Gly Asn Ala Thr His Trp
    290                 295                 300

Ser Asn Gly Cys Asn Cys Cys Asn Thr Thr Tyr Gly Ala Tyr Thr Gly
305                 310                 315                 320
```

Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn
325 330 335

Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp
340 345 350

Ser Asn

<210> 682
<211> 345
<212> PRT
<213> Homo Sapiens

<400> 682

Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Gly Cys Asn Thr Ala Tyr
85 90 95

Trp Ser Asn Ala Thr Gly Ala Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Trp Ser Asn Thr Ala Tyr Ala Thr His Trp Ser Asn Trp Ser Asn Trp
145 150 155 160

Ser Asn Gly Gly Asn Met Gly Asn Cys Ala Asn Ala Thr His Thr Ala

```
                165                 170                 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
            180                 185                 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
        195                 200                 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Gly Cys
    210                 215                 220

Asn Ala Ala Arg Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Thr Thr Tyr
225                 230                 235                 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
                245                 250                 255

Thr Asn Met Gly Asn Gly Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Ala
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Tyr Thr Asn Thr Gly Gly Gly Cys Asn Cys Cys Asn Thr
    290                 295                 300

Thr Tyr Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala
305                 310                 315                 320

Arg Gly Gly Asn Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys Ala Asn
                325                 330                 335

Gly Thr Asn Trp Ser Asn Trp Ser Asn
            340                 345
```

<210> 683
<211> 375
<212> PRT
<213> Homo Sapiens

<400> 683

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Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1               5                   10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Tyr Thr
            20                  25                  30
```

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Trp Ser Asn Ala Thr Gly Ala Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Trp Ser Asn Cys Ala Tyr Ala Thr His Trp Ser Asn Trp Ser Asn Trp
145 150 155 160

Ser Asn Trp Ser Asn Met Gly Asn Cys Ala Asn Ala Thr His Thr Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
195 200 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Gly Cys
210 215 220

Asn Ala Ala Arg Ala Ala Tyr Trp Ser Asn Gly Thr Asn Thr Ala Tyr
225 230 235 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
245 250 255

Thr Asn Met Gly Asn Gly Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Ala
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Gly Ala Tyr Gly Gly Asn Thr Ala Tyr Ala
290 295 300

Ala Tyr Thr Gly Gly Ala Ala Tyr Gly Gly Asn Gly Gly Asn Gly Gly
305 310 315 320

Asn Ala Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly
325 330 335

Gly Ala Tyr Gly Thr Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly
340 345 350

Gly Asn Cys Ala Asn Cys Ala Asn Gly Thr Asn Cys Ala Asn Gly Thr
355 360 365

Asn Trp Ser Asn Trp Ser Asn
370 375

<210> 684
<211> 375
<212> PRT
<213> Homo Sapiens

<400> 684

Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Trp Ser Asn Ala Thr Gly Ala Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala

115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Trp Ser Asn Cys Ala Tyr Ala Thr His Trp Ser Asn Met Gly Asn Trp
145 150 155 160

Ser Asn Trp Ser Asn Met Gly Asn Cys Ala Asn Ala Thr His Thr Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
195 200 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Gly Cys
210 215 220

Asn Ala Ala Arg Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Thr Ala Tyr
225 230 235 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
245 250 255

Thr Asn Met Gly Asn Gly Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Ala
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Gly Ala Tyr Gly Gly Asn Thr Ala Tyr Ala
290 295 300

Ala Tyr Thr Gly Gly Ala Ala Tyr Ala Ala Tyr Gly Gly Asn Gly Gly
305 310 315 320

Asn Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly
325 330 335

Gly Ala Tyr Gly Thr Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly
340 345 350

Gly Asn Cys Ala Asn Cys Ala Asn Gly Thr Asn Cys Ala Asn Gly Thr
355 360 365

Asn Trp Ser Asn Trp Ser Asn
370 375

<210> 685
<211> 354
<212> PRT
<213> Homo Sapiens

<400> 685

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Gly Asn
85 90 95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Cys
145 150 155 160

Ala Tyr Trp Ser Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Cys Ala
165 170 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
180 185 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Cys
195 200 205

Ala Asn Ala Thr His Trp Ser Asn Gly Thr Asn Gly Ala Tyr Cys Ala
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225 230 235 240

Trp Ser Asn Tyr Thr Asn Ala Ala Tyr Tyr Thr Asn Trp Ser Asn Trp
245 250 255

Ser Asn Gly Thr Asn Cys Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala
260 265 270

Tyr Cys Ala Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Gly Gly Asn Cys Cys Asn Thr
290 295 300

Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr
305 310 315 320

Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn
325 330 335

Cys Ala Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp
340 345 350

Ser Asn

<210> 686
<211> 381
<212> PRT
<213> Homo Sapiens

<400> 686

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr

50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Met Gly Asn Gly Gly Asn
85 90 95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Thr
145 150 155 160

Ala Tyr Cys Ala Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Cys Ala
165 170 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
180 185 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Ala
195 200 205

Ala Tyr Ala Thr Gly Trp Ser Asn Gly Thr Asn Gly Ala Tyr Cys Ala
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225 230 235 240

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Tyr Thr Asn Trp Ser Asn Trp
245 250 255

Ser Asn Gly Thr Asn Cys Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala
260 265 270

Tyr Cys Ala Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Gly Cys Asn Tyr Thr Asn Met
290 295 300

Gly Asn Gly Gly Asn Ala Thr His Gly Thr Asn Tyr Thr Asn Ala Thr
305 310 315 320

Gly Gly Thr Asn Thr Ala Tyr Gly Thr Asn Tyr Thr Asn Gly Gly Asn
325 330 335

Gly Cys Asn Tyr Thr Asn Gly Ala Tyr Ala Thr His Thr Gly Gly Gly
340 345 350

Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Ala Ala Arg Gly Thr
355 360 365

Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
370 375 380

<210> 687
<211> 381
<212> PRT
<213> Homo Sapiens

<400> 687

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
85 90 95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg
130 135 140

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Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Cys Ala
                165                 170                 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
            180                 185                 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Cys
        195                 200                 205

Ala Asn Ala Thr His Trp Ser Asn Gly Thr Asn Gly Ala Tyr Cys Ala
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225                 230                 235                 240

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Tyr Thr Asn Trp Ser Asn Trp
                245                 250                 255

Ser Asn Gly Thr Asn Cys Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala
            260                 265                 270

Tyr Cys Ala Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Gly Ala Tyr Gly Ala Arg Cys
    290                 295                 300

Ala Asn Gly Thr Asn Gly Thr Asn Met Gly Asn Gly Gly Asn Tyr Thr
305                 310                 315                 320

Asn Ala Thr His Met Gly Asn Thr Ala Tyr Thr Gly Tyr Thr Ala Tyr
                325                 330                 335

Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr Gly Gly Gly
            340                 345                 350

Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Cys Ala Asn Gly Thr
        355                 360                 365

Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
    370                 375                 380
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<210> 688
<211> 366
<212> PRT
<213> Homo Sapiens

<400> 688

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Ala Ala Tyr Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
85 90 95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Cys
145 150 155 160

Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Cys Ala
165 170 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
180 185 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Ala Thr His Cys
195 200 205

Ala Asn Ala Thr His Trp Ser Asn Gly Cys Asn Gly Ala Tyr Cys Ala
210 215 220

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Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225                 230                 235                 240

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Tyr Thr Asn Ala Ala Tyr Trp
                245                 250                 255

Ser Asn Gly Thr Asn Cys Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala
            260                 265                 270

Tyr Cys Ala Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Gly Ala Tyr Met Gly Asn Gly
    290                 295                 300

Gly Asn Gly Gly Asn Gly Gly Asn Gly Ala Tyr Thr Ala Tyr Gly Gly
305                 310                 315                 320

Asn Met Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr Gly Gly
                325                 330                 335

Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Cys Ala Asn Gly
            340                 345                 350

Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
        355                 360                 365


<210>  689
<211>  366
<212>  PRT
<213>  Homo Sapiens

<400>  689

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1               5                   10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
            20                  25                  30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
        35                  40                  45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Ala Ala Tyr Thr
    50                  55                  60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65                  70                  75                  80
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Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
                85                  90                  95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
            100                 105                 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Cys
145                 150                 155                 160

Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Cys Ala
                165                 170                 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
            180                 185                 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Ala Thr His Cys
        195                 200                 205

Ala Asn Ala Thr His Trp Ser Asn Gly Cys Asn Gly Ala Tyr Cys Ala
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225                 230                 235                 240

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Tyr Thr Asn Ala Ala Tyr Trp
                245                 250                 255

Ser Asn Gly Thr Asn Cys Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala
            260                 265                 270

Tyr Cys Ala Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Gly Ala Tyr Met Gly Asn Gly
    290                 295                 300

Gly Asn Gly Gly Asn Gly Gly Asn Gly Ala Tyr Thr Ala Tyr Gly Gly
305                 310                 315                 320
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Asn Met Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr Gly Gly
325 330 335

Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Cys Ala Asn Gly
340 345 350

Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
355 360 365

<210> 690
<211> 357
<212> PRT
<213> Homo Sapiens

<400> 690

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
85 90 95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Cys
145 150 155 160

Ala Tyr Trp Ser Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Cys Ala
165 170 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
180 185 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Ala Thr His Cys
195 200 205

Ala Asn Ala Ala Arg Trp Ser Asn Gly Thr Asn Gly Ala Tyr Cys Ala
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225 230 235 240

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Tyr Thr Asn Trp Ser Asn Trp
245 250 255

Ser Asn Gly Thr Asn Cys Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala
260 265 270

Tyr Cys Ala Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Trp Ser Asn Ala Ala Tyr Ala
290 295 300

Ala Tyr Thr Ala Tyr Gly Gly Asn Thr Gly Tyr Thr Thr Tyr Gly Cys
305 310 315 320

Asn Tyr Thr Asn Thr Gly Gly Gly Gly Asn Met Gly Asn Gly Gly Asn
325 330 335

Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp
340 345 350

Ser Asn Trp Ser Asn
355

<210> 691
<211> 357
<212> PRT
<213> Homo Sapiens

<400> 691

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
85 90 95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Cys
145 150 155 160

Ala Tyr Trp Ser Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Cys Ala
165 170 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
180 185 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Ala Thr His Cys
195 200 205

Ala Asn Ala Ala Arg Trp Ser Asn Gly Thr Asn Gly Ala Tyr Cys Ala
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225 230 235 240

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Tyr Thr Asn Trp Ser Asn Trp
245 250 255

Ser Asn Gly Thr Asn Cys Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala
260 265 270

Tyr Cys Ala Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Trp Ser Asn Ala Ala Tyr Ala
290 295 300

Ala Tyr Thr Ala Tyr Gly Gly Asn Thr Gly Tyr Thr Thr Tyr Gly Cys
305 310 315 320

Asn Tyr Thr Asn Thr Gly Gly Gly Gly Asn Met Gly Asn Gly Gly Asn
325 330 335

Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp
340 345 350

Ser Asn Trp Ser Asn
355

<210> 692
<211> 399
<212> PRT
<213> Homo Sapiens

<400> 692

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
85 90 95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Cys
145 150 155 160

Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Cys Ala
165 170 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
180 185 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Cys
195 200 205

Ala Asn Ala Thr His Trp Ser Asn Gly Thr Asn Gly Ala Tyr Cys Ala
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225 230 235 240

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Tyr Thr Asn Trp Ser Asn Trp
245 250 255

Ser Asn Gly Thr Asn Cys Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala
260 265 270

Tyr Cys Ala Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Ala Tyr Ala
290 295 300

Ala Tyr Thr Ala Tyr Gly Gly Asn Tyr Thr Asn Thr Ala Tyr Thr Ala
305 310 315 320

Tyr Thr Ala Tyr Gly Ala Tyr Trp Ser Asn Trp Ser Asn Gly Gly Asn
325 330 335

Thr Ala Tyr Cys Cys Asn Trp Ser Asn Thr Ala Tyr Thr Ala Tyr Thr
340 345 350

Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr Gly
355 360 365

Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Cys Ala Asn

370 375 380

Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
385 390 395

<210> 693
<211> 375
<212> PRT
<213> Homo Sapiens

<400> 693

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
85 90 95

Gly Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Ala Ala Tyr Thr
100 105 110

Gly Gly Gly Thr Asn Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Thr
145 150 155 160

Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Gly Gly Asn Cys Ala
165 170 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
180 185 190

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Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Cys
        195                 200                 205

Ala Asn Ala Thr His Trp Ser Asn Gly Thr Asn Gly Ala Tyr Cys Ala
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225                 230                 235                 240

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Tyr Thr Asn Thr Thr Tyr Trp
                245                 250                 255

Ser Asn Gly Thr Asn Cys Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala
            260                 265                 270

Tyr Cys Ala Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Thr Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Cys Ala Asn Thr Ala Tyr Thr
    290                 295                 300

Ala Tyr Gly Ala Tyr Ala Thr His Tyr Thr Asn Cys Ala Asn Gly Gly
305                 310                 315                 320

Asn Thr Ala Tyr Cys Cys Asn Thr Thr Tyr Thr Ala Tyr Thr Thr Tyr
                325                 330                 335

Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly
            340                 345                 350

Gly Asn Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr
        355                 360                 365

Asn Trp Ser Asn Trp Ser Asn
    370                 375
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<210> 694
<211> 375
<212> PRT
<213> Homo Sapiens

<400> 694

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Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1               5                   10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
            20                  25                  30
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Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
85 90 95

Gly Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Ala Ala Tyr Thr
100 105 110

Gly Gly Gly Thr Asn Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Thr
145 150 155 160

Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Gly Gly Asn Cys Ala
165 170 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
180 185 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Cys
195 200 205

Ala Asn Ala Thr His Trp Ser Asn Gly Thr Asn Gly Ala Tyr Cys Ala
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225 230 235 240

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Tyr Thr Asn Thr Thr Tyr Trp
245 250 255

Ser Asn Gly Thr Asn Cys Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala
260 265 270

Tyr Cys Ala Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Thr Tyr

275 280 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Cys Ala Asn Thr Ala Tyr Thr
290 295 300

Ala Tyr Gly Ala Tyr Ala Thr His Tyr Thr Asn Cys Ala Asn Gly Gly
305 310 315 320

Asn Thr Ala Tyr Cys Cys Asn Thr Thr Tyr Thr Ala Tyr Thr Thr Tyr
325 330 335

Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly
340 345 350

Gly Asn Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr
355 360 365

Asn Trp Ser Asn Trp Ser Asn
370 375

<210> 695
<211> 360
<212> PRT
<213> Homo Sapiens

<400> 695

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Cys
1 5 10 15

Ala Arg Thr Gly Gly Gly Gly Asn Gly Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Tyr Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Gly Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Thr Asn Thr Ala Tyr Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Ala Tyr
85 90 95

Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr Gly Gly Ala Thr His Met
100 105 110

Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr His
130 135 140

Gly Gly Asn Gly Ala Arg Ala Thr His Ala Ala Tyr Cys Ala Tyr Trp
145 150 155 160

Ser Asn Gly Gly Asn Trp Ser Asn Cys Ala Asn Ala Ala Tyr Thr Ala
165 170 175

Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg
180 185 190

Trp Ser Asn Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Trp
195 200 205

Ser Asn Gly Thr Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala
210 215 220

Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn
225 230 235 240

Ala Ala Arg Tyr Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Cys
245 250 255

Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala Tyr Cys Ala Asn Gly Cys
260 265 270

Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn
275 280 285

Met Gly Asn Gly Gly Asn Gly Gly Asn Thr Ala Tyr Trp Ser Asn Trp
290 295 300

Ser Asn Trp Ser Asn Thr Gly Gly Thr Ala Tyr Thr Gly Gly Thr Thr
305 310 315 320

Tyr Gly Ala Tyr Cys Cys Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg
325 330 335

Gly Gly Asn Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly
340 345 350

Thr Asn Trp Ser Asn Trp Ser Asn
355 360

<210> 696
<211> 360
<212> PRT
<213> Homo Sapiens

<400> 696

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Cys
1 5 10 15

Ala Arg Thr Gly Gly Gly Gly Asn Gly Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Tyr Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Gly Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Thr Asn Thr Ala Tyr Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Ala Tyr
85 90 95

Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr Gly Gly Ala Thr His Met
100 105 110

Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr His
130 135 140

Gly Gly Asn Gly Ala Arg Ala Thr His Ala Ala Tyr Cys Ala Tyr Trp
145 150 155 160

Ser Asn Gly Gly Asn Trp Ser Asn Cys Ala Asn Ala Ala Tyr Thr Ala
165 170 175

Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg
180 185 190

Trp Ser Asn Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Trp
195 200 205

Ser Asn Gly Thr Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala

210 215 220

Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn
225 230 235 240

Ala Ala Arg Tyr Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Cys
245 250 255

Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala Tyr Cys Ala Asn Gly Cys
260 265 270

Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn
275 280 285

Met Gly Asn Gly Gly Asn Gly Gly Asn Thr Ala Tyr Trp Ser Asn Trp
290 295 300

Ser Asn Trp Ser Asn Thr Gly Gly Thr Thr Tyr Thr Gly Gly Thr Thr
305 310 315 320

Tyr Gly Ala Tyr Cys Cys Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg
325 330 335

Gly Gly Asn Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly
340 345 350

Thr Asn Trp Ser Asn Trp Ser Asn
355 360

<210> 697
<211> 369
<212> PRT
<213> Homo Sapiens

<400> 697

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Gly Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

```
Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65                  70                  75                  80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr
                85                  90                  95

Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr Gly Gly Ala Thr His Met
            100                 105                 110

Gly Asn Cys Ala Arg Cys Cys Asn Gly Cys Asn Gly Gly Asn Ala Ala
        115                 120                 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr His
    130                 135                 140

Gly Gly Asn Met Gly Asn Ala Thr His Thr Ala Tyr Cys Ala Asn Trp
145                 150                 155                 160

Ser Asn Gly Gly Asn Cys Ala Asn Cys Ala Asn Ala Ala Tyr Thr Ala
                165                 170                 175

Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg
            180                 185                 190

Trp Ser Asn Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr Gly Trp
        195                 200                 205

Ser Asn Gly Thr Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala
    210                 215                 220

Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn
225                 230                 235                 240

Ala Ala Arg Tyr Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Cys
                245                 250                 255

Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala Tyr Cys Ala Asn Gly Cys
            260                 265                 270

Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn
        275                 280                 285

Met Gly Asn Gly Ala Tyr Gly Gly Asn Thr Ala Tyr Trp Ser Asn Thr
    290                 295                 300

Ala Tyr Gly Gly Asn Cys Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala
305                 310                 315                 320
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Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn
325 330 335

Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Cys
340 345 350

Ala Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser
355 360 365

Asn

<210> 698
<211> 378
<212> PRT
<213> Homo Sapiens

<400> 698

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Gly Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Gly Asn
85 90 95

Gly Gly Asn Trp Ser Asn Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Thr

145 150 155 160

Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Cys Ala
165 170 175

Asn Ala Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
180 185 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Cys
195 200 205

Ala Asn Ala Thr His Trp Ser Asn Ala Thr His Gly Thr Asn Cys Ala
210 215 220

Asn Trp Ser Asn Met Gly Asn Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225 230 235 240

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Tyr Thr Asn Trp Ser Asn Trp
245 250 255

Ser Asn Gly Thr Asn Cys Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala
260 265 270

Tyr Cys Ala Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Trp Ser Asn Gly Cys Asn Tyr
290 295 300

Thr Asn Met Gly Asn Thr Ala Tyr Thr Thr Tyr Gly Ala Tyr Thr Gly
305 310 315 320

Gly Tyr Thr Asn Thr Thr Tyr Trp Ser Asn Gly Ala Tyr Gly Thr Asn
325 330 335

Trp Ser Asn Gly Ala Tyr Ala Thr His Thr Gly Gly Gly Gly Asn Cys
340 345 350

Ala Arg Gly Gly Asn Cys Ala Asn Ala Thr Gly Gly Thr Asn Cys Ala
355 360 365

Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
370 375

<210> 699
<211> 360
<212> PRT

<213> Homo Sapiens

<400> 699

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Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Cys
1               5                  10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Tyr Thr
            20                  25                  30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Ala Arg
        35                  40                  45

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Ala Thr His Trp Ser Asn Thr
    50                  55                  60

Gly Tyr Ala Ala Arg Gly Gly Asn Trp Ser Asn Gly Gly Asn Thr Ala
65                  70                  75                  80

Tyr Met Gly Asn Thr Thr Tyr Cys Ala Asn Trp Ser Asn Thr Ala Tyr
                85                  90                  95

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Gly Gly Gly Thr Asn Met
            100                 105                 110

Gly Asn Cys Ala Arg Ala Thr Gly Cys Cys Asn Gly Gly Asn Ala Ala
        115                 120                 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
    130                 135                 140

Gly Gly Asn Ala Thr His Ala Thr His Thr Ala Tyr Cys Cys Asn Gly
145                 150                 155                 160

Ala Tyr Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Cys Ala Asn Met Gly
                165                 170                 175

Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn Thr Thr Tyr
            180                 185                 190

Cys Ala Arg Gly Gly Asn Cys Ala Arg Gly Thr Asn Cys Ala Asn Ala
        195                 200                 205

Thr His Trp Ser Asn Gly Cys Asn Gly Ala Tyr Ala Ala Arg Trp Ser
    210                 215                 220

Asn Ala Thr His Trp Ser Asn Cys Ala Asn Gly Cys Asn Thr Ala Tyr
225                 230                 235                 240
```

```
Tyr Thr Asn Cys Ala Arg Thr Gly Gly Trp Ser Asn Trp Ser Asn Tyr
                245                 250                 255

Thr Asn Ala Ala Arg Gly Cys Asn Trp Ser Asn Gly Ala Tyr Cys Ala
            260                 265                 270

Asn Gly Cys Asn Ala Thr Gly Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Met Gly Asn Cys Ala Arg Ala Ala Arg Trp Ser Asn Thr
    290                 295                 300

Ala Tyr Gly Gly Asn Thr Ala Tyr Trp Ser Asn Thr Ala Tyr Thr Thr
305                 310                 315                 320

Tyr Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg
                325                 330                 335

Gly Gly Asn Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly
            340                 345                 350

Thr Asn Trp Ser Asn Trp Ser Asn
        355                 360
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<210> 700
<211> 363
<212> PRT
<213> Homo Sapiens

<400> 700

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Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Cys
1               5                   10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
            20                  25                  30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Ala Arg
        35                  40                  45

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Ala Thr His Trp Ser Asn Thr
    50                  55                  60

Gly Tyr Ala Ala Arg Gly Gly Asn Trp Ser Asn Gly Gly Asn Thr Ala
65                  70                  75                  80

Tyr Trp Ser Asn Thr Thr Tyr Cys Ala Asn Trp Ser Asn Thr Ala Tyr
```

```
                85                  90                  95

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Gly Gly Gly Thr Asn Met
            100                 105                 110

Gly Asn Cys Ala Arg Ala Thr Gly Cys Cys Asn Gly Gly Asn Ala Ala
        115                 120                 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
    130                 135                 140

Gly Gly Asn Ala Thr His Ala Thr His Thr Ala Tyr Cys Cys Asn Gly
145                 150                 155                 160

Ala Tyr Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Cys Asn Met Gly
                165                 170                 175

Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn Thr Thr Tyr
            180                 185                 190

Cys Ala Arg Gly Gly Asn Cys Ala Arg Gly Thr Asn Cys Ala Asn Ala
        195                 200                 205

Thr His Trp Ser Asn Gly Cys Asn Gly Ala Tyr Ala Ala Arg Trp Ser
    210                 215                 220

Asn Ala Thr His Ala Ala Tyr Cys Ala Asn Gly Cys Asn Thr Ala Tyr
225                 230                 235                 240

Tyr Thr Asn Cys Ala Arg Thr Gly Gly Trp Ser Asn Trp Ser Asn Tyr
                245                 250                 255

Thr Asn Ala Ala Arg Gly Cys Asn Trp Ser Asn Gly Ala Tyr Cys Ala
            260                 265                 270

Asn Gly Cys Asn Ala Thr Gly Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Met Gly Asn Cys Ala Arg Gly Gly Asn Thr Ala Tyr Gly
    290                 295                 300

Gly Asn Trp Ser Asn Gly Gly Asn Thr Gly Gly Gly Gly Asn Thr Ala
305                 310                 315                 320

Tyr Thr Thr Tyr Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn
                325                 330                 335
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Cys Ala Arg Gly Gly Asn Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys
340 345 350

Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
355 360

<210> 701
<211> 381
<212> PRT
<213> Homo Sapiens

<400> 701

Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
20 25 30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Ala Arg
35 40 45

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Ala Thr His Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Gly Asn Trp Ser Asn Gly Gly Asn Thr Ala
65 70 75 80

Tyr Trp Ser Asn Thr Thr Tyr Cys Ala Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Ala Thr Gly Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
130 135 140

Gly Gly Asn Ala Thr His Ala Thr His Thr Ala Tyr Cys Cys Asn Gly
145 150 155 160

Gly Asn Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Ala Thr His Met Gly
165 170 175

Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn Thr Thr Tyr
180 185 190

Cys Ala Arg Gly Gly Asn Cys Ala Arg Gly Thr Asn Cys Ala Asn Ala
195 200 205

Thr His Trp Ser Asn Gly Cys Asn Gly Ala Tyr Ala Ala Arg Trp Ser
210 215 220

Asn Ala Thr His Trp Ser Asn Cys Ala Asn Gly Cys Asn Thr Ala Tyr
225 230 235 240

Tyr Thr Asn Cys Ala Arg Thr Gly Gly Trp Ser Asn Trp Ser Asn Tyr
245 250 255

Thr Asn Ala Ala Arg Gly Cys Asn Trp Ser Asn Gly Ala Tyr Cys Ala
260 265 270

Asn Gly Cys Asn Ala Thr Gly Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Cys Ala Arg Gly Gly Asn Tyr Thr Asn Gly
290 295 300

Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Ala Asn Trp Ser
305 310 315 320

Asn Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr
325 330 335

Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr Gly Gly Gly
340 345 350

Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Cys Ala Asn Gly Thr
355 360 365

Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
370 375 380

<210> 702
<211> 375
<212> PRT
<213> Homo Sapiens

<400> 702

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr

20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Ala Thr His Trp Ser Asn Gly Gly Asn Gly Ala
65 70 75 80

Tyr Trp Ser Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Trp Ser Asn Gly Cys Asn Gly Cys Asn Thr Gly Gly Ala Ala Tyr Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Trp Ser Asn Cys Cys
115 120 125

Asn Trp Ser Asn Met Gly Asn Gly Gly Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Tyr Thr Asn Gly Gly Asn Met Gly Asn Cys Ala Asn Thr
145 150 155 160

Ala Tyr Thr Gly Tyr Met Gly Asn Trp Ser Asn Ala Ala Arg Thr Gly
165 170 175

Gly Thr Ala Tyr Ala Ala Tyr Gly Ala Tyr Thr Ala Tyr Gly Cys Asn
180 185 190

Gly Thr Asn Trp Ser Asn Gly Thr Asn Ala Ala Arg Trp Ser Asn Met
195 200 205

Gly Asn Ala Thr His Cys Ala Asn Ala Thr His Ala Ala Tyr Cys Cys
210 215 220

Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr
225 230 235 240

Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Cys Ala Arg Tyr
245 250 255

Thr Asn Ala Ala Tyr Trp Ser Asn Gly Thr Asn Cys Ala Asn Cys Cys
260 265 270

Asn Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr Asn
275 280 285

Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn Gly
290 295 300

Ala Tyr Met Gly Asn Gly Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly
305 310 315 320

Asn Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly
325 330 335

Gly Ala Tyr Gly Thr Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly
340 345 350

Gly Asn Cys Ala Asn Cys Ala Asn Gly Thr Asn Cys Ala Asn Gly Thr
355 360 365

Asn Trp Ser Asn Trp Ser Asn
370 375

<210> 703
<211> 324
<212> DNA
<213> Homo Sapiens

<400> 703
cgaactgtgg ctgcaccatc tgtcttcatc ttcccgccat ctgatgagca gttgaaatct
60

ggaactgcta gcgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag
120

tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac
180

agcaaggaca gcacctacag cctcagcagc accctgacgc tgagcaaagc agactacgag
240

aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag
300

agcttcaaca ggggagagtg ttag
324

<210> 704
<211> 981
<212> DNA
<213> Homo Sapiens

<400> 704
gcctccacca agggcccatc ggtcttcccc ctggcgccct gctctagaag cacctccgag
60

agcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg
120

tggaactcag gcgctctgac cagcggcgtg cacaccttcc cagctgtcct acagtcctca
180

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcaacttcgg cacccagacc
240

tacacatgca acgtagatca caagcccagc aacaccaagg tggacaagac agttgagcgc
300

aaatgttgtg tcgagtgccc accgtgccca gcaccacctg tggcaggacc gtcagtcttc
360

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacgtgc
420

gtggtggtgg acgtgagcca cgaagacccc gaggtccagt tcaactggta cgtggacggc
480

gtggaggtgc ataatgccaa gacaaagcca cgggaggagc agttcaacag cacgttccgt
540

gtggtcagcg tcctcaccgt tgtgcaccag gactggctga acggcaagga gtacaagtgc
600

aaggtctcca acaaaggcct cccagccccc atcgagaaaa ccatctccaa aaccaaaggg
660

cagccccgag aaccacaggt gtacaccctg cccccatccc gggaggagat gaccaagaac
720

caggtcagcc tgacctgcct ggtcaaaggc ttctacccca gcgacatcgc cgtggagtgg
780

gagagcaatg ggcagccgga gaacaactac aagaccacac ctcccatgct ggactccgac
840

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac
900

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc
960

tccctgtctc cgggtaaatg a
981

<210> 705
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 705

Met Gly Asn Trp Ser Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Tyr
1 5 10 15

Thr Asn Gly Thr Asn Thr Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Gly

20 25 30

Asn Ala Ala Tyr Cys Ala Asn Thr Ala Tyr Tyr Thr Asn Ala Ala Tyr
35 40 45

<210> 706
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 706

Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Tyr
1 5 10 15

Thr Asn Tyr Thr Asn Cys Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Gly
20 25 30

Asn Ala Ala Arg Cys Ala Asn Thr Ala Tyr Tyr Thr Asn Thr Ala Tyr
35 40 45

<210> 707
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 707

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Gly Gly Asn Ala
1 5 10 15

Thr His Gly Cys Asn Ala Ala Tyr Thr Ala Tyr Tyr Thr Asn Gly Cys
20 25 30

Asn

<210> 708
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 708

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Gly Gly Asn Ala
1 5 10 15

Thr His Trp Ser Asn Ala Ala Tyr Gly Ala Tyr Tyr Thr Asn Gly Cys
20 25 30

Asn

<210> 709
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 709

Met Gly Asn Trp Ser Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Tyr
1 5 10 15

Thr Asn Gly Thr Asn Cys Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Gly
20 25 30

Asn Ala Ala Tyr Cys Ala Asn Thr Ala Tyr Tyr Thr Asn Trp Ser Asn
35 40 45

<210> 710
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 710

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Cys Ala Asn Gly
1 5 10 15

Thr Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr Tyr Thr
20 25 30

Asn Gly Cys Asn
35

<210> 711
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 711

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Gly
1 5 10 15

Thr Asn Trp Ser Asn Met Gly Asn Tyr Thr Asn Gly Cys Asn
20 25 30

<210> 712
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 712

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Gly Gly Asn Ala
1 5 10 15

Thr His Met Gly Asn Ala Ala Tyr Gly Ala Tyr Tyr Thr Asn Gly Gly
20 25 30

Asn

<210> 713
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 713

Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Gly
1 5 10 15

Thr Asn Tyr Thr Asn Thr Ala Tyr Trp Ser Asn Trp Ser Asn Ala Ala
20 25 30

Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr Ala Tyr Tyr Thr Asn
35 40 45

Gly Thr Asn
50

<210> 714
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 714

Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Gly
1 5 10 15

Thr Asn Tyr Thr Asn Thr Ala Tyr Trp Ser Asn Trp Ser Asn Ala Ala
20 25 30

Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr Ala Tyr Tyr Thr Asn
35 40 45

Gly Cys Asn
50

<210> 715
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 715

Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala Arg Ala Ala Tyr Gly
1 5 10 15

Thr Asn Tyr Thr Asn Thr Ala Tyr Trp Ser Asn Trp Ser Asn Ala Ala
20 25 30

Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr Ala Tyr Tyr Thr Asn
35 40 45

Gly Cys Asn
50

<210> 716
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 716

Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Gly
1 5 10 15

Thr Asn Tyr Thr Asn Thr Ala Tyr Ala Ala Tyr Trp Ser Asn Ala Ala
20 25 30

Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr Ala Tyr Tyr Thr Asn
35 40 45

Gly Cys Asn
50

<210> 717
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 717

Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Gly
1 5 10 15

Thr Asn Tyr Thr Asn Gly Ala Tyr Trp Ser Asn Trp Ser Asn Ala Ala
20 25 30

Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr Ala Tyr Tyr Thr Asn
35 40 45

Gly Cys Asn

50

<210> 718
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 718

Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Ala
1 5 10 15

Thr His Tyr Thr Asn Thr Ala Tyr Met Gly Asn Trp Ser Asn Ala Ala
20 25 30

Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr Ala Tyr Tyr Thr Asn
35 40 45

Gly Cys Asn
50

<210> 719
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 719

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Gly Ala Tyr Ala
1 5 10 15

Thr His Trp Ser Asn Cys Ala Tyr Thr Ala Tyr Tyr Thr Asn Gly Cys
20 25 30

Asn

<210> 720
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 720

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Gly Ala Tyr Ala
1 5 10 15

Thr His Trp Ser Asn Ala Ala Tyr Thr Ala Tyr Tyr Thr Asn Gly Cys
20 25 30

Asn

<210> 721
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 721

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Gly
1 5 10 15

Thr Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr Tyr Thr Asn Gly Cys
20 25 30

Asn

<210> 722
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 722

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Gly Ala Tyr Ala
1 5 10 15

Thr His Trp Ser Asn Met Gly Asn Thr Gly Gly Tyr Thr Asn Gly Cys
20 25 30

Asn

<210> 723
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 723

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Ala
1 5 10 15

Thr His Trp Ser Asn Cys Ala Asn Thr Ala Tyr Tyr Thr Asn Ala Ala
20 25 30

Tyr

<210> 724
<211> 33
<212> PRT

<213> Homo Sapiens

<400> 724

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Cys Ala Asn Ala
1 5 10 15

Thr His Trp Ser Asn Ala Thr His Thr Ala Tyr Tyr Thr Asn Ala Ala
20 25 30

Tyr

<210> 725
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 725

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Ala
1 5 10 15

Thr His Met Gly Asn Trp Ser Asn Thr Ala Tyr Tyr Thr Asn Ala Ala
20 25 30

Tyr

<210> 726
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 726

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Cys Ala Asn Ala
1 5 10 15

Thr His Trp Ser Asn Met Gly Asn Thr Ala Tyr Tyr Thr Asn Ala Ala
20 25 30

Tyr

<210> 727
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 727

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Met Gly Asn Ala

1 5 10 15

Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr Tyr Thr Asn Ala Ala
20 25 30

Tyr

<210> 728
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 728

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Ala
1 5 10 15

Thr His Trp Ser Asn Met Gly Asn Thr Ala Tyr Tyr Thr Asn Ala Ala
20 25 30

Tyr

<210> 729
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 729

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Ala
1 5 10 15

Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr Tyr Thr Asn Ala Ala
20 25 30

Tyr

<210> 730
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 730

Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala Arg Gly Ala Tyr Ala
1 5 10 15

Thr His Trp Ser Asn Ala Ala Tyr Thr Ala Tyr Tyr Thr Asn Ala Ala
20 25 30

Tyr

<210> 731
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 731

Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala Arg Gly Ala Tyr Ala
1 5 10 15

Thr His Trp Ser Asn Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Ala Ala
20 25 30

Tyr

<210> 732
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 732

Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala Arg Gly Ala Tyr Ala
1 5 10 15

Thr His Trp Ser Asn Gly Ala Tyr Thr Ala Tyr Tyr Thr Asn Ala Ala
20 25 30

Tyr

<210> 733
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 733

Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala Arg Gly Ala Tyr Ala
1 5 10 15

Thr His Cys Ala Asn Ala Ala Tyr Thr Ala Tyr Tyr Thr Asn Ala Ala
20 25 30

Tyr

<210> 734
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 734

Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Thr Gly Gly Gly
1 5 10 15

Ala Tyr Trp Ser Asn
20

<210> 735
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 735

Gly Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn
20

<210> 736
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 736

Gly Thr Asn Gly Cys Asn Trp Ser Asn Cys Ala Asn Tyr Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn
20

<210> 737
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 737

Gly Cys Asn Gly Cys Asn Trp Ser Asn Cys Ala Asn Tyr Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn
20

<210> 738

<211> 21
<212> PRT
<213> Homo Sapiens

<400> 738

Ala Ala Arg Ala Thr His Trp Ser Asn Ala Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn
20

<210> 739
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 739

Gly Gly Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Met Gly Asn Gly
1 5 10 15

Cys Asn Cys Ala Asn
20

<210> 740
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 740

Gly Gly Asn Gly Cys Asn Trp Ser Asn Met Gly Asn Met Gly Asn Gly
1 5 10 15

Cys Asn Cys Ala Asn
20

<210> 741
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 741

Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn
20

<210> 742
<211> 21
<212> PRT

<213> Homo Sapiens

<400> 742

Thr Gly Gly Gly Cys Asn Trp Ser Asn Cys Ala Asn Met Gly Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn
20

<210> 743
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 743

Thr Gly Gly Gly Cys Asn Trp Ser Asn Cys Ala Asn Met Gly Asn Ala
1 5 10 15

Ala Arg Trp Ser Asn
20

<210> 744
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 744

Thr Gly Gly Gly Cys Asn Trp Ser Asn Gly Cys Asn Met Gly Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn
20

<210> 745
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 745

Gly Cys Asn Gly Ala Arg Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn
20

<210> 746
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 746

Cys Ala Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn
20

<210> 747
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 747

Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn
20

<210> 748
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 748

Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Tyr Thr Asn Gly
1 5 10 15

Ala Arg Cys Ala Asn
20

<210> 749
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 749

Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Thr His Tyr Thr Asn Gly
1 5 10 15

Ala Arg Cys Ala Asn
20

<210> 750
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 750

Ala Thr Gly Cys Ala Arg Trp Ser Asn Cys Ala Asn Cys Ala Tyr Thr
1 5 10 15

Gly Gly Cys Cys Asn Ala Thr His Cys Ala Asn
20 25

<210> 751
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 751

Ala Thr His Cys Ala Arg Gly Gly Asn Cys Ala Asn Cys Ala Tyr Thr
1 5 10 15

Gly Gly Cys Cys Asn Cys Ala Asn Cys Ala Asn
20 25

<210> 752
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 752

Ala Thr Gly Cys Ala Arg Gly Gly Asn Cys Ala Asn Cys Ala Tyr Thr
1 5 10 15

Gly Gly Cys Cys Asn Ala Thr His Cys Ala Asn
20 25

<210> 753
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 753

Ala Thr Gly Cys Ala Arg Gly Gly Asn Ala Thr His Cys Ala Arg Tyr
1 5 10 15

Thr Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn
20 25

<210> 754
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 754

Ala Thr Gly Cys Ala Arg Trp Ser Asn Ala Thr His Cys Ala Arg Tyr
1 5 10 15

Thr Asn Cys Cys Asn Tyr Thr Asn Cys Ala Asn
20 25

<210> 755
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 755

Ala Thr Gly Cys Ala Arg Trp Ser Asn Ala Thr His Cys Ala Arg Tyr
1 5 10 15

Thr Asn Cys Cys Asn Ala Thr His Cys Ala Asn
20 25

<210> 756
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 756

Cys Ala Arg Ala Ala Tyr Thr Ala Tyr Ala Ala Tyr Trp Ser Asn Gly
1 5 10 15

Cys Asn Cys Cys Asn Thr Thr Tyr Cys Ala Asn
20 25

<210> 757
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 757

Cys Ala Arg Ala Ala Arg Thr Ala Tyr Ala Ala Tyr Trp Ser Asn Gly
1 5 10 15

Thr Asn Cys Cys Asn Tyr Thr Asn Cys Ala Asn
20 25

<210> 758
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 758

Ala Thr Gly Cys Ala Arg Gly Cys Asn Cys Ala Asn Cys Ala Arg Thr
1 5 10 15

Thr Tyr Cys Cys Asn Cys Ala Tyr Cys Ala Asn
20 25

<210> 759
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 759

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Gly Gly Asn Trp Ser Asn Trp
1 5 10 15

Ser Asn Cys Cys Asn Met Gly Asn Cys Ala Asn
20 25

<210> 760
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 760

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Gly Gly Asn Trp Ser Asn Trp
1 5 10 15

Ser Asn Cys Cys Asn Met Gly Asn Trp Ser Asn
20 25

<210> 761
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 761

Tyr Thr Asn Cys Ala Arg Cys Ala Tyr Ala Ala Tyr Trp Ser Asn Thr
1 5 10 15

Ala Tyr Cys Cys Asn Cys Cys Asn Cys Ala Asn
20 25

<210> 762
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 762

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Thr
1 5 10 15

Thr Tyr Cys Cys Asn Thr Gly Gly Cys Ala Asn
20 25

<210> 763
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 763

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Cys
1 5 10 15

Ala Asn Cys Ala Asn Thr Gly Gly Cys Ala Asn
20 25

<210> 764
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 764

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Cys
1 5 10 15

Ala Asn Cys Cys Asn Met Gly Asn Cys Ala Asn
20 25

<210> 765
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 765

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Ala
1 5 10 15

Thr His Trp Ser Asn Met Gly Asn Cys Ala Asn
20 25

<210> 766
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 766

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Cys
1 5 10 15

Ala Asn Ala Thr Gly Thr Thr Tyr Trp Ser Asn
20 25

<210> 767
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 767

Cys Ala Tyr Cys Ala Arg Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Cys
1 5 10 15

Ala Asn Cys Cys Asn Tyr Thr Asn Cys Ala Asn
20 25

<210> 768
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 768

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Thr Thr Tyr Ala Thr His Cys
1 5 10 15

Ala Asn Cys Cys Asn Tyr Thr Asn Cys Ala Asn
20 25

<210> 769
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 769

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Ala Ala Tyr Ala Ala Tyr Thr
1 5 10 15

Ala Tyr Cys Cys Asn Thr Thr Tyr Cys Ala Asn
20 25

<210> 770
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 770

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Ala Ala Tyr Cys Ala Asn Thr
1 5 10 15

Ala Tyr Cys Cys Asn Thr Thr Tyr Cys Ala Asn
20 25

<210> 771
<211> 30

<212> PRT
<213> Homo Sapiens

<400> 771

Cys Ala Arg Cys Ala Arg Cys Ala Tyr Ala Ala Tyr Ala Ala Tyr Thr
1 5 10 15

Gly Gly Cys Cys Asn Cys Cys Asn Thr Gly Gly Cys Ala Asn
20 25 30

<210> 772
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 772

Cys Ala Arg Cys Ala Arg Gly Cys Asn Ala Ala Tyr Trp Ser Asn Thr
1 5 10 15

Thr Tyr Cys Cys Asn Cys Cys Asn Cys Ala Asn
20 25

<210> 773
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 773

Cys Ala Arg Cys Ala Arg Trp Ser Asn Cys Ala Tyr Trp Ser Asn Gly
1 5 10 15

Cys Asn Cys Cys Asn Thr Thr Tyr Cys Ala Asn
20 25

<210> 774
<211> 24
<212> PRT
<213> Homo Sapiens

<400> 774

Cys Ala Arg Cys Ala Arg Trp Ser Asn Thr Ala Tyr Trp Ser Asn Cys
1 5 10 15

Ala Asn Tyr Thr Asn Cys Ala Asn
20

<210> 775
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 775

Cys Ala Arg Cys Ala Arg Trp Ser Asn Thr Ala Tyr Trp Ser Asn Ala
1 5 10 15

Thr His Cys Cys Asn Tyr Thr Asn Cys Ala Asn
20 25

<210> 776
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 776

Cys Ala Arg Cys Ala Arg Ala Thr His Thr Ala Tyr Trp Ser Asn Cys
1 5 10 15

Ala Asn Trp Ser Asn Ala Thr His Cys Ala Asn
20 25

<210> 777
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 777

Cys Ala Arg Cys Ala Arg Trp Ser Asn Thr Ala Tyr Ala Thr His Cys
1 5 10 15

Ala Asn Cys Cys Asn Ala Thr His Cys Ala Asn
20 25

<210> 778
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 778

Cys Ala Arg Cys Ala Arg Trp Ser Asn Thr Ala Tyr Thr Thr Tyr Cys
1 5 10 15

Ala Asn Cys Cys Asn Ala Thr His Cys Ala Asn
20 25

<210> 779
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 779

Cys Ala Arg Cys Ala Arg Trp Ser Asn Thr Ala Tyr Thr Thr Tyr Trp
1 5 10 15

Ser Asn Cys Cys Asn Ala Thr His Cys Ala Asn
20 25

<210> 780
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 780

Cys Ala Arg Cys Ala Arg Trp Ser Asn Thr Thr Tyr Thr Ala Tyr Cys
1 5 10 15

Ala Asn Cys Cys Asn Ala Thr His Cys Ala Asn
20 25

<210> 781
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 781

Cys Ala Arg Cys Ala Arg Trp Ser Asn Thr Thr Tyr Thr Ala Tyr Gly
1 5 10 15

Cys Asn Cys Cys Asn Ala Thr His Cys Ala Asn
20 25

<210> 782
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 782

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Gly Ala Tyr Thr Ala Tyr Tyr
1 5 10 15

Thr Asn Cys Cys Asn Thr Thr Tyr Cys Ala Asn
20 25

<210> 783
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 783

Cys Ala Arg Cys Ala Arg Thr Gly Tyr Gly Ala Tyr Gly Ala Tyr Tyr

1 5 10 15

Thr Asn Cys Cys Asn Tyr Thr Asn Cys Ala Asn
20 25

<210> 784
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 784

Cys Ala Arg Cys Ala Tyr Thr Ala Tyr Gly Ala Tyr Ala Ala Tyr Tyr
1 5 10 15

Thr Asn Cys Cys Asn Tyr Thr Asn Cys Ala Asn
20 25

<210> 785
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 785

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Gly Ala Tyr Ala Ala Tyr Tyr
1 5 10 15

Thr Asn Cys Cys Asn Tyr Thr Asn Cys Ala Asn
20 25

<210> 786
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 786

Cys Ala Arg Cys Ala Arg Thr Gly Tyr Gly Ala Tyr Ala Thr His Tyr
1 5 10 15

Thr Asn Cys Cys Asn Tyr Thr Asn Trp Ser Asn
20 25

<210> 787
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 787

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Gly Ala Tyr Ala Ala Tyr Tyr
1 5 10 15

Thr Asn Cys Cys Asn Tyr Thr Asn Gly Cys Asn
20 25

<210> 788
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 788

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Gly Ala Tyr Trp Ser Asn Tyr
1 5 10 15

Thr Asn Cys Cys Asn Ala Thr His Cys Ala Asn
20 25

<210> 789
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 789

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Gly Ala Tyr Ala Ala Tyr Tyr
1 5 10 15

Thr Asn Cys Cys Asn Ala Thr His Cys Ala Asn
20 25

<210> 790
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 790

Cys Ala Arg Cys Ala Tyr Thr Ala Tyr Gly Ala Tyr Ala Ala Tyr Tyr
1 5 10 15

Thr Asn Cys Cys Asn Ala Thr His Cys Ala Asn
20 25

<210> 791
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 791

Gly Gly Asn Thr Ala Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Trp
1 5 10 15

Ser Asn Thr Ala Tyr Gly Gly Asn Ala Thr His Trp Ser Asn

20 25 30

<210> 792
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 792

Gly Gly Asn Thr Ala Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Gly
1 5 10 15

Gly Asn Cys Ala Tyr Thr Ala Tyr Ala Thr Gly Cys Ala Tyr
20 25 30

<210> 793
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 793

Gly Gly Asn Thr Ala Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Gly
1 5 10 15

Gly Asn Thr Ala Tyr Thr Ala Tyr Ala Thr Gly Cys Ala Tyr
20 25 30

<210> 794
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 794

Gly Gly Asn Thr Ala Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Gly
1 5 10 15

Ala Arg Tyr Thr Asn Trp Ser Asn Ala Thr Gly Cys Ala Tyr
20 25 30

<210> 795
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 795

Gly Gly Asn Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Trp Ser Asn Ala
1 5 10 15

Ala Tyr Gly Cys Asn Met Gly Asn Ala Thr Gly Gly Gly Asn Gly Thr
20 25 30

Asn Trp Ser Asn
35

<210> 796
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 796

Gly Gly Asn Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Trp Ser Asn Cys
1 5 10 15

Ala Asn Gly Gly Asn Gly Gly Asn Gly Thr Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Gly Asn
35

<210> 797
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 797

Gly Gly Asn Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Ala Ala Tyr Cys
1 5 10 15

Ala Asn Gly Gly Asn Gly Gly Asn Gly Thr Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Gly Asn
35

<210> 798
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 798

Gly Gly Asn Thr Thr Tyr Cys Cys Asn Thr Thr Tyr Trp Ser Asn Met
1 5 10 15

Gly Asn Thr Ala Tyr Trp Ser Asn Ala Thr Gly Ala Ala Tyr
20 25 30

<210> 799
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 799

Gly Gly Asn Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp
1 5 10 15

Ser Asn Thr Ala Tyr Gly Cys Asn Ala Thr Gly Ala Ala Tyr
20 25 30

<210> 800
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 800

Gly Gly Asn Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp
1 5 10 15

Ser Asn Thr Ala Tyr Gly Cys Asn Ala Thr Gly Trp Ser Asn
20 25 30

<210> 801
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 801

Gly Gly Asn Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp
1 5 10 15

Ser Asn Thr Ala Tyr Gly Gly Asn Ala Thr Gly Cys Ala Tyr
20 25 30

<210> 802
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 802

Gly Gly Asn Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp
1 5 10 15

Ser Asn Thr Ala Tyr Gly Ala Tyr Ala Thr Gly Cys Ala Tyr
20 25 30

<210> 803
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 803

Gly Gly Asn Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Met Gly Asn Trp
1 5 10 15

Ser Asn Cys Ala Tyr Gly Gly Asn Ala Thr Gly Cys Ala Tyr
20 25 30

<210> 804
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 804

Gly Gly Asn Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Gly
1 5 10 15

Cys Asn Thr Ala Tyr Trp Ser Asn Ala Thr Gly Ala Ala Tyr
20 25 30

<210> 805
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 805

Gly Gly Asn Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp
1 5 10 15

Ser Asn Thr Ala Tyr Trp Ser Asn Ala Thr Gly Ala Ala Tyr
20 25 30

<210> 806
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 806

Gly Gly Asn Gly Gly Asn Trp Ser Asn Gly Thr Asn Trp Ser Asn Trp
1 5 10 15

Ser Asn Gly Gly Asn Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly
20 25 30

Gly Trp Ser Asn
35

<210> 807
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 807

Gly Gly Asn Gly Gly Asn Trp Ser Asn Ala Thr His Trp Ser Asn Met
1 5 10 15

Gly Asn Gly Gly Asn Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly
20 25 30

Gly Trp Ser Asn
35

<210> 808
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 808

Gly Gly Asn Gly Gly Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp
1 5 10 15

Ser Asn Gly Gly Asn Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly
20 25 30

Gly Trp Ser Asn
35

<210> 809
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 809

Gly Gly Asn Gly Gly Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp
1 5 10 15

Ser Asn Gly Gly Asn Gly Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Gly
20 25 30

Gly Ala Ala Tyr
35

<210> 810
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 810

Gly Gly Asn Gly Gly Asn Trp Ser Asn Thr Thr Tyr Trp Ser Asn Gly
1 5 10 15

Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn
20 25 30

<210> 811
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 811

Gly Gly Asn Gly Gly Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp
1 5 10 15

Ser Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn
20 25 30

<210> 812
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 812

Gly Gly Asn Gly Gly Asn Trp Ser Asn Gly Thr Asn Trp Ser Asn Trp
1 5 10 15

Ser Asn Gly Gly Asn Gly Gly Asn Trp Ser Asn Thr Ala Tyr Thr Gly
20 25 30

Gly Trp Ser Asn
35

<210> 813
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 813

Gly Gly Asn Thr Ala Tyr Met Gly Asn Thr Thr Tyr Cys Ala Asn Trp
1 5 10 15

Ser Asn Thr Ala Tyr Thr Gly Gly Ala Thr His Gly Gly Asn
20 25 30

<210> 814
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 814

Gly Gly Asn Thr Ala Tyr Trp Ser Asn Thr Thr Tyr Cys Ala Asn Trp
1 5 10 15

Ser Asn Thr Ala Tyr Thr Gly Gly Ala Thr His Gly Gly Asn
20 25 30

<210> 815
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 815

Gly Gly Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn Trp Ser Asn Trp
1 5 10 15

Ser Asn Thr Ala Tyr Trp Ser Asn Gly Cys Asn Gly Cys Asn Thr Gly
20 25 30

Gly Ala Ala Tyr
35

<210> 816
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 816

Thr Gly Gly Ala Thr His Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala
1 5 10 15

Ala Tyr Gly Gly Asn Ala Ala Tyr Cys Ala Asn Ala Ala Tyr Thr Ala
20 25 30

Tyr Gly Cys Asn Cys Ala Arg Ala Ala Arg Tyr Thr Asn Cys Ala Arg
35 40 45

Gly Ala Tyr
50

<210> 817
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 817

Thr Gly Gly Ala Thr His Ala Ala Tyr Cys Cys Asn Ala Ala Tyr Trp
1 5 10 15

Ser Asn Gly Gly Asn Gly Gly Asn Cys Ala Asn Ala Ala Tyr Thr Gly

20 25 30

Tyr Gly Cys Asn Cys Ala Arg Ala Ala Arg Thr Thr Tyr Cys Ala Arg
35 40 45

Gly Gly Asn
50

<210> 818
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 818

Thr Gly Gly Ala Thr His Ala Ala Tyr Cys Cys Asn Ala Ala Tyr Trp
1 5 10 15

Ser Asn Gly Gly Asn Gly Gly Asn Cys Ala Asn Ala Ala Tyr Cys Ala
20 25 30

Tyr Cys Ala Asn Cys Ala Arg Ala Ala Arg Thr Thr Tyr Cys Ala Arg
35 40 45

Gly Gly Asn
50

<210> 819
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 819

Trp Ser Asn Thr Thr Tyr Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly
1 5 10 15

Ala Tyr Gly Gly Asn Gly Ala Arg Cys Ala Asn Ala Thr His Thr Ala
20 25 30

Tyr Gly Cys Asn Cys Ala Arg Ala Ala Arg Thr Thr Tyr Cys Ala Arg
35 40 45

Gly Gly Asn
50

<210> 820
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 820

Cys Ala Tyr Ala Thr His Thr Thr Tyr Trp Ser Asn Ala Ala Tyr Gly
1 5 10 15

Ala Tyr Gly Ala Arg Ala Ala Arg Trp Ser Asn Thr Ala Tyr Trp Ser
20 25 30

Asn Cys Ala Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg Trp Ser Asn
35 40 45

<210> 821
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 821

Tyr Thr Asn Ala Thr His Thr Thr Tyr Trp Ser Asn Ala Ala Tyr Gly
1 5 10 15

Ala Tyr Gly Ala Arg Ala Ala Arg Trp Ser Asn Thr Ala Tyr Trp Ser
20 25 30

Asn Cys Ala Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg Trp Ser Asn
35 40 45

<210> 822
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 822

Tyr Thr Asn Ala Thr His Thr Ala Tyr Thr Gly Gly Ala Ala Tyr Gly
1 5 10 15

Ala Tyr Gly Ala Tyr Ala Ala Arg Met Gly Asn Thr Ala Tyr Trp Ser
20 25 30

Asn Cys Cys Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg Trp Ser Asn
35 40 45

<210> 823
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 823

Tyr Thr Asn Ala Thr His Thr Ala Tyr Thr Gly Gly Ala Ala Tyr Gly
1 5 10 15

Thr Asn Gly Ala Arg Ala Ala Arg Met Gly Asn Thr Ala Tyr Trp Ser
20 25 30

Asn Cys Cys Asn Trp Ser Asn Tyr Thr Asn Met Gly Asn Trp Ser Asn
35 40 45

<210> 824
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 824

Gly Cys Asn Ala Thr His Trp Ser Asn Trp Ser Asn Trp Ser Asn Trp
1 5 10 15

Ser Asn Trp Ser Asn Thr Ala Tyr Ala Thr His Thr Ala Tyr Thr Ala
20 25 30

Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn Ala Ala Arg
35 40 45

Gly Gly Asn
50

<210> 825
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 825

Gly Cys Asn Ala Thr His Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly
1 5 10 15

Gly Asn Gly Gly Asn Trp Ser Asn Cys Ala Asn Thr Ala Tyr Thr Ala
20 25 30

Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn Ala Ala Arg
35 40 45

Gly Gly Asn
50

<210> 826
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 826

Thr Thr Tyr Ala Thr His Trp Ser Asn Gly Ala Tyr Gly Ala Tyr Gly
1 5 10 15

Gly Asn Trp Ser Asn Cys Ala Asn Ala Ala Arg Thr Ala Tyr Thr Ala
20 25 30

Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn Ala Ala Arg
35 40 45

Gly Gly Asn
50

<210> 827
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 827

Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly Ala Tyr Gly
1 5 10 15

Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Thr Ala Tyr Thr Ala
20 25 30

Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn Ala Ala Arg
35 40 45

Gly Gly Asn
50

<210> 828
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 828

Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly Ala Tyr Gly
1 5 10 15

Gly Asn Trp Ser Asn Ala Thr His Ala Ala Arg Thr Ala Tyr Thr Ala
20 25 30

Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn Ala Ala Arg
35 40 45

Gly Gly Asn
50

<210> 829
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 829

Gly Thr Asn Ala Thr His Thr Gly Gly Trp Ser Asn Gly Ala Tyr Gly
1 5 10 15

Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Thr Ala Tyr Thr Ala
20 25 30

Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn Ala Ala Arg
35 40 45

Gly Gly Asn
50

<210> 830
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 830

Gly Thr Asn Ala Thr His Thr Gly Gly Gly Ala Tyr Gly Ala Tyr Gly
1 5 10 15

Gly Asn Trp Ser Asn Ala Ala Tyr Cys Ala Arg Thr Ala Tyr Thr Ala
20 25 30

Tyr Cys Ala Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn Ala Ala Arg
35 40 45

Gly Gly Asn
50

<210> 831
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 831

Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly Ala Tyr Gly
1 5 10 15

Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Met Gly Asn Thr Ala
20 25 30

Tyr Gly Thr Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn Ala Ala Arg

35 40 45

Gly Gly Asn
50

<210> 832
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 832

Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly Ala Tyr Gly
1 5 10 15

Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr Ala
20 25 30

Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn Met Gly Asn
35 40 45

Gly Gly Asn
50

<210> 833
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 833

Thr Ala Tyr Ala Thr His Trp Ser Asn Trp Ser Asn Trp Ser Asn Gly
1 5 10 15

Gly Asn Met Gly Asn Cys Ala Asn Ala Thr His Thr Ala Tyr Thr Ala
20 25 30

Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn Ala Ala Arg
35 40 45

Gly Gly Asn
50

<210> 834
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 834

Cys Ala Tyr Ala Thr His Trp Ser Asn Trp Ser Asn Trp Ser Asn Trp
1 5 10 15

Ser Asn Met Gly Asn Cys Ala Asn Ala Thr His Thr Ala Tyr Thr Ala
20 25 30

Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn Ala Ala Arg
35 40 45

Gly Gly Asn
50

<210> 835
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 835

Cys Ala Tyr Ala Thr His Trp Ser Asn Met Gly Asn Trp Ser Asn Trp
1 5 10 15

Ser Asn Met Gly Asn Cys Ala Asn Ala Thr His Thr Ala Tyr Thr Ala
20 25 30

Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn Ala Ala Arg
35 40 45

Gly Gly Asn
50

<210> 836
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 836

Thr Ala Tyr Ala Thr His Cys Ala Tyr Trp Ser Asn Trp Ser Asn Gly
1 5 10 15

Gly Asn Trp Ser Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Ala Ala
20 25 30

Tyr Cys Cys Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg Trp Ser Asn
35 40 45

<210> 837
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 837

Thr Ala Tyr Ala Thr His Thr Ala Tyr Cys Ala Tyr Trp Ser Asn Gly
1 5 10 15

Gly Asn Trp Ser Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Ala Ala
20 25 30

Tyr Cys Cys Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg Trp Ser Asn
35 40 45

<210> 838
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 838

Thr Ala Tyr Ala Thr His Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Gly
1 5 10 15

Gly Asn Trp Ser Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Ala Ala
20 25 30

Tyr Cys Cys Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg Trp Ser Asn
35 40 45

<210> 839
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 839

Thr Ala Tyr Ala Thr His Cys Ala Tyr Thr Ala Tyr Trp Ser Asn Gly
1 5 10 15

Gly Asn Trp Ser Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Ala Ala
20 25 30

Tyr Cys Cys Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg Trp Ser Asn
35 40 45

<210> 840
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 840

Thr Ala Tyr Ala Thr His Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Gly
1 5 10 15

Gly Asn Gly Gly Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Ala Ala
20 25 30

Tyr Cys Cys Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg Trp Ser Asn
35 40 45

<210> 841
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 841

Gly Ala Arg Ala Thr His Ala Ala Tyr Cys Ala Tyr Trp Ser Asn Gly
1 5 10 15

Gly Asn Trp Ser Asn Cys Ala Asn Ala Ala Tyr Thr Ala Tyr Ala Ala
20 25 30

Tyr Cys Cys Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg Trp Ser Asn
35 40 45

<210> 842
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 842

Met Gly Asn Ala Thr His Thr Ala Tyr Cys Ala Asn Trp Ser Asn Gly
1 5 10 15

Gly Asn Cys Ala Asn Cys Ala Asn Ala Ala Tyr Thr Ala Tyr Ala Ala
20 25 30

Tyr Cys Cys Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg Trp Ser Asn
35 40 45

<210> 843
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 843

Thr Ala Tyr Ala Thr His Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Gly
1 5 10 15

Gly Asn Trp Ser Asn Cys Ala Asn Ala Ala Tyr Thr Ala Tyr Ala Ala
20 25 30

Tyr Cys Cys Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg Trp Ser Asn

35 40 45

<210> 844
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 844

Ala Thr His Ala Thr His Thr Ala Tyr Cys Cys Asn Gly Ala Tyr Gly
1 5 10 15

Ala Tyr Trp Ser Asn Gly Ala Tyr Cys Ala Asn Met Gly Asn Thr Ala
20 25 30

Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn Thr Thr Tyr Cys Ala Arg
35 40 45

Gly Gly Asn
50

<210> 845
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 845

Ala Thr His Ala Thr His Thr Ala Tyr Cys Cys Asn Gly Ala Tyr Gly
1 5 10 15

Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Cys Asn Met Gly Asn Thr Ala
20 25 30

Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn Thr Thr Tyr Cys Ala Arg
35 40 45

Gly Gly Asn
50

<210> 846
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 846

Ala Thr His Ala Thr His Thr Ala Tyr Cys Cys Asn Gly Gly Asn Gly
1 5 10 15

Ala Tyr Trp Ser Asn Gly Ala Tyr Ala Thr His Met Gly Asn Thr Ala
20 25 30

Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn Thr Thr Tyr Cys Ala Arg
35 40 45

Gly Gly Asn
50

<210> 847
<211> 54
<212> PRT
<213> Homo Sapiens

<400> 847

Met Gly Asn Cys Ala Asn Thr Ala Tyr Thr Gly Tyr Met Gly Asn Trp
1 5 10 15

Ser Asn Ala Ala Arg Thr Gly Gly Thr Ala Tyr Ala Ala Tyr Gly Ala
20 25 30

Tyr Thr Ala Tyr Gly Cys Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn
35 40 45

Ala Ala Arg Trp Ser Asn
50

<210> 848
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 848

Gly Ala Arg Gly Ala Tyr Ala Ala Tyr Thr Gly Gly Ala Ala Tyr Thr
1 5 10 15

Ala Tyr Gly Gly Asn Thr Thr Tyr Thr Thr Tyr Gly Ala Tyr Thr Ala
20 25 30

Tyr

<210> 849
<211> 24
<212> PRT
<213> Homo Sapiens

<400> 849

Trp Ser Asn Ala Thr His Gly Cys Asn Gly Thr Asn Gly Cys Asn Tyr
1 5 10 15

Thr Asn Gly Ala Tyr Thr Ala Tyr
20

<210> 850
<211> 39
<212> PRT
<213> Homo Sapiens

<400> 850

Gly Ala Arg Gly Gly Asn Gly Ala Tyr Gly Gly Asn Gly Gly Asn Thr
1 5 10 15

Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Thr
20 25 30

Gly Gly Ala Tyr Gly Thr Asn
35

<210> 851
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 851

Ala Thr Gly Thr Ala Tyr Trp Ser Asn Trp Ser Asn Gly Gly Asn Thr
1 5 10 15

Gly Gly Thr Ala Tyr Gly Gly Asn Gly Thr Asn Thr Thr Tyr Gly Ala
20 25 30

Tyr Thr Ala Tyr
35

<210> 852
<211> 39
<212> PRT
<213> Homo Sapiens

<400> 852

Gly Thr Asn Thr Ala Tyr Trp Ser Asn Trp Ser Asn Gly Gly Asn Thr
1 5 10 15

Gly Gly Trp Ser Asn Thr Thr Tyr Thr Ala Tyr Gly Gly Asn Ala Thr
20 25 30

Gly Gly Ala Tyr Gly Thr Asn
35

<210> 853
<211> 24
<212> PRT
<213> Homo Sapiens

<400> 853

Met Gly Asn Met Gly Asn Gly Ala Arg Tyr Thr Asn Cys Cys Asn Thr
1 5 10 15

Thr Tyr Gly Ala Tyr Thr Ala Tyr
20

<210> 854
<211> 24
<212> PRT
<213> Homo Sapiens

<400> 854

Met Gly Asn Ala Ala Tyr Thr Gly Gly Cys Ala Asn Cys Cys Asn Thr
1 5 10 15

Thr Tyr Gly Ala Tyr Thr Ala Tyr
20

<210> 855
<211> 24
<212> PRT
<213> Homo Sapiens

<400> 855

Met Gly Asn Tyr Thr Asn Gly Ala Arg Tyr Thr Asn Cys Cys Asn Thr
1 5 10 15

Thr Tyr Gly Ala Tyr Thr Ala Tyr
20

<210> 856
<211> 24
<212> PRT
<213> Homo Sapiens

<400> 856

Met Gly Asn Met Gly Asn Gly Ala Arg Gly Thr Asn Cys Cys Asn Thr
1 5 10 15

Thr Tyr Gly Ala Tyr Thr Ala Tyr
20

<210> 857
<211> 24

<212> PRT
<213> Homo Sapiens

<400> 857

Met Gly Asn Cys Ala Tyr Cys Ala Asn Ala Ala Tyr Cys Cys Asn Thr
1 5 10 15

Thr Tyr Gly Ala Arg Thr Ala Tyr
20

<210> 858
<211> 24
<212> PRT
<213> Homo Sapiens

<400> 858

Met Gly Asn Gly Gly Asn Gly Ala Arg Tyr Thr Asn Cys Cys Asn Thr
1 5 10 15

Thr Tyr Gly Ala Tyr Thr Ala Tyr
20

<210> 859
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 859

Gly Ala Tyr Met Gly Asn Gly Thr Asn Gly Gly Asn Gly Cys Asn Cys
1 5 10 15

Ala Asn Cys Cys Asn Gly Ala Tyr Gly Cys Asn Thr Thr Tyr Gly Ala
20 25 30

Tyr Ala Thr His
35

<210> 860
<211> 57
<212> PRT
<213> Homo Sapiens

<400> 860

Gly Ala Arg Gly Gly Asn Ala Thr His Gly Cys Asn Gly Thr Asn Gly
1 5 10 15

Cys Asn Gly Gly Asn Cys Ala Asn Gly Cys Asn Gly Ala Arg Thr Ala
20 25 30

Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Cys Asn
35 40 45

Ala Thr Gly Gly Ala Tyr Gly Thr Asn
50 55

<210> 861
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 861

Gly Ala Arg Gly Gly Asn Ala Thr His Gly Cys Asn Gly Cys Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Trp Ser Asn Thr Ala Tyr Thr Ala Tyr Thr Ala
20 25 30

Tyr Thr Ala Tyr Gly Cys Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn
35 40 45

<210> 862
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 862

Gly Ala Arg Gly Gly Asn Ala Thr His Gly Cys Asn Gly Gly Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Trp Ser Asn Thr Ala Tyr Thr Ala Tyr Thr Ala
20 25 30

Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn
35 40 45

<210> 863
<211> 42
<212> PRT
<213> Homo Sapiens

<400> 863

Trp Ser Asn Thr Ala Tyr Thr Ala Tyr Gly Ala Tyr Trp Ser Asn Trp
1 5 10 15

Ser Asn Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Gly
20 25 30

Asn Thr Thr Tyr Gly Ala Tyr Thr Ala Tyr

35 40

<210> 864
<211> 15
<212> PRT
<213> Homo Sapiens

<400> 864

Ala Ala Tyr Gly Thr Asn Ala Thr His Gly Ala Tyr Thr Ala Tyr
1 5 10 15

<210> 865
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 865

Gly Gly Asn Gly Gly Asn Gly Cys Asn Cys Ala Asn Gly Gly Asn Gly
1 5 10 15

Cys Asn Gly Ala Arg Thr Ala Tyr Thr Thr Tyr Cys Ala Arg Cys Ala
20 25 30

Tyr

<210> 866
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 866

Tyr Thr Asn Thr Gly Gly Thr Thr Tyr Gly Gly Asn Gly Ala Arg Cys
1 5 10 15

Ala Asn Thr Thr Tyr Gly Ala Tyr Thr Ala Tyr
20 25

<210> 867
<211> 18
<212> PRT
<213> Homo Sapiens

<400> 867

Ala Ala Tyr Tyr Thr Asn Cys Cys Asn Thr Thr Tyr Gly Ala Tyr Thr
1 5 10 15

Ala Tyr

<210> 868
<211> 42
<212> PRT
<213> Homo Sapiens

<400> 868

Trp Ser Asn Cys Ala Tyr Thr Ala Tyr Gly Gly Asn Gly Gly Asn Gly
1 5 10 15

Ala Tyr Thr Ala Tyr Gly Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Gly
20 25 30

Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn
35 40

<210> 869
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 869

Gly Ala Tyr Gly Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg Cys
1 5 10 15

Ala Arg Gly Cys Asn Cys Cys Asn Thr Thr Tyr Gly Ala Tyr Thr Ala
20 25 30

Tyr

<210> 870
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 870

Thr Gly Gly Gly Gly Asn Ala Thr His Trp Ser Asn Gly Cys Asn Cys
1 5 10 15

Cys Asn Thr Thr Tyr Gly Ala Tyr Thr Gly Tyr
20 25

<210> 871
<211> 18
<212> PRT
<213> Homo Sapiens

<400> 871

Thr Gly Gly Gly Cys Asn Cys Cys Asn Thr Thr Tyr Gly Ala Tyr Thr

1 5 10 15

Ala Tyr

<210> 872
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 872

Gly Ala Tyr Gly Gly Asn Thr Ala Tyr Ala Ala Tyr Thr Gly Gly Ala
1 5 10 15

Ala Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Ala Ala Tyr Thr Ala
20 25 30

Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn
35 40 45

<210> 873
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 873

Gly Ala Tyr Gly Gly Asn Thr Ala Tyr Ala Ala Tyr Thr Gly Gly Ala
1 5 10 15

Ala Tyr Ala Ala Tyr Gly Gly Asn Gly Gly Asn Thr Ala Tyr Thr Ala
20 25 30

Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn
35 40 45

<210> 874
<211> 24
<212> PRT
<213> Homo Sapiens

<400> 874

Gly Gly Asn Cys Cys Asn Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala
1 5 10 15

Thr Gly Gly Ala Tyr Gly Thr Asn
20

<210> 875
<211> 51

<212> PRT
<213> Homo Sapiens

<400> 875

Gly Cys Asn Tyr Thr Asn Met Gly Asn Gly Gly Asn Ala Thr His Gly
1 5 10 15

Thr Asn Tyr Thr Asn Ala Thr Gly Gly Thr Asn Thr Ala Tyr Gly Thr
20 25 30

Asn Tyr Thr Asn Gly Gly Asn Gly Cys Asn Tyr Thr Asn Gly Ala Tyr
35 40 45

Ala Thr His
50

<210> 876
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 876

Gly Ala Tyr Gly Ala Arg Cys Ala Asn Gly Thr Asn Gly Thr Asn Met
1 5 10 15

Gly Asn Gly Gly Asn Tyr Thr Asn Ala Thr His Met Gly Asn Thr Ala
20 25 30

Tyr Thr Gly Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr
35 40 45

Gly Thr Asn
50

<210> 877
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 877

Gly Ala Tyr Met Gly Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly
1 5 10 15

Ala Tyr Thr Ala Tyr Gly Gly Asn Met Gly Asn Ala Thr Gly Gly Ala
20 25 30

Tyr Gly Thr Asn
35

<210> 878
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 878

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr Gly Gly Asn Thr
1 5 10 15

Gly Tyr Thr Thr Tyr Gly Cys Asn Tyr Thr Asn
20 25

<210> 879
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 879

Gly Gly Asn Thr Ala Tyr Ala Ala Tyr Thr Ala Tyr Gly Gly Asn Tyr
1 5 10 15

Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Ala Tyr Trp Ser
20 25 30

Asn Trp Ser Asn Gly Gly Asn Thr Ala Tyr Cys Cys Asn Trp Ser Asn
35 40 45

Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly Gly
50 55 60

Ala Tyr Gly Thr Asn
65

<210> 880
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 880

Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Gly Ala Tyr Ala Thr His Tyr
1 5 10 15

Thr Asn Cys Ala Asn Gly Gly Asn Thr Ala Tyr Cys Cys Asn Thr Thr
20 25 30

Tyr Thr Ala Tyr Thr Thr Tyr Gly Ala Tyr Thr Ala Tyr
35 40 45

<210> 881
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 881

Gly Gly Asn Gly Gly Asn Thr Ala Tyr Trp Ser Asn Trp Ser Asn Trp
1 5 10 15

Ser Asn Thr Gly Gly Thr Ala Tyr Thr Gly Gly Thr Thr Tyr Gly Ala
20 25 30

Tyr Cys Cys Asn
35

<210> 882
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 882

Gly Gly Asn Gly Gly Asn Thr Ala Tyr Trp Ser Asn Trp Ser Asn Trp
1 5 10 15

Ser Asn Thr Gly Gly Thr Thr Tyr Thr Gly Gly Thr Thr Tyr Gly Ala
20 25 30

Tyr Cys Cys Asn
35

<210> 883
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 883

Gly Ala Tyr Gly Gly Asn Thr Ala Tyr Trp Ser Asn Thr Ala Tyr Gly
1 5 10 15

Gly Asn Cys Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala
20 25 30

Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn
35 40 45

<210> 884
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 884

Trp Ser Asn Gly Cys Asn Tyr Thr Asn Met Gly Asn Thr Ala Tyr Thr
1 5 10 15

Thr Tyr Gly Ala Tyr Thr Gly Gly Tyr Thr Asn Thr Thr Tyr Trp Ser
20 25 30

Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Gly Ala Tyr Ala Thr His
35 40 45

<210> 885
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 885

Cys Ala Arg Ala Ala Arg Trp Ser Asn Thr Ala Tyr Gly Gly Asn Thr
1 5 10 15

Ala Tyr Trp Ser Asn Thr Ala Tyr Thr Thr Tyr Gly Ala Tyr Thr Ala
20 25 30

Tyr

<210> 886
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 886

Cys Ala Arg Gly Gly Asn Thr Ala Tyr Gly Gly Asn Trp Ser Asn Gly
1 5 10 15

Gly Asn Thr Gly Gly Gly Gly Asn Thr Ala Tyr Thr Thr Tyr Gly Ala
20 25 30

Tyr Thr Ala Tyr
35

<210> 887
<211> 54
<212> PRT
<213> Homo Sapiens

<400> 887

Cys Ala Arg Gly Gly Asn Tyr Thr Asn Gly Cys Asn Gly Thr Asn Gly
1 5 10 15

Cys Asn Gly Gly Asn Cys Ala Asn Trp Ser Asn Thr Ala Tyr Thr Ala
20 25 30

Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly
35 40 45

Gly Ala Tyr Gly Thr Asn
50

<210> 888
<211> 39
<212> PRT
<213> Homo Sapiens

<400> 888

Gly Ala Tyr Met Gly Asn Gly Cys Asn Gly Thr Asn Gly Cys Asn Gly
1 5 10 15

Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Thr
20 25 30

Gly Gly Ala Tyr Gly Thr Asn
35

<210> 889
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 889

Gly Ala Tyr Gly Thr Asn Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Tyr Thr Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Cys Cys Asn Gly Thr Asn Cys Ala Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr
65

<210> 890
<211> 69
<212> PRT

<213> Homo Sapiens

<400> 890

Gly Ala Tyr Gly Thr Asn Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Tyr Thr Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Cys Cys Asn Gly Thr Asn Cys Ala Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr
65

<210> 891
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 891

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Cys Ala Asn Cys Cys Asn Tyr Thr Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Thr Asn Cys Ala Asn Cys Cys Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr
65

<210> 892
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 892

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Cys Ala Asn Cys Cys Asn Tyr Thr Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Thr Asn Cys Ala Asn Cys Cys Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr
65

<210> 893
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 893

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Ala
50 55 60

Thr His Thr Gly Tyr
65

<210> 894
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 894

Ala Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Cys Ala Asn Cys Cys Asn Tyr Thr Asn Trp Ser Asn Trp Ser
20 25 30

Asn Cys Cys Asn Gly Thr Asn Cys Ala Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr
65

<210> 895
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 895

Gly Ala Arg Ala Thr His Gly Thr Asn Tyr Thr Asn Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Gly Asn Cys Ala Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Tyr Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Tyr Thr Asn Trp
50 55 60

Ser Asn Thr Gly Tyr
65

<210> 896
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 896

Gly Ala Arg Ala Thr His Gly Thr Asn Tyr Thr Asn Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Gly Asn Cys Ala Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Tyr Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Tyr Thr Asn Trp
50 55 60

Ser Asn Thr Gly Tyr
65

<210> 897
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 897

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 898
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 898

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Tyr Thr
20 25 30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr
65

<210> 899
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 899

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys

1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Tyr Thr
20 25 30

Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr
65

<210> 900
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 900

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Tyr Thr
20 25 30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr
65

<210> 901
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 901

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn

35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 902
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 902

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Gly Cys Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 903
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 903

Gly Ala Arg Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Cys Asn Cys Ala Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Tyr Thr Asn Trp
50 55 60

Ser Asn Thr Gly Tyr

65

<210> 904
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 904

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Gly Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 905
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 905

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 906
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 906

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 907
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 907

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 908
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 908

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 909
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 909

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 910
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 910

Thr Gly Gly Tyr Thr Asn Cys Ala Arg Cys Ala Arg Met Gly Asn Cys
1 5 10 15

Cys Asn Gly Gly Asn Cys Ala Arg Trp Ser Asn Cys Cys Asn Met Gly
20 25 30

Asn Met Gly Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 911
<211> 45

<212> PRT
<213> Homo Sapiens

<400> 911

Thr Gly Gly Thr Ala Tyr Tyr Thr Asn Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys Asn Cys Ala
20 25 30

Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 912
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 912

Thr Gly Gly Thr Thr Tyr Tyr Thr Asn Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys Asn Cys Ala
20 25 30

Arg Cys Cys Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 913
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 913

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Thr Asn Cys Cys Asn Ala Ala
20 25 30

Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 914
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 914

Thr Gly Gly Tyr Thr Asn Cys Ala Arg Cys Ala Arg Met Gly Asn Cys
1 5 10 15

Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys Asn Met Gly
20 25 30

Asn Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 915
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 915

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Met Gly
20 25 30

Asn Tyr Thr Asn Tyr Thr Asn Ala Thr His Trp Ser Asn
35 40 45

<210> 916
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 916

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Met Gly
20 25 30

Asn Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 917
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 917

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Cys Cys Asn Ala Ala

20 25 30

Arg Met Gly Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 918
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 918

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys Asn Ala Ala
20 25 30

Arg Tyr Thr Asn Thr Thr Tyr Ala Thr His Thr Ala Tyr
35 40 45

<210> 919
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 919

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys Asn Ala Ala
20 25 30

Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 920
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 920

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys Asn Ala Ala
20 25 30

Arg Gly Thr Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 921
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 921

Thr Gly Gly Thr Thr Tyr Cys Ala Arg Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Cys Cys Asn Ala Ala
20 25 30

Arg Trp Ser Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 922
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 922

Thr Gly Gly Tyr Thr Asn Cys Ala Arg Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Cys Cys Asn Ala Ala
20 25 30

Arg Trp Ser Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 923
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 923

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Gly Ala Tyr Cys
1 5 10 15

Cys Asn Gly Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Met Gly
20 25 30

Asn Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 924
<211> 45
<212> PRT

<213> Homo Sapiens

<400> 924

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Cys Cys Asn Ala Ala
20 25 30

Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 925
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 925

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Cys Cys Asn Ala Ala
20 25 30

Arg Thr Thr Tyr Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 926
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 926

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Met Gly Asn Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Tyr Gly Cys Asn Cys Cys Asn Ala Ala
20 25 30

Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 927
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 927

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala Ala Arg Cys

1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Cys Cys Asn Ala Ala
20 25 30

Arg Gly Thr Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 928
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 928

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Cys Cys Asn Gly Ala
20 25 30

Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 929
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 929

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala Ala Arg Tyr
1 5 10 15

Thr Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Cys Cys Asn Ala Ala
20 25 30

Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His Cys Ala Tyr
35 40 45

<210> 930
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 930

Gly Gly Asn Gly Thr Asn Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Ala Ala Tyr Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Ala Ala Arg Ala Thr His Trp Ser Asn Met Gly Asn Gly
50 55 60

Thr Asn Gly Ala Arg Gly Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr
65 70 75 80

Asn Gly Gly Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 931
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 931

Gly Gly Asn Gly Thr Asn Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Ala Ala Arg Ala Thr His Trp Ser Asn Met Gly Asn Gly
50 55 60

Thr Asn Gly Ala Arg Gly Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr
65 70 75 80

Asn Gly Gly Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 932
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 932

Gly Gly Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr
65 70 75 80

Asn Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 933
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 933

Gly Gly Asn Gly Thr Asn Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Gly Cys
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Ala Ala Arg Ala Thr His Trp Ser Asn Met Gly Asn Gly
50 55 60

Thr Asn Gly Ala Arg Gly Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr
65 70 75 80

Asn Gly Gly Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 934
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 934

Gly Gly Asn Gly Thr Asn Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly Gly Asn Gly Cys
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Ala Ala Arg Ala Thr His Trp Ser Asn Met Gly Asn Gly
50 55 60

Thr Asn Gly Ala Arg Gly Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr
65 70 75 80

Asn Gly Gly Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 935
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 935

Gly Gly Asn Ala Thr His Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Met Gly Asn Tyr
50 55 60

Thr Asn Gly Ala Arg Cys Cys Asn Gly Ala Arg Gly Ala Tyr Thr Thr
65 70 75 80

Tyr Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 936
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 936

Gly Gly Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Arg Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Gly Ala Tyr Thr Thr
65 70 75 80

Tyr Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 937
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 937

Gly Gly Asn Gly Thr Asn Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Cys Ala Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Gly Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr
65 70 75 80

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 938
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 938

Gly Gly Asn Gly Thr Asn Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Gly Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr
65 70 75 80

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 939
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 939

Gly Gly Asn Gly Thr Asn Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Gly Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr
65 70 75 80

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Thr Tyr Thr Gly Tyr
85 90 95

<210> 940
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 940

Gly Gly Asn Gly Thr Asn Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Gly Gly Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Gly Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr
65 70 75 80

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 941
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 941

Gly Gly Asn Gly Thr Asn Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Gly Cys Asn Gly Ala Tyr Gly Ala Tyr Gly Thr
65 70 75 80

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 942
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 942

Gly Gly Asn Gly Thr Asn Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Gly Gly Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Gly Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr
65 70 75 80

Asn Gly Cys Asn Tyr Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 943
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 943

Gly Gly Asn Gly Thr Asn Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Gly Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr
65 70 75 80

Asn Gly Cys Asn Gly Thr Asn Thr Thr Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 944
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 944

Gly Gly Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Ala Ala Arg Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Gly Ala Tyr Thr Thr
65 70 75 80

Tyr Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 945
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<400> 945

Gly Gly Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Gly Ala Tyr Thr Thr
65 70 75 80

Tyr Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 946
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<400> 946

Gly Gly Asn Ala Thr His Cys Cys Asn Gly Cys Asn Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Arg Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Trp Ser Asn Gly Ala Arg Gly Ala Tyr Thr Thr
65 70 75 80

Tyr Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 947
<211> 96
<212> PRT
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<400> 947

Gly Gly Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Gly Ala Tyr Thr Thr
65 70 75 80

Tyr Gly Cys Asn Gly Cys Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 948
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 948

Gly Gly Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Met Gly Asn Gly
1 5 10 15

Thr Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Met Gly Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Gly Ala Tyr Thr Thr
65 70 75 80

Tyr Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 949
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 949

Gly Gly Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Tyr Thr Asn Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Gly Ala Tyr Thr Thr
65 70 75 80

Tyr Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 950
<211> 96
<212> PRT
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<400> 950

Gly Gly Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr Thr Thr
65 70 75 80

Tyr Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 951
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 951

Gly Gly Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Gly Ala Tyr Thr Thr
65 70 75 80

Tyr Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 952
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 952

Gly Gly Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Tyr Thr Asn Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Gly Ala Tyr Thr Thr
65 70 75 80

Tyr Gly Cys Asn Trp Ser Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 953
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 953

Gly Gly Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Gly Ala Tyr Thr Thr
65 70 75 80

Tyr Gly Cys Asn Trp Ser Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 954
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 954

Gly Gly Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Thr Thr Tyr Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Gly Ala Tyr Ala Thr
65 70 75 80

His Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 955
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 955

Gly Gly Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Ala Arg Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Thr Thr Tyr Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Gly Ala Tyr Ala Thr
65 70 75 80

His Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 956
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 956

Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Met
1 5 10 15

Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
20 25 30

<210> 957
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 957

Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Met
1 5 10 15

Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Thr His
20 25 30

<210> 958
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 958

Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Ala
1 5 10 15

Ala Arg Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
20 25 30

<210> 959
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 959

Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Cys Ala Asn Ala
1 5 10 15

Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
20 25 30

<210> 960
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 960

Thr Thr Tyr Gly Gly Asn Cys Ala Tyr Gly Gly Asn Cys Ala Asn Met
1 5 10 15

Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
20 25 30

<210> 961
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 961

Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala Asn Ala
1 5 10 15

Ala Arg Gly Thr Asn Gly Ala Tyr Ala Thr His Ala Ala Arg
20 25 30

<210> 962
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 962

Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Ala
1 5 10 15

Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
20 25 30

<210> 963
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 963

Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala Asn Ala
1 5 10 15

Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
20 25 30

<210> 964
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 964

Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Cys Ala Asn Ala
1 5 10 15

Ala Arg Gly Thr Asn Gly Cys Asn Ala Thr His Ala Ala Arg
20 25 30

<210> 965
<211> 30

<212> PRT
<213> Homo Sapiens

<400> 965

Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala Asn Ala
1 5 10 15

Ala Arg Ala Thr Gly Gly Ala Tyr Ala Thr His Ala Ala Arg
20 25 30

<210> 966
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 966

Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Ala
1 5 10 15

Ala Arg Gly Thr Asn Gly Ala Arg Thr Thr Tyr Ala Ala Arg
20 25 30

<210> 967
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 967

Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Cys Ala Asn Ala
1 5 10 15

Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Met Gly Asn
20 25 30

<210> 968
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 968

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
20 25 30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Cys Asn
35 40 45

Trp Ser Asn Gly Thr Asn Ala Ala Arg Gly Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Cys Asn Trp Ser Asn
65 70 75

<210> 969
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 969

Cys Ala Arg Gly Thr Asn Cys Ala Tyr Tyr Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
20 25 30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Cys Asn
35 40 45

Trp Ser Asn Gly Thr Asn Ala Ala Arg Gly Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn
65 70 75

<210> 970
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 970

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
20 25 30

Asn Met Gly Asn Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Cys Asn
35 40 45

Trp Ser Asn Gly Thr Asn Ala Ala Arg Gly Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn
65 70 75

<210> 971
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 971

Cys Ala Arg Gly Thr Asn Cys Ala Asn Tyr Thr Asn Ala Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Thr Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Cys Ala Asn Gly Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Cys Ala Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn
65 70 75

<210> 972
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 972

Cys Ala Arg Ala Thr His Cys Ala Asn Tyr Thr Asn Ala Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Cys Ala Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Cys Ala Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Cys Ala Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn
65 70 75

<210> 973
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 973

Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly

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1               5                   10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Tyr Thr
            20                  25                  30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
        35                  40                  45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
    50                  55                  60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn
65                  70                  75
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<210> 974
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 974

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Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Tyr Thr Asn Gly
1               5                   10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Tyr Thr
            20                  25                  30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
        35                  40                  45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
    50                  55                  60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn
65                  70                  75
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<210> 975
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 975

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Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Tyr Thr Asn Gly
1               5                   10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Tyr Thr
            20                  25                  30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
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35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Cys Asn Trp Ser Asn
65 70 75

<210> 976
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 976

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn
65 70 75

<210> 977
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 977

Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn

65 70 75

<210> 978
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 978

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn
65 70 75

<210> 979
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 979

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Ala Ala Tyr Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn
65 70 75

<210> 980
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 980

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Cys
1 5 10 15

Ala Arg Thr Gly Gly Gly Gly Asn Gly Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Tyr Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Gly Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Thr Asn Thr Ala Tyr
65 70 75

<210> 981
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 981

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Gly Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn
65 70 75

<210> 982
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 982

Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Tyr Thr
20 25 30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Ala Arg
35 40 45

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Ala Thr His Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Gly Asn Trp Ser Asn
65 70 75

<210> 983
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 983

Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
20 25 30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Ala Arg
35 40 45

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Ala Thr His Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Gly Asn Trp Ser Asn
65 70 75

<210> 984
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 984

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Ala Thr His Trp Ser Asn
65 70 75

<210> 985
<211> 42
<212> PRT
<213> Homo Sapiens

<400> 985

Thr Gly Gly Gly Thr Asn Met Gly Asn Cys Ala Arg Gly Cys Asn Cys
1 5 10 15

Cys Asn Gly Gly Asn Cys Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala
20 25 30

Arg Thr Gly Gly Ala Thr Gly Gly Gly Asn
35 40

<210> 986
<211> 42
<212> PRT
<213> Homo Sapiens

<400> 986

Thr Gly Gly Gly Thr Asn Met Gly Asn Cys Ala Arg Gly Cys Asn Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala
20 25 30

Arg Thr Gly Gly Ala Thr Gly Gly Gly Asn
35 40

<210> 987
<211> 42
<212> PRT
<213> Homo Sapiens

<400> 987

Thr Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Tyr Thr Asn Gly Ala
20 25 30

Arg Thr Gly Gly Tyr Thr Asn Gly Cys Asn
35 40

<210> 988
<211> 42
<212> PRT
<213> Homo Sapiens

<400> 988

Thr Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Tyr Thr Asn Gly Ala
20 25 30

Arg Thr Gly Gly Tyr Thr Asn Gly Thr Asn
35 40

<210> 989
<211> 42
<212> PRT
<213> Homo Sapiens

<400> 989

Thr Gly Gly Gly Thr Asn Met Gly Asn Cys Ala Arg Gly Cys Asn Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala
20 25 30

Arg Thr Gly Gly Gly Thr Asn Trp Ser Asn
35 40

<210> 990
<211> 42
<212> PRT
<213> Homo Sapiens

<400> 990

Thr Gly Gly Gly Thr Asn Met Gly Asn Cys Ala Arg Gly Cys Asn Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala
20 25 30

Arg Thr Gly Gly Gly Thr Asn Gly Cys Asn
35 40

<210> 991
<211> 42
<212> PRT
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<400> 991

Thr Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala
20 25 30

Arg Thr Gly Gly Ala Thr His Gly Gly Asn
35 40

<210> 992
<211> 42
<212> PRT
<213> Homo Sapiens

<400> 992

Thr Gly Gly Gly Thr Asn Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala
20 25 30

Arg Thr Gly Gly Ala Thr His Gly Gly Asn
35 40

<210> 993
<211> 42
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<400> 993

Thr Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala
20 25 30

Arg Thr Gly Gly Ala Thr His Gly Gly Asn
35 40

<210> 994
<211> 42
<212> PRT
<213> Homo Sapiens

<400> 994

Thr Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Gly
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala
20 25 30

Arg Thr Gly Gly Ala Thr His Gly Gly Asn
35 40

<210> 995
<211> 42
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<400> 995

Thr Gly Gly Gly Thr Asn Met Gly Asn Cys Ala Arg Ala Thr Gly Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala
20 25 30

Arg Thr Gly Gly Ala Thr Gly Gly Gly Asn
35 40

<210> 996
<211> 42
<212> PRT
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<400> 996

Thr Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Trp Ser Asn Cys
1 5 10 15

Cys Asn Trp Ser Asn Met Gly Asn Gly Gly Asn Tyr Thr Asn Gly Ala
20 25 30

Arg Thr Gly Gly Tyr Thr Asn Gly Gly Asn
35 40

<210> 997
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 997

Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Cys Ala Asn Trp Ser
20 25 30

Asn Cys Ala Asn Gly Cys Asn Thr Ala Tyr Ala Thr Gly Gly Ala Arg
35 40 45

Tyr Thr Asn Met Gly Asn Trp Ser Asn Tyr Thr Asn Met Gly Asn Trp
50 55 60

Ser Asn Gly Ala Tyr Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 998
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 998

Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr Gly Cys Ala Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Thr His Trp Ser
20 25 30

Asn Cys Ala Asn Gly Cys Asn Thr Ala Tyr Ala Thr Gly Gly Ala Arg
35 40 45

Tyr Thr Asn Trp Ser Asn Met Gly Asn Tyr Thr Asn Met Gly Asn Trp
50 55 60

Ser Asn Gly Ala Tyr Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 999
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 999

Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr Gly Tyr Thr Asn Gly
1 5 10 15

Ala Arg Gly Ala Tyr Cys Ala Asn Trp Ser Asn Cys Ala Asn Gly Ala
20 25 30

Tyr Cys Ala Asn Gly Cys Asn Thr Ala Tyr Ala Thr Gly Gly Ala Arg
35 40 45

Tyr Thr Asn Trp Ser Asn Trp Ser Asn Tyr Thr Asn Met Gly Asn Trp
50 55 60

Ser Asn Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Cys Ala Asn
85 90 95

<210> 1000
<211> 96
<212> PRT
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<400> 1000

Met Gly Asn Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Ala
1 5 10 15

Ala Arg Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Trp Ser
20 25 30

Asn Cys Ala Arg Gly Thr Asn Gly Thr Asn Tyr Thr Asn Cys Ala Asn
35 40 45

Ala Thr Gly Cys Ala Asn Ala Ala Tyr Ala Thr Gly Gly Ala Tyr Cys
50 55 60

Cys Asn Gly Thr Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Cys Ala
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1001
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1001

Met Gly Asn Tyr Thr Asn Cys Ala Asn Ala Thr His Cys Ala Asn Ala
1 5 10 15

Ala Arg Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

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Tyr Cys Ala Arg Gly Thr Asn Gly Thr Asn Tyr Thr Asn Cys Ala Asn
        35                  40                  45

Ala Thr Gly Cys Ala Asn Ala Ala Tyr Ala Thr Gly Gly Ala Tyr Cys
    50                  55                  60

Cys Asn Gly Thr Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Cys Ala
65                  70                  75                  80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Cys Ala Tyr
                85                  90                  95
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<210> 1002
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1002

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Met Gly Asn Tyr Thr Asn Cys Ala Asn Ala Thr His Cys Ala Asn Ala
1               5                   10                  15

Ala Arg Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Cys Ala
            20                  25                  30

Asn Cys Ala Arg Gly Thr Asn Gly Thr Asn Tyr Thr Asn Cys Ala Asn
        35                  40                  45

Gly Thr Asn Cys Ala Asn Gly Ala Tyr Ala Thr Gly Gly Ala Tyr Cys
    50                  55                  60

Cys Asn Gly Thr Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Cys Ala
65                  70                  75                  80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Cys Ala Tyr
                85                  90                  95
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<210> 1003
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1003

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Met Gly Asn Tyr Thr Asn Cys Ala Asn Ala Thr His Cys Ala Asn Ala
1               5                   10                  15

Ala Arg Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Ala Ala
            20                  25                  30
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Tyr Cys Ala Arg Gly Thr Asn Gly Thr Asn Tyr Thr Asn Cys Ala Asn
35 40 45

Ala Thr Gly Cys Ala Asn Ala Ala Tyr Tyr Thr Asn Gly Ala Tyr Cys
50 55 60

Cys Asn Gly Thr Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Cys Ala
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Cys Ala Tyr
85 90 95

<210> 1004
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1004

Met Gly Asn Tyr Thr Asn Cys Ala Asn Ala Thr His Cys Ala Asn Ala
1 5 10 15

Ala Arg Gly Cys Asn Cys Ala Asn Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Arg Gly Thr Asn Gly Thr Asn Tyr Thr Asn Cys Ala Asn
35 40 45

Ala Thr Gly Cys Ala Asn Ala Ala Tyr Ala Thr Gly Gly Ala Tyr Cys
50 55 60

Cys Asn Gly Thr Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Cys Ala
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Cys Ala Tyr
85 90 95

<210> 1005
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1005

Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala Thr His Trp Ser Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Trp Ser Asn Tyr Thr Asn Thr Ala Tyr Tyr Thr Asn Cys Ala Arg
35 40 45

Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Met Gly Asn Gly
50 55 60

Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1006
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1006

Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala Thr His Trp Ser Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr Tyr Thr Asn Cys Ala Arg
35 40 45

Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Met Gly Asn Gly
50 55 60

Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Ala Ala Arg
85 90 95

<210> 1007
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1007

Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala Thr His Trp Ser Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr Tyr Thr Asn Cys Ala Arg
35 40 45

Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Met Gly Asn Gly
50 55 60

Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Ala
65 70 75 80

Arg Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Ala Ala Arg
85 90 95

<210> 1008
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1008

Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala Thr His Trp Ser Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser Asn Ala Thr Gly Ala Ala
20 25 30

Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr Tyr Thr Asn Cys Ala Arg
35 40 45

Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Met Gly Asn Gly
50 55 60

Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1009
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1009

Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala Thr His Trp Ser Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr Tyr Thr Asn Cys Ala Arg
35 40 45

Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Met Gly Asn Gly
50 55 60

Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1010
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1010

Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala Thr His Trp Ser Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr Tyr Thr Asn Cys Ala Arg
35 40 45

Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Met Gly Asn Gly
50 55 60

Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Thr Asn Tyr Thr Asn
85 90 95

<210> 1011
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1011

Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala Thr His Trp Ser Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Asn Tyr Thr Asn Gly Ala Tyr Tyr Thr Asn Cys Ala Arg
35 40 45

Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Met Gly Asn Gly
50 55 60

Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1012
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1012

Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala Thr His Trp Ser Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Trp Ser Asn Tyr Thr Asn Thr Thr Tyr Tyr Thr Asn Cys Ala Arg
35 40 45

Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Met Gly Asn Gly
50 55 60

Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Tyr Thr Asn
85 90 95

<210> 1013
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1013

Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala Thr His Trp Ser Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Trp Ser Asn Gly Thr Asn Thr Ala Tyr Tyr Thr Asn Cys Ala Arg
35 40 45

Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Met Gly Asn Gly
50 55 60

Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1014
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1014

Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala Thr His Trp Ser Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Trp Ser Asn Tyr Thr Asn Thr Ala Tyr Tyr Thr Asn Cys Ala Arg
35 40 45

Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Met Gly Asn Gly
50 55 60

Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1015
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1015

Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Gly
1 5 10 15

Thr Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Ala Ala Tyr
35 40 45

Tyr Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Cys Ala Asn Gly
50 55 60

Cys Asn Gly Cys Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1016
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1016

Met Gly Asn Gly Thr Asn Ala Ala Tyr Ala Thr Gly Trp Ser Asn Gly
1 5 10 15

Thr Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Ala Ala Arg
35 40 45

Tyr Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Cys Ala Asn Gly
50 55 60

Cys Asn Gly Cys Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1017
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1017

Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Gly
1 5 10 15

Thr Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Ala Ala Arg
35 40 45

Tyr Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Cys Ala Asn Gly
50 55 60

Cys Asn Gly Cys Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1018
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1018

Met Gly Asn Ala Thr His Cys Ala Asn Ala Thr His Trp Ser Asn Gly
1 5 10 15

Cys Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Ala Ala Arg
35 40 45

Tyr Thr Asn Ala Ala Tyr Trp Ser Asn Gly Thr Asn Cys Ala Asn Gly
50 55 60

Cys Asn Gly Cys Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1019
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1019

Met Gly Asn Ala Thr His Cys Ala Asn Ala Ala Arg Trp Ser Asn Gly
1 5 10 15

Thr Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Ala Ala Arg
35 40 45

Tyr Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Cys Ala Asn Gly
50 55 60

Cys Asn Gly Cys Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1020
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1020

Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Gly
1 5 10 15

Thr Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Ala Ala Arg
35 40 45

Tyr Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Cys Ala Asn Gly
50 55 60

Cys Asn Gly Cys Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Trp Ser Asn
85 90 95

<210> 1021
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<212> PRT
<213> Homo Sapiens

<400> 1021

Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Gly
1 5 10 15

Thr Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Ala Ala Arg
35 40 45

Tyr Thr Asn Thr Thr Tyr Trp Ser Asn Gly Thr Asn Cys Ala Asn Gly
50 55 60

Cys Asn Gly Cys Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Thr Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1022
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1022

Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr Gly Trp Ser Asn Gly
1 5 10 15

Thr Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Ala Ala Arg
35 40 45

Tyr Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Cys Ala Asn Gly
50 55 60

Cys Asn Gly Cys Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1023
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1023

Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Ala
1 5 10 15

Thr His Gly Thr Asn Cys Ala Asn Trp Ser Asn Met Gly Asn Ala Ala
20 25 30

Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Ala Ala Arg
35 40 45

Tyr Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Cys Ala Asn Gly
50 55 60

Cys Asn Gly Cys Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1024
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1024

Cys Ala Arg Gly Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Gly
1 5 10 15

Cys Asn Gly Ala Tyr Ala Ala Arg Trp Ser Asn Ala Thr His Trp Ser
20 25 30

Asn Cys Ala Asn Gly Cys Asn Thr Ala Tyr Tyr Thr Asn Cys Ala Arg
35 40 45

Thr Gly Gly Trp Ser Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg Gly
50 55 60

Cys Asn Trp Ser Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Ala Thr
65 70 75 80

Gly Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1025
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1025

Cys Ala Arg Gly Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Gly
1 5 10 15

Cys Asn Gly Ala Tyr Ala Ala Arg Trp Ser Asn Ala Thr His Ala Ala
20 25 30

Tyr Cys Ala Asn Gly Cys Asn Thr Ala Tyr Tyr Thr Asn Cys Ala Arg
35 40 45

Thr Gly Gly Trp Ser Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg Gly
50 55 60

Cys Asn Trp Ser Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Ala Thr
65 70 75 80

Gly Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1026
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1026

Met Gly Asn Ala Thr His Cys Ala Asn Ala Thr His Ala Ala Tyr Cys
1 5 10 15

Cys Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Cys Ala Arg
35 40 45

Tyr Thr Asn Ala Ala Tyr Trp Ser Asn Gly Thr Asn Cys Ala Asn Cys
50 55 60

Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1027
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 1027

Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Tyr
1 5 10 15

Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser
20 25 30

Asn

<210> 1028
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 1028

Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Cys
1 5 10 15

Ala Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser
20 25 30

Asn

<210> 1029
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 1029

Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Ala
1 5 10 15

Thr Gly Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser
20 25 30

Asn

<210> 1030
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 1030

Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Trp Ser Asn Tyr
1 5 10 15

Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Cys Cys
20 25 30

Asn

<210> 1031
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 1031

Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Ala
1 5 10 15

Ala Arg Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser
20 25 30

Asn

<210> 1032
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 1032

Thr Gly Gly Gly Gly Asn Met Gly Asn Gly Gly Asn Cys Ala Asn Tyr
1 5 10 15

Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser
20 25 30

Asn

<210> 1033
<211> 16
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(1)
<223> X1 is selected from the group consisting of H and LI

<400> 1033

Xaa Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 1034
<211> 16
<212> PRT
<213> Homo sapiens

<220>

<221> MISC_FEATURE
<222> (6)..(6)
<223> X1 is selected from the group consisting of D and V

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> X2 is selected from the group consisting of D and E

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> X3 is selected from the group consisting of K and R

<400> 1034

Leu Ile Tyr Trp Asn Xaa Xaa Lys Arg Tyr Ser Pro Ser Leu Xaa Ser
1 5 10 15

<210> 1035
<211> 13
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(1)
<223> X1 is selected from the group consisting of E and S

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> X2 is selected from the group consisting of D, G and no amino
acid

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> X3 is selected from the group consisting of D, N and no amino
acid

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> X4 is selected from the group consisting of G and no amino acid

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> X5 is selected from the group consisting of G and no amino acid

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> X6 is selected from the group consisting of W, Y and no amino

acid

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> X7 is selected from the group consisting of I, N and Y

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> X8 is selected from the group consisting of A and Y

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> X9 is selected from the group consisting of G, V and Y

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> X10 is selected from the group consisting of A, F and G

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> X11 is selected from the group consisting of F, L and M

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> X12 is selected from the group consisting of V and Y

<400> 1035

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa
1 5 10

<210> 1036
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> X1 is selected from the group consisting of G and no amino acid

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> X2 is selected from the group consisting of K, L and Y

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> X3 is selected from the group consisting of A, G and S

<220>
<221> MISC_FEATURE

<222> (5)..(5)
<223> X4 is selected from the group consisting of S, V and Y

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> X5 is selected from the group consisting of A and G

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> X6 is selected from the group consisting of G and no amino acid

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> X7 is selected from the group consisting of T and no amino acid

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> X8 is selected from the group consisting of S and no amino acid

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> X9 is selected from the group consisting of Y and no amino acid

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> X10 is selected from the group consisting of W and Y

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> X11 is selected from the group consisting of G, S and Y

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> X12 is selected from the group consisting of F and Y

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> X13 is selected from the group consisting of G and no amino acid

<220>
<221> MISC_FEATURE
<222> (16)..(16)
<223> X14 is selected from the group consisting of M and no amino acid

<220>
<221> MISC_FEATURE
<222> (18)..(18)

<223> X15 is selected from the group consisting of V and Y

<400> 1036

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Xaa Xaa
1 5 10 15

Asp Xaa

<210> 1037
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(1)
<223> X1 is selected from the group consisting of D, G, L, S and no
amino acid

<220>
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amino acid

<220>
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acid

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acid

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<220>
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<220>
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<220>
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<400> 1037

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> 1038
<211> 19
<212> PRT
<213> Homo sapiens

<220>
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<223> X1 is selected from the group consisting of E, D and no amino
acid

<220>
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<220>
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<223> X3 is selected from the group consisting of I, V, Y and no amino
acid

<220>
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<223> X4 is selected from the group consisting of A, G, L and N

<220>
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<220>
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<220>
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acid

<220>
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<222> (8)..(8)
<223> X8 is selected from the group consisting of G, T and no amino
acid

<220>
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acid

<220>
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acid

<220>
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acid

<220>
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<220>
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<220>
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acid

<220>
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<223> X17 is selected from the group consisting of F and M

<220>
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<400> 1038

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Asp Xaa

<210> 1039
<211> 23
<212> PRT
<213> Homo sapiens

<220>
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<223> X1 is selected from the group consisting of A, D, G, S and T

<220>
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<223> X2 is selected from the group consisting of A, E, G, L, N, R, Y
and no amino acid

<220>
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and no amino acid

<220>
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<223> X4 is selected from the group consisting of D, G, R, S, V, Y and
no amino acid

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> X5 is selected from the group consisting of A, G, I, S, V, Y and
no amino acid

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> X6 is selected from the group consisting of F, G, L, R, V and no
amino acid

<220>
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<222> (7)..(7)
<223> X7 is selected from the group consisting of L, T, Y and no amino
acid

<220>
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<222> (8)..(8)
<223> X8 is selected from the group consisting of Y and no amino acid

<220>
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<222> (9)..(9)
<223> X9 is selected from the group consisting of Y and no amino acid

<220>
<221> MISC_FEATURE

<222> (10)..(10)
<223> X10 is selected from the group consisting of D and no amino acid

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> X11 is selected from the group consisting of S and no amino acid

<220>
<221> MISC_FEATURE
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<223> X12 is selected from the group consisting of S and no amino acid

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> X13 is selected from the group consisting of G and no amino acid

<220>
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<222> (14)..(14)
<223> X14 is selected from the group consisting of D, L, M, S, Y and no
amino acid

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> X15 is selected from the group consisting of H, I, P, V, W and no
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<220>
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<223> X16 is selected from the group consisting of F, G, L, R, S, Y and
no amino acid

<220>
<221> MISC_FEATURE
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<223> X17 is selected from the group consisting of D, F, V, W, Y and no
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<220>
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<222> (18)..(18)
<223> X18 is selected from the group consisting of C, F, L, P, S and Y

<220>
<221> MISC_FEATURE
<222> (19)..(19)
<223> X19 is selected from the group consisting of D, F, G and Y

<220>

<221> MISC_FEATURE
<222> (20)..(20)
<223> X20 is selected from the group consisting of A, C, G, P, R, V and
Y

<220>
<221> MISC_FEATURE
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<223> X21 is selected from the group consisting of F, L, M, S and no
amino acid

<220>
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<222> (22)..(22)
<223> X22 is selected from the group consisting of A, D and no amino
acid

<220>
<221> MISC_FEATURE
<222> (23)..(23)
<223> X23 is selected from the group consisting of I, L, V, Y and no
amino acid

<400> 1039

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20

<210> 1040
<211> 14
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(1)
<223> X1 is selected from the group consisting of M and V

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> X2 is selected from the group consisting of S and no amino acid

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> X3 is selected from the group consisting of F and no amino acid

<220>
<221> MISC_FEATURE

<222> (11)..(11)
<223> X4 is selected from the group consisting of V and no amino acid

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> X5 is selected from the group consisting of F and M

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> X6 is selected from the group consisting of V and Y

<400> 1040

Xaa Tyr Ser Ser Gly Trp Xaa Xaa Tyr Gly Xaa Xaa Asp Xaa
1 5 10

<210> 1041
<211> 8
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> X1 is selected from the group consisting of G, H, L, N and R

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> X2 is selected from the group consisting of E, T and W

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> X3 is selected from the group consisting of L, N, T and V

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> X4 is selected from the group consisting of D and E

<400> 1041

Arg Xaa Xaa Xaa Pro Phe Xaa Tyr
1 5

<210> 1042
<211> 208
<212> PRT
<213> Homo sapiens

<400> 1042

Met Lys Leu Leu Pro Ser Val Val Leu Lys Leu Phe Leu Ala Ala Val
1 5 10 15

Leu Ser Ala Leu Val Thr Gly Glu Ser Leu Glu Arg Leu Arg Arg Gly
20 25 30

Leu Ala Ala Gly Thr Ser Asn Pro Asp Pro Pro Thr Val Ser Thr Asp
35 40 45

Gln Leu Leu Pro Leu Gly Gly Gly Arg Asp Arg Lys Val Arg Asp Leu
50 55 60

Gln Glu Ala Asp Leu Asp Leu Leu Arg Val Thr Leu Ser Ser Lys Pro
65 70 75 80

Gln Ala Leu Ala Thr Pro Asn Lys Glu Glu His Gly Lys Arg Lys Lys
85 90 95

Lys Gly Lys Gly Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr
100 105 110

Lys Asp Phe Cys Ile His Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg
115 120 125

Ala Pro Ser Cys Ile Cys His Pro Gly Tyr His Gly Glu Arg Cys His
130 135 140

Gly Leu Ser Leu Pro Val Glu Asn Arg Leu Tyr Thr Tyr Asp His Thr
145 150 155 160

Thr Ile Leu Ala Val Val Ala Val Val Leu Ser Ser Val Cys Leu Leu
165 170 175

Val Ile Val Gly Leu Leu Met Phe Arg Tyr His Arg Arg Gly Gly Tyr
180 185 190

Asp Val Glu Asn Glu Glu Lys Val Lys Leu Gly Met Thr Asn Ser His
195 200 205

<210> 1043
<211> 19
<212> PRT
<213> Homo sapiens

<400> 1043

Met Lys Leu Leu Pro Ser Val Val Leu Lys Leu Phe Leu Ala Ala Val
1 5 10 15

Leu Ser Ala

<210> 1044
<211> 149
<212> PRT
<213> Homo sapiens

<400> 1044

Met Lys Leu Leu Pro Ser Val Val Leu Lys Leu Phe Leu Ala Ala Val
1 5 10 15

Leu Ser Ala Leu Val Thr Gly Glu Ser Leu Glu Arg Leu Arg Arg Gly
20 25 30

Leu Ala Ala Gly Thr Ser Asn Pro Asp Pro Pro Thr Val Ser Thr Asp
35 40 45

Gln Leu Leu Pro Leu Gly Gly Gly Arg Asp Arg Lys Val Arg Asp Leu
50 55 60

Gln Glu Ala Asp Leu Asp Leu Leu Arg Val Thr Leu Ser Ser Lys Pro
65 70 75 80

Gln Ala Leu Ala Thr Pro Asn Lys Glu Glu His Gly Lys Arg Lys Lys
85 90 95

Lys Gly Lys Gly Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr
100 105 110

Lys Asp Phe Cys Ile His Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg
115 120 125

Ala Pro Ser Cys Ile Cys His Pro Gly Tyr His Gly Glu Arg Cys His
130 135 140

Gly Leu Ser Leu Pro
145

<210> 1045
<211> 87
<212> PRT
<213> Homo sapiens

<400> 1045

Asp Leu Gln Glu Ala Asp Leu Asp Leu Leu Arg Val Thr Leu Ser Ser
1 5 10 15

Lys Pro Gln Ala Leu Ala Thr Pro Asn Lys Glu Glu His Gly Lys Arg

20 25 30

Lys Lys Lys Gly Lys Gly Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg
35 40 45

Lys Tyr Lys Asp Phe Cys Ile His Gly Glu Cys Lys Tyr Val Lys Glu
50 55 60

Leu Arg Ala Pro Ser Cys Ile Cys His Pro Gly Tyr His Gly Glu Arg
65 70 75 80

Cys His Gly Leu Ser Leu Pro
85

<210> 1046
<211> 43
<212> PRT
<213> Homo sapiens

<400> 1046

Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys Ile His Gly Glu Cys Lys
1 5 10 15

Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys Ile Cys His Pro Gly Tyr
20 25 30

His Gly Glu Arg Cys His Gly Leu Ser Leu Pro
35 40

<210> 1047
<211> 149
<212> PRT
<213> Homo sapiens

<400> 1047

Met Lys Leu Leu Pro Ser Val Val Leu Lys Leu Phe Leu Ala Ala Val
1 5 10 15

Leu Ser Ala Leu Val Thr Gly Glu Ser Leu Glu Arg Leu Arg Arg Gly
20 25 30

Leu Ala Ala Gly Thr Ser Asn Pro Asp Pro Pro Thr Val Ser Thr Asp
35 40 45

Gln Leu Leu Pro Leu Gly Gly Gly Arg Asp Arg Lys Val Arg Asp Leu
50 55 60

Gln Glu Ala Asp Leu Asp Leu Leu Arg Val Thr Leu Ser Ser Lys Pro

65 70 75 80

Gln Ala Leu Ala Thr Pro Asn Lys Glu Glu His Gly Lys Arg Lys Lys
85 90 95

Lys Gly Lys Gly Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr
100 105 110

Lys Asp Phe Cys Ile His Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg
115 120 125

Ala Pro Ser Cys Ile Cys His Pro Gly Tyr His Gly Glu Arg Cys His
130 135 140

Gly Leu Ser Leu Pro
145

<210> 1048
<211> 32
<212> DNA
<213> Artificial

<220>
<223> forward primer

<400> 1048
gggttaacgc caccatgaag ctgctgccgt cg
32

<210> 1049
<211> 28
<212> DNA
<213> Artificial

<220>
<223> reverse primer

<400> 1049
ccgctcgagg tgggaattag tcatgccc
28

<210> 1050
<211> 31
<212> DNA
<213> Artificial

<220>
<223> forward primer

<400> 1050
ggaattcgcc accatgaagc tgctgccgtc g
31

<210> 1051
<211> 30
<212> DNA
<213> Artificial

<220>
<223> reverse primer

<400> 1051
ccgctcgagg tgggagctag cagccacgcc
30

<210> 1052
<211> 44
<212> PRT
<213> Homo sapiens

<400> 1052

Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys Ile His Gly Glu Cys
1 5 10 15

Lys Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys Ile Cys His Pro Gly
20 25 30

Tyr His Gly Glu Arg Cys His Gly Leu Ser Leu Pro
35 40

<210> 1053
<211> 49
<212> PRT
<213> Homo sapiens

<400> 1053

Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Tyr Cys
1 5 10 15

Ile His Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys
20 25 30

Ile Cys His Pro Gly Tyr His Gly Glu Arg Cys His Gly Leu Ser Leu
35 40 45

Pro

<210> 1054
<211> 49
<212> PRT
<213> Homo sapiens

<400> 1054

Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys
1 5 10 15

Ile His Gly Glu Cys Lys Tyr Val Lys Glu Phe Arg Ala Pro Ser Cys
20 25 30

Ile Cys His Pro Gly Tyr His Gly Glu Arg Cys His Gly Leu Ser Leu
35 40 45

Pro

<210> 1055
<211> 49
<212> PRT
<213> Homo sapiens

<400> 1055

Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys
1 5 10 15

Ile His Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys
20 25 30

Ile Cys His Pro Gly Tyr His Gly His Arg Cys His Gly Leu Ser Leu
35 40 45

Pro

<210> 1056
<211> 49
<212> PRT
<213> Homo sapiens

<400> 1056

Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys
1 5 10 15

Ile His Gly Glu Cys Arg Tyr Leu Gln Glu Leu Arg Ala Pro Ser Cys
20 25 30

Ile Cys His Pro Gly Tyr His Gly Glu Arg Cys His Gly Leu Ser Leu
35 40 45

Pro

<210> 1057
<211> 49
<212> PRT
<213> Homo sapiens

<400> 1057

Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Tyr Cys
1 5 10 15

Ile His Gly Glu Cys Arg Tyr Leu Gln Glu Leu Arg Ala Pro Ser Cys
20 25 30

Ile Cys His Pro Gly Tyr His Gly Glu Arg Cys His Gly Leu Ser Leu
35 40 45

Pro

<210> 1058
<211> 49
<212> PRT
<213> Homo sapiens

<400> 1058

Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys
1 5 10 15

Ile His Gly Glu Cys Arg Tyr Leu Gln Glu Leu Arg Ala Pro Ser Cys
20 25 30

Ile Cys His Pro Gly Tyr His Gly His Arg Cys His Gly Leu Ser Leu
35 40 45

Pro

<210> 1059
<211> 49
<212> PRT
<213> Homo sapiens

<400> 1059

Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys
1 5 10 15

Ile His Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys
20 25 30

Lys Cys Leu Pro Gly Tyr His Gly Glu Arg Cys His Gly Leu Ser Leu

35 40 45

Pro

<210> 1060
<211> 49
<212> PRT
<213> Homo sapiens

<400> 1060

Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Tyr Cys
1 5 10 15

Ile His Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys
20 25 30

Lys Cys Leu Pro Gly Tyr His Gly Glu Arg Cys His Gly Leu Ser Leu
35 40 45

Pro

<210> 1061
<211> 49
<212> PRT
<213> Homo sapiens

<400> 1061

Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys
1 5 10 15

Ile His Gly Glu Cys Lys Tyr Val Lys Glu Phe Arg Ala Pro Ser Cys
20 25 30

Lys Cys Leu Pro Gly Tyr His Gly Glu Arg Cys His Gly Leu Ser Leu
35 40 45

Pro

<210> 1062
<211> 49
<212> PRT
<213> Homo sapiens

<400> 1062

Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys
1 5 10 15

Ile His Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys
20 25 30

Ile Cys His Pro Gly Tyr His Gly Glu Arg Cys His Gly Leu Ser Thr
35 40 45

Pro

<210> 1063
<211> 49
<212> PRT
<213> Homo sapiens

<400> 1063

Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys
1 5 10 15

Ile His Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys
20 25 30

Ile Cys His Pro Gly Tyr His Gly His Arg Cys His Gly Leu Ser Thr
35 40 45

Pro

<210> 1064
<211> 50
<212> PRT
<213> Homo sapiens

<400> 1064

Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys
1 5 10 15

Leu His Asp Gly Val Cys Lys Tyr Val Lys Glu Leu Arg Ala Pro Ser
20 25 30

Cys Ile Cys His Pro Gly Tyr His Gly Glu Arg Cys His Gly Leu Ser
35 40 45

Leu Pro
50

<210> 1065
<211> 214

<212> PRT
<213> Homo Sapiens

<400> 1065

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                  10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Leu Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Ser Phe Tyr Thr Pro Ile
                85                  90                  95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
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<210> 1066

<211> 23
<212> PRT
<213> Homo Sapiens

<400> 1066

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys
20

<210> 1067
<211> 23
<212> PRT
<213> Homo Sapiens

<400> 1067

Asn Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys
20

<210> 1068
<211> 23
<212> PRT
<213> Homo Sapiens

<400> 1068

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Thr Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys
20

<210> 1069
<211> 23
<212> PRT
<213> Homo Sapiens

<400> 1069

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Gly Val Thr Ile Thr Cys
20

<210> 1070
<211> 23
<212> PRT

<213> Homo Sapiens

<400> 1070

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Ala Ile Thr Cys
20

<210> 1071
<211> 23
<212> PRT
<213> Homo Sapiens

<400> 1071

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys
20

<210> 1072
<211> 23
<212> PRT
<213> Homo Sapiens

<400> 1072

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Arg Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys
20

<210> 1073
<211> 23
<212> PRT
<213> Homo Sapiens

<400> 1073

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys
20

<210> 1074
<211> 15
<212> PRT
<213> Homo Sapiens

<400> 1074

Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
1 5 10 15

<210> 1075
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 1075

Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 1076
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 1076

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 1077
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 1077

Gly Ala Arg Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Cys Ala Asn Cys Cys Asn Tyr Thr Asn Trp Ser Asn Trp Ser
20 25 30

Asn Cys Cys Asn Gly Thr Asn Cys Ala Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr
65

<210> 1078
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 1078

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Tyr Thr
20 25 30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr
65

<210> 1079
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 1079

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Gly
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 1080
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 1080

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Gly Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 1081
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 1081

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 1082
<211> 69
<212> PRT

<213> Homo Sapiens

<400> 1082

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Gly Cys Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 1083
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 1083

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 1084
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 1084

Thr Gly Gly Thr Thr Tyr Cys Ala Arg Cys Ala Arg Met Gly Asn Cys
1 5 10 15

1335

Cys Asn Gly Gly Asn Cys Ala Arg Trp Ser Asn Cys Cys Asn Met Gly
20 25 30

Asn Met Gly Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 1085
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 1085

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn
65 70 75

<210> 1086
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 1086

Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Cys
1 5 10 15

Ala Arg Thr Gly Gly Gly Gly Asn Gly Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Tyr Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Gly Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Thr Asn Thr Ala Tyr
65 70 75

<210> 1087
<211> 42
<212> PRT
<213> Homo Sapiens

<400> 1087

Thr Gly Gly Gly Thr Asn Met Gly Asn Cys Ala Arg Gly Cys Asn Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala
20 25 30

Arg Thr Gly Gly Gly Thr Asn Trp Ser Asn
35 40

<210> 1088
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1088

Met Gly Asn Thr Thr Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Asn Tyr Thr Asn Thr Thr Tyr Tyr Thr Asn Cys Ala Arg
35 40 45

Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Met Gly Asn Gly
50 55 60

Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1089
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<400> 1089

Xaa Gln Xaa Xaa Xaa Xaa Pro Xaa Xaa
1 5

<210> 1090
<211> 9
<212> PRT
<213> Homo sapiens

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<400> 1090

Gln Gln Xaa Xaa Xaa Xaa Xaa Ile Thr
1 5

<210> 1091
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<212> PRT
<213> Homo sapiens

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<400> 1091

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr

1 5

<210> 1092
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<212> PRT
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<220>
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<400> 1092

Gln Xaa Xaa Asp Xaa Leu Pro Xaa Xaa
1 5

<210> 1093
<211> 10
<212> PRT
<213> Homo sapiens

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<400> 1093

Gln Gln Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa
1 5 10

<210> 1094
<211> 10
<212> PRT
<213> Homo sapiens

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<220>
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<400> 1094

Xaa Gln Tyr Xaa Xaa Xaa Xaa Xaa Xaa Phe
1 5 10

<210> 1095
<211> 10
<212> PRT
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<400> 1095

Gly Tyr Thr Xaa Thr Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> 1096
<211> 10
<212> PRT
<213> Homo sapiens

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<400> 1096

Gly Tyr Xaa Phe Thr Ser Tyr Trp Ile Gly
1 5 10

<210> 1097
<211> 10
<212> PRT
<213> Homo sapiens

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<400> 1097

Gly Phe Thr Phe Xaa Ser Xaa Xaa Met His
1 5 10

<210> 1098
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<212> PRT
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<400> 1098

Gly Phe Xaa Phe Ser Xaa Tyr Xaa Met Xaa
1 5 10

<210> 1099
<211> 12
<212> PRT
<213> Homo sapiens

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<400> 1099

Gly Xaa Ser Xaa Ser Xaa Xaa Xaa Xaa Xaa Trp Xaa
1 5 10

<210> 1100
<211> 12
<212> PRT
<213> Homo sapiens

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<400> 1100

Gly Phe Ser Leu Xaa Thr Gly Gly Val Gly Val Gly
1 5 10

<210> 1101
<211> 16
<212> PRT
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<400> 1101

Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Thr Xaa Xaa Xaa Gln Lys Xaa Xaa
1 5 10 15

<210> 1102
<211> 17
<212> PRT
<213> Homo sapiens

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<220>
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<400> 1102

Ile Ile Tyr Pro Xaa Asp Ser Asp Xaa Arg Tyr Ser Pro Ser Phe Gln
1 5 10 15

Gly

<210> 1103
<211> 17
<212> PRT
<213> Homo sapiens

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<400> 1103

Xaa Ile Xaa Xaa Asp Gly Ser Xaa Xaa Xaa Tyr Xaa Asp Ser Val Xaa
1 5 10 15

Gly

<210> 1104
<211> 17
<212> PRT
<213> Homo sapiens

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<221> MISC_FEATURE
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<400> 1104

Xaa Ile Ser Xaa Ser Xaa Xaa Xaa Xaa Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 1105
<211> 18
<212> PRT
<213> Homo sapiens

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<400> 1105

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Xaa Ser Xaa
1 5 10 15

Lys Ser

<210> 1106
<211> 16

<212> PRT
<213> Homo sapiens

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<400> 1106

Xaa Ser Ser Gln Ser Leu Xaa Xaa Ser Asp Gly Xaa Thr Tyr Leu Xaa
1 5 10 15

<210> 1107
<211> 11
<212> PRT
<213> Homo sapiens

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<220>
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<223> X2 is selected from the group consisting of R and S

<400> 1107

Arg Ala Ser Gln Xaa Ile Ser Xaa Tyr Leu Asn
1 5 10

<210> 1108
<211> 11
<212> PRT
<213> Homo sapiens

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<220>
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<400> 1108

Arg Ala Ser Gln Xaa Ile Xaa Xaa Xaa Leu Xaa
1 5 10

<210> 1109
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> X1 is selected from the group consisting of S and T

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> X2 is selected from the group consisting of D and N

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> X3 is selected from the group consisting of S and Y

<400> 1109

Gln Ala Ser Gln Asp Ile Xaa Xaa Xaa Leu Asn
1 5 10

<210> 1110
<211> 12

<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> X1 is selected from the group consisting of S and T

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> X2 is selected from the group consisting of I and S

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> X3 is selected from the group consisting of R and S

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> X4 is selected from the group consisting of S, N and no amino
acid

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> X5 is selected from the group consisting of Y and no amino acid

<400> 1110

Arg Ala Ser Gln Xaa Val Xaa Xaa Xaa Xaa Leu Ala
1 5 10

<210> 1111
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> X1 is selected from the group consisting of N and S

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> X2 is selected from the group consisting of I and V

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> X3 is selected from the group consisting of D and Y

<220>
<221> MISC_FEATURE
<222> (9)..(9)

<223> X4 is selected from the group consisting of N, R and S

<220>
<221> MISC_FEATURE
<222> (17)..(17)
<223> X5 is selected from the group consisting of A and V

<400> 1111

Lys Ser Ser Gln Xaa Xaa Leu Xaa Xaa Ser Asn Asn Lys Asn Tyr Leu
1 5 10 15

Xaa

<210> 1112
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> X1 is selected from the group consisting of E and K

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> X2 is selected from the group consisting of I and V

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> X3 is selected from the group consisting of R and W

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> X4 is selected from the group consisting of D and F

<400> 1112

Xaa Xaa Ser Asn Xaa Xaa Ser
1 5

<210> 1113
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> X1 is selected from the group consisting of A and T

<220>
<221> MISC_FEATURE

<222> (2)..(2)
<223> X2 is selected from the group consisting of A, E and V

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> X3 is selected from the group consisting of S and T

<400> 1113

Xaa Xaa Ser Xaa Leu Gln Ser
1 5

<210> 1114
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> X1 is selected from the group consisting of A and V

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> X2 is selected from the group consisting of S and T

<400> 1114

Xaa Ala Ser Xaa Leu Gln Ser
1 5

<210> 1115
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> X1 is selected from the group consisting of I and N

<400> 1115

Asp Ala Ser Xaa Leu Glu Thr
1 5

<210> 1116
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (4)..(4)

<223> X1 is selected from the group consisting of A and T

<400> 1116

Trp Ala Ser Xaa Arg Glu Ser
1 5

PROTEINAS DE UNION A ANTIGENO DE FACTOR DE CRECIMIENTO TIPO FACTOR DE CRECIMIENTO EPIDERMICO DE UNION A HEPARINA

Antecedentes de la invención

La familia del receptor de factor de crecimiento epidérmico humano (HER) comprende cuatro tirosina cinasas receptoras distintas conocidas como HER1 (o erbB1), HER2 (o erbB2), HER3 (o erbB3) y HER4 (o erbB4). HER1 también se conoce comúnmente como receptor de factor de crecimiento epidérmico (EGFR). Con la excepción de HER3, estos receptores tienen actividades de proteína tirosina cinasa intrínsecas específicas objetivo de fosfo-receptor. Los miembros de la familia HER son expresados en la mayoría de las células epiteliales así como en un número de diferentes tipos de células tumorales. Por ejemplo, los receptores de la familia HER son expresados en células tumorales de origen epitelial, y de origen mesenquimático. Más aún, las tirosina cinasas receptoras de HER están implicadas en la proliferación celular y angiogénesis, las cuales están asociadas con enfermedades tales como cáncer. Por ejemplo, EGFR es frecuentemente sobre-expresado o activado aberrantemente en cánceres de seno, cánceres hepáticos, cánceres renales, leucemia, cánceres bronquiales, cánceres pancreáticos y cánceres gastrointestinales tales como cánceres de colon, rectal o de estómago. Altos niveles del

receptor de EGF se correlacionan también con un pronóstico y respuesta a tratamiento deficientes (Wright *et al.*, 1992, *Br. J. Cancer* 65: 118-121). Así, la interrupción de la traducción de señales desde y hacia estas cinasas tendría un efecto antiproliferativo, y de esta manera, terapéutico en un número de tipos de células tumorales y cánceres.

La actividad enzimática de las tirosina cinasas receptoras puede ser estimulada mediante sobre-expresión y/o mediante dimerización mediada por ligandos (Heldin, 1995, *Cell* 80: 213-223). La activación de homodímeros y heterodímeros receptores da como resultado la fosforilación de residuos de tirosina en los receptores, los cuales a su vez fosforilan residuos de tirosina de otras moléculas, incluyendo proteínas intracelulares. (Ullrich *et al.*, 1990, *Cell* 61:203-212). Esto es seguido por la activación de vías de señalización intracelular tales como aquellas que incluyen la proteína cinasa activada por mitógeno (cinasa MAP) (Dhillon et al., 2007, *Oncogene* 26: 3279-3290) y la fosfatidilinositol 3-cinasa (cinasa PI3). Aunque la activación de estas vías ha mostrado incrementar la proliferación celular e inhibir apoptosis, la inhibición de señalización mediada por miembros de la familia de HER ya sea por inhibidores de molécula pequeña o anticuerpos monoclonales ha mostrado inhibir la proliferación de células y promover apoptosis (Prenzel *et al.*, 2001, *Endocr. Relat.*

1957

Cancer 8: 11-31).

El factor de crecimiento tipo factor de crecimiento epidérmico de unión a heparina (HB-EGF) es una proteína O-glicosilada de 22 kDa (Higahiyama *et al.*, 1992, *J Biol Chem* 267: 6205-6212). En su forma madura, HB-EGF se une a y activa al receptor EGF y HER4 (Elenius et al., 1997, EMBO 16:1268-1278). HB-EGF es el mediador clave de la proliferación celular inducida por receptor acoplado a proteína G (GPCR) mediante un proceso llamado señalización de paso de triple membrana (TMPS) (Prenzel *et al.*, 1999, *Nature* 402:884-888, revisión en Fischer *et al.*, 2003, *Biochem. Soc. Trans* 31:1203-1208). Se ha demostrado que HB-EGF promueve proliferación celular así como angiogénesis (Zushi *et al.*, 1997, *Int J Cancer* 73:917-923; Abramovitch *et al.*, 1998, *FEBS letters* 425:441-447). HB-EGF también ha demostrado jugar un papel en un número de cánceres, es decir, ha estado ligado al comportamiento agresivo de tumores ováricos (Tanaka *et al.*, 2005, *Clin. Cancer Res.* 11:4783-4792). Más aún, HB-EGF es esencial para la formación de tumores de xenoinjerto mediante líneas de células de cáncer ovárico. La sobre-expresión de HB-EGF (tipo silvestre o una forma secretada) acelera la formación de tumores en células SKOV3 y RMG-1. La supresión de HB-EGF endógeno usando ARNsi, no obstante, detuvo o retrasó la formación de tumores por células SKOV3 y RMG-1. Miyamoto, 2004, *Cancer Res.* 64:5720. Como se sugiere por la

evidencia anterior, la inhibición de la expresión de HB-EGF o actividad puede inhibir la formación de tumores.

De manera similar, HB-EGF es un marcador de pronóstico deficiente en algunos cánceres, incluyendo cánceres de vejiga humanos (Thogersen *et al.*, 2001, *Cancer Res.* 61:6227-6233). Estudios *in vitro* indican que células de vejiga EJ humanas que fueron manipuladas para expresar HB-EGF (*tipo silvestre*, soluble o no cortable) exhiben un incremento en crecimiento, crecimiento independiente de anclaje y producción de VEGF, y migración incrementada. Cuando estas células de vejiga EJ que expresan HB-EGF fueron transplantadas en ratones desnudos, un incremento en la formación de tumores, tamaño y densidad de vasos sanguíneos se observó en esos tumores. (Ongusaha, 2004, *Cancer Res.* 64:5283-5290).

Breve descripción de la invención

En la presente se proporcionan proteínas de unión a antígeno aislados que se unen a HB-EGF. Algunas de estas proteínas de unión a antígeno comprenden A) una o más regiones de determinación de complementariedad de la cadena ligera (CDRL) que consisten en: (i) una CDRL1 seleccionada de SEQ ID NOs: **189-217**; (ii) una CDRL2 seleccionada de SEQ ID NOs: **218-233**; (iii) una CDRL3 seleccionada de SEQ ID NO: **234-274**; o (iv) una CDRL de (i), (ii) o (iii) que contiene una o más sustituciones, supresiones o inserciones de aminoácido de

no más de cuatro aminoácidos. Como alternativa, la proteína de unión a antígeno HB-EGF puede comprender B) una o más regiones de determinación de complementariedad de la cadena pesada (CDRH) que consisten en: (i) una CDRH1 seleccionada de SEQ ID NO: **275-299**; (ii) una CDRH2 seleccionada de SEQ ID NO: **300-331**; (iii) una CDRH3 seleccionada de SEQ ID NO: **332-372**; o (iv) una CDRH de (i), (ii) o (iii) que contiene una o más sustituciones, supresiones o inserciones de aminoácido de no más de cuatro aminoácidos.

En una modalidad, la proteína de unión a antígeno aislada puede comprender una, dos o más de las CDRL de la cadena ligera mencionadas arriba y una, dos o más de las CDRH de la cadena pesada mencionadas arriba. En un aspecto, la proteína de unión a antígeno aislada comprende CDRH1, CDRH2, CDRH3, CDRL1, CDRL2 y CDRL3. En otro aspecto, la proteína de unión a antígeno aislada de A), arriba, se selecciona del grupo que consiste en: una CDRL1 de SEQ ID Nos: **189-217**; una CDRL2 de SEQ ID NOs: **218-233**; una CDRL3 de SEQ ID Nos: **234-274**; y una CDRL de cualquiera de los (i), (ii) o (ii) mencionados arriba que contiene una o más sustituciones, supresiones o inserciones de aminoácido de no más de dos aminoácidos. Además, la CDRH de la cadena pesada de B), arriba, se selecciona de una CDRH1 de SEQ ID NOs: **275-299**; una CDRH2 de SEQ ID NOs: **300-331**; una secuencia de aminoácidos de CDRH3 de SEQ ID NOs: **332-372** y una CDRH de las

1960.

mencionadas anteriormente que contiene uno o más sustituciones, supresiones o inserciones de aminoácido de no más de dos aminoácidos. Más aún, la proteína de unión a antígeno aislada puede comprender una o más CDRL de la cadena ligera de A), arriba; y una o más CDRH de la cadena pesada de B), arriba.

En otra modalidad, la proteína de unión a antígeno comprende una CDRL seleccionada de las siguientes: una CDRL1 de SEQ ID NOs: **189-217**; una CDRL2 de SEQ ID NOs: **218-233**; y una CDRL3 de SEQ ID NOs: **234-274**. La proteína de unión a antígeno también puede comprender una CDRH seleccionada de una de las siguientes: una CDRH1 de SEQ ID NOs: **275-299**; una CDRH2 de SEQ ID NOs: **300-331**; y una CDRH3 seleccionada de SEQ ID NOs: **332-372**. Como alternativa, la proteína de unión a antígeno aislada puede comprender una o más CDRL de la cadena ligera listadas en A), arriba, y una o más CDRH de la cadena pesada de B), arriba. En particular, la proteína de unión a antígeno aislada puede comprender una CDRL1 de SEQ ID NOs: **189-217**, una CDRL2 de SEQ ID NOs: **218-233** y una CDRL3 de SEQ ID NOs: **234-274** y/o una CDRH1 de SEQ ID NOs: **275-299**, una CDRH2 de SEQ ID NOs: **300-331** y una CDRH3 de SEQ ID NOs: **332-372**.

En un aspecto, la proteína de unión a antígeno aislada comprende una región variable de la cadena ligera (V_L) que tiene al menos 80%, 90% o 100% de identidad de

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secuencia con una secuencia de aminoácidos seleccionada de SEQ ID NOs: **94-141**. En otro aspecto, la proteína de unión a antígeno aislada comprende una región variable de la cadena pesada (V_H) que tiene al menos 80%, 90% o 100% de identidad de secuencia con una secuencia de aminoácidos de SEQ ID NOs: **142-186**.

En otra modalidad, la proteína de unión a antígeno aislada reconoce específicamente al menos un epítopo que contiene IHGE y/o un dominio tipo EGF de HB-EGF.

Además, en la presente se proporciona una proteína de unión a antígeno aislada que compite para la unión con la proteína de unión a antígeno aislada que se une a HB-EGF, como la descrita arriba.

También se proporciona en la presente una proteína de unión a antígeno aislada que se une a HB-EGF y que comprende A) una o más CDR de la cadena ligera (CDRL) del grupo que consiste en: (i) una CDRL1 con al menos 80%, o al menos 90% de identidad de secuencia con SEQ ID NOs: **189-217**; (ii) una CDRL2 con al menos 80%, o al menos 90% de identidad de secuencia con SEQ ID NOs: **218-233**; y (iii) una CDRL3 con al menos 80%, o al menos 90% de identidad de secuencia con SEQ ID NOs: **234-274**. Como alternativa, la proteína de unión a antígeno aislada que se une a HB-EGF, comprende B) una o más CDR de la cadena pesada (CDRH) del grupo que consiste en (i) una CDRH1 con al menos 80%, o al menos 90% de identidad

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de secuencia con SEQ ID NOs: **275-299**; (ii) una CDRH2 con al menos 80%, o al menos 90% de identidad de secuencia con SEQ ID NOs: **300-331**; y (iii) una CDRH3 con al menos 80%, o al menos 90% de identidad de secuencia con SEQ ID NOs: **332-372**. La proteína de unión a antígeno aislada también puede comprender C) una o más CDRL de la cadena ligera de A) y una o más CDRH de la cadena pesada de B).

En otra modalidad, la proteína de unión a antígeno aislada se une a HB-EGF y comprende: A) una región de determinación de complementariedad de la cadena ligera (CDRL) seleccionada de: (i) una CDRL3 seleccionada del grupo que consiste en SEQ ID NOs: **234-274**; (ii) una CDRL3 que difiere en secuencia de aminoácidos de la CDRL3 de (i) por una adición, supresión o sustitución de aminoácido de no más de dos aminoácidos y (iii) una secuencia de aminoácidos de CDRL3 seleccionada de las siguientes:

$X_1QX_2X_3X_4X_5PX_6X_7$ (SEQ ID NO: 1046), en donde

X_1 es I o M,

X_2 es A, G o S,

X_3 es I o T,

X_4 es H o Q,

X_5 es F, L o W,

X_6 es C, I, H, L o T,

X_7 es S o T;

$QQX_1X_2X_3X_4X_5IT$ (SEQ ID NO: 1047), en donde

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X_1 es I o S,

X_2 es F o Y,

X_3 es F, I, S o Y,

X_4 es A, S o T,

X_5 es P o S;

$X_1X_2X_3X_4X_5X_6X_7X_8T$ (SEQ ID NO: 1048), en donde

X_1 es L o Q,

X_2 es K, N o Q,

X_3 es A, H, S o Y,

X_4 es H, N o Y,

X_5 es N, S o T,

X_6 es A, F, I, T, V o Y,

X_7 es P o ningún aminoácido,

X_8 es F, L o P;

$QX_1X_2DX_3LPX_4X_5$ (SEQ ID NO: 1049), en donde

X_1 es H o Q,

X_2 es C o Y,

X_3 es D, I, N, S o Y,

X_4 es F, I o L,

X_5 es A, S o T;

$QQ_1X_2X_3X_4PX_5X_6X_7$ (SEQ ID NO: 1050), en donde

X_1 es H o Y,

X_2 es G o N,

X_3 es N o S,

X_4 es S o W,

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X_5 es P o ningún aminoácido,

X_6 es R o W,

X_7 es S o T; o

$X_1QYX_2X_3X_4X_5X_6X_7F$ (SEQ ID NO: 1051)., en donde

X_1 es H o Q,

X_2 es F o Y,

X_3 es G, I o S,

X_4 es F, I o T,

X_5 es M, P, S o T,

X_6 es F, L, R o W,

X_7 es S o T.

La proteína de unión a antígeno aislada también puede comprender B) una región de determinación de complementariedad de la cadena pesada (CDRH) seleccionada del grupo que consiste en: (i) una CDRH3 seleccionada del grupo que consiste en SEQ ID NOs: **332-372**; (ii) una CDRH3 que difiere en secuencia de aminoácidos de la CDRH3 de (i) por una adición, supresión o sustitución de aminoácido de no más de dos aminoácidos y (iii) una secuencia de aminoácidos de CDRH3 seleccionada de las siguientes:

$X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}DX_{12}$ (SEQ ID NO: 1065), en donde

X_1 es E o S,

X_2 es D, G o ningún aminoácido,

X_3 es D, N o ningún aminoácido,

X_4 es G o ningún aminoácido,

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X_5 es G o ningún aminoácido,

X_6 es W, Y o ningún aminoácido,

X_7 es I, N o Y,

X_8 es A o Y,

X_9 es G, V o Y,

X_{10} es A, F o G,

X_{11} es F, L o M,

X_{12} es V o Y;

$QX_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}YX_{12}X_{13}X_{14}DX_{15}$ (SEQ ID NO: 1066),

en donde

X_1 es G o ningún aminoácido,

X_2 es K, L o Y,

X_3 es A, G o S,

X_4 es S, V o Y,

X_5 es A o G,

X_6 es G o ningún aminoácido,

X_7 es t o ningún aminoácido,

X_8 es S o ningún aminoácido,

X_9 es Y o ningún aminoácido,

X_{10} es W o Y,

X_{11} es G, S o Y,

X_{12} es F o Y,

X_{13} es G o ningún aminoácido,

X_{14} es M o ningún aminoácido,

X_{15} es V o Y;

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$X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}$ (SEQ ID NO: 1067), en donde

X_1 es D, G, L, S o ningún aminoácido,

X_2 es g, H, W, Y o ningún aminoácido,

X_3 es A, F, W, Y o ningún aminoácido,

X_4 es D, G, Q, T o ningún aminoácido,

X_5 es G, I, Q, S o ningún aminoácido,

X_6 es A, D, N, Q, S o ningún aminoácido,

X_7 es G, Y o ningún aminoácido,

X_8 es D, Y o ningún aminoácido,

X_9 es Y o ningún aminoácido,

X_{10} es A, E, N o Y,

X_{11} es G, P, T, V o Y,

X_{12} es F o I,

X_{13} es D o Q,

X_{14} es C, H, V o Y;

$X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}DX_{18}$ (SEQ ID NO: 1068), en donde

X_1 es E, D o ningún aminoácido,

X_2 es G, R o ningún aminoácido,

X_3 es I, V, Y o ningún aminoácido,

X_4 es A, G, L o N,

X_5 es A, G, V o W,

X_6 es A, N, R o T,

X_7 es G, N, P o ningún aminoácido,

X_8 es G, T o ningún aminoácido,

X_9 es A o ningún aminoácido,

X_{10} es D, E o ningún aminoácido,

X_{11} es S, Y o ningún aminoácido,

X_{12} es G, Y o ningún aminoácido,

X_{13} es N, Y o ningún aminoácido,

X_{14} es Y o ningún aminoácido,

X_{15} es D, Y o ningún aminoácido,

X_{16} es A, G o ningún aminoácido,

X_{17} es F o M,

X_{18} es I, V o y;

$X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}X_{18}X_{19}X_{20}X_{21}X_{22}X_{23}$

(SEQ ID NO: 1069), en donde

X_1 es A, D, G, S o T,

X_2 es A, E, G, L, N, R, Y o ningún aminoácido,

X_3 es A, G, L, N, R, T, Y o ningún aminoácido,

X_4 es D, G, R, S, V, Y o ningún aminoácido,

X_5 es A, G, I, S, V, Y o ningún aminoácido,

X_6 es F, G, L, R, V o ningún aminoácido,

X_7 es L, T, Y o ningún aminoácido,

X_8 es Y o ningún aminoácido,

X_9 es Y o ningún aminoácido,

X_{10} es D o ningún aminoácido,

X_{11} es S o ningún aminoácido,

X_{12} es S o ningún aminoácido,

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X_{13} es G o ningún aminoácido,

X_{14} es D, L, M, S, Y o ningún aminoácido,

X_{15} es H, I, P, V, W o ningún aminoácido,

X_{16} es F, G, L, R, S, Y o ningún aminoácido,

X_{17} es D, F, V, W, Y o ningún aminoácido,

X_{18} es C, F, L, P, S o Y,

X_{19} es D, F, G o Y,

X_{20} es A, C, G, P, R, V o Y,

X_{21} es F, L, M, S o ningún aminoácido,

X_{22} es A, D o ningún aminoácido,

X_{23} es I, L, V, Y o ningún aminoácido,

$X_1YSSGWX_2X_3YGX_4X_5DX_6$ (SEQ ID NO: 17070), en donde

X_1 es M o V,

X_2 es S o ningún aminoácido,

X_3 es F o ningún aminoácido,

X_4 es V o ningún aminoácido,

X_5 es F o M,

X_6 es V o Y; o

$RX_1X_2X_3PFX_4Y$ (SEQ ID NO: 1071), en donde

X_1 es G, H, L, N o R,

X_2 es E, T o W,

X_3 es L, N, T o V,

X_4 es D o E.

En otro aspecto, la proteína de unión a antígeno aislada puede comprender además A) una CDRL seleccionada de:

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(i) una CDRL1 seleccionada de SEQ ID NOs: **189-217**; (ii) una CDRL que difiere en secuencia de aminoácidos de la CDRH1 de (i) por una adición, supresión o sustitución de aminoácido de no más de dos aminoácidos; o (iii) una secuencia de aminoácidos de CDRL1 seleccionada de las siguientes:

X_1 es K o R,

X_2 es L o V,

X_3 es H o Y,

X_4 es K o N,

X_5 es N, S o Y;

$RASQX_1ISX_2YLN$ (SEQ ID NO:1036), en donde

X_1 es R, S o T,

X_2 es R o S;

$RASQX_1IX_2X_3X_4LX_5$ (SEQ ID NO: 1037), en donde

X_1 es D, G, S o T,

X_2 es A, R o S,

X_3 es H, I, N, R, S o T,

X_4 es D, W o Y,

X_5 es A, G o N;

$QASQDIX_1X_2X_3LN$ (SEQ ID NO: 1038), en donde

X_1 es S o T,

X_2 es D o N,

X_3 es S o Y;

$RASQX_1VX_2X_3X_4X_5LA$ (SEQ ID NO:1039), en donde

X_1 es S o T,

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X_2 es I o S,

X_3 es R o S,

X_4 es S, N o ningún aminoácido,

X_5 es Y o ningún aminoácido;

$KSSQX_1X_2LX_3X_4SNNKNYLX_5$ (SEQ ID NO: 1040), en donde

X_1 es N o S,

X_2 es I o V,

X_3 es D o Y,

X_4 es N, R o S,

X_5 es A o V;

(iv) una CDRL2 del grupo que consiste en SEQ ID NOs: **218-233**; (v) una CDRL2 que difiere en secuencia de aminoácidos de la CDRL2 de (iv) por una adición, supresión o sustitución de aminoácido de no más de dos aminoácidos; o (vi) una secuencia de aminoácidos de CDRL2 seleccionada de las siguientes:

$X_1X_2SNX_3X_4S$ (SEQ ID NO: 1041); en donde

X_1 es E o K,

X_2 es I o V,

X_3 es R o W,

X_4 es D o F;

$X_1X_2SX_3LQS$ (SEQ ID NO: 1042), en donde

X_1 es A o T,

X_2 es A, E o V,

X_3 es S o T;

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X_1ASX_2LQS (SEQ ID NO: 1043), en donde

X_1 es A o V;

X_2 es S o T;

$DASX_1LET$ (SEQ ID NO: 1044); en donde

X_1 es I o N;

GASSRAT (SEQ ID NO: 223); o

$WASX_1RES$ (SEQ ID NO: 1045), en donde

X_1 es A o T.

Las proteínas de unión a antígeno aisladas pueden comprender además B) una CDRH del grupo que consiste en: (i) una CDRH1 del grupo que consiste en SEQ ID NOs: **275-299**; (ii) una CDRH1 que difiere en secuencia de aminoácidos de la CDRH1 de (i) por una adición, supresión o sustitución de aminoácido de no más de dos aminoácidos; (iii) una secuencia de aminoácidos de CDRH1 seleccionada de:

$GYTX_1TX_2X_3X_4X_5X_6$ (SEQ ID NO: 1052), en donde

X_1 es F o L,

X_2 es E, G o S,

X_3 es H, L o Y,

X_4 es G, S o Y,

X_5 es I o M,

X_6 es H o S;

$GYX_1FTSYWIG$ (SEQ ID NO: 1053), en donde

X_1 es R o S;

$GFTFX_1SX_2X_3MH$ (SEQ ID NO: 1054), en donde

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X_1 es R o S,

X_2 es H o Y,

X_3 es D o G;

$GFX_1FSX_2YX_3MX_4$ (SEQ ID NO: 1055), en donde

X_1 es P o T,

X_2 es A, R o S,

X_3 es A o S,

X_4 es N o S;

$GX_1SX_2SX_3X_4X_5X_6X_7XW_8$ (SEQ ID NO: 1056), en donde

X_1 es D o G,

X_2 es F, I o V,

X_3 es R, S o ningún aminoácido,

X_4 es G, Y o ningún aminoácido,

X_5 es D, G, S o ningún aminoácido,

X_6 es A, S o Y,

X_7 es A o Y,

X_8 es N o S;

GFSLSNARMGVS (SEQ ID NO: 279); o

$GFSLX_1TGGVGVG$ (SEQ ID NO: 1057), en donde

X_1 es S o N,

(iv) una CDRH2 seleccionada del grupo que consiste en SEQ ID NOs: **300-331**; (v) una CDRH2 que difiere en secuencia de aminoácidos de la CDRH2 de (iv) por una adición, supresión o sustitución de aminoácido de no más de dos aminoácidos; o (vi) una secuencia de aminoácidos de CDRH2 de

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las siguientes:

$X_1X_2X_3X_4X_5X_6GX_7TX_8X_9X_{10}QKX_{11}X_{12}$ (SEQ ID NO: 1058), en donde

X_1 es S o W,

X_2 es F o I,

X_3 es D, N o S,

X_4 es A o P,

X_5 es E, N o S,

X_6 es D, N o S,

X_7 es E, G o N,

X_8 es I o N,

X_9 es C, H o Y,

X_{10} es A o T,

X_{11} es F o L,

X_{12} es D o G,

$IIYPX_1DSDX_2RYSPSFQG$ (SEQ ID NO: 1059), en donde

X_1 es D o G,

X_2 es A, I o T;

$X_1IX_2X_3DGSX_4X_5X_6YX_7DSVX_8G$ (SEQ ID NO: 1060), en donde

X_1 es F o V,

X_2 es S o W,

X_3 es D, S o Y,

X_4 es I, N o T,

X_5 es K o Q,

X_6 es N, R o Y,

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X_7 es A, T o V,

X_8 es K o R;

$X_1ISX_2SX_3X_4X_5X_6YYADSVKG$ (SEQ ID NO: 1061), en donde

X_1 es A, H o Y,

X_2 es G, R o S,

X_3 es G o S,

X_4 es G, R o S,

X_5 es S, T o Y,

X_6 es I o T;

$X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}YX_{12}X_{13}SX_{14}KS$ (SEQ ID NO: 1062), en donde

X_1 es E, R o Y,

X_2 es I o T,

X_3 es H, N o Y,

X_4 es C, H, S, T o Y,

X_5 es S o R,

X_6 es G o S,

X_7 es G, K, S o T,

X_8 es T o W,

X_9 es N o Y,

X_{10} es N o ningún aminoácido,

X_{11} es D o ningún aminoácido,

X_{12} es A o N,

X_{13} es P o V,

X_{14} es L o V;

X_1IFSNDEKSYSTSLKS (SEQ ID NO: 1063), en donde

X_1 es H o LI; o

LIYWNX_1X_2KRYSPSLX_3S (SEQ ID NO: 1064), en donde

X_1 es D o V,

X_2 es D o E,

X_3 es K o R.

En otra modalidad más, la proteína de unión a antígeno aislada descrita anteriormente en la presente comprende la primera secuencia de aminoácidos y la segunda secuencia de aminoácidos, ambas secuencias de las cuales son enlazadas covalentemente una a otra. La primera secuencia de aminoácidos comprende también CDRL3 de SEQ ID NOs: **234-274**; CDRL2 de SEQ ID NOs: **218-233** y CDRL1 de SEQ ID NOs: **189-217**, y la segunda secuencia de aminoácidos comprende las CDRH3 de SEQ ID NOs: **332-372**, CDRH2 de SEQ ID NOs: **300-331**, y CDRH1 de SEQ ID NOs: **275-299**.

En un aspecto, las proteínas de unión a antígeno aisladas pueden ser un anticuerpo monoclonal, un anticuerpo policlonal, un anticuerpo recombinante, un anticuerpo humano, un anticuerpo humanizado, un anticuerpo quimérico, un anticuerpo multiespecífico o un fragmento de anticuerpo de los mismos. El fragmento de anticuerpo puede ser un fragmento Fab, un fragmento Fab', un fragmento $F(ab')_2$, un fragmento Fv, un dicuerpo o una molécula de anticuerpo de cadena individual. En una modalidad, la proteína de unión a

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antígeno aislada de la presente invención es un anticuerpo humano. En otra modalidad, la proteína de unión a antígeno aislada es un anticuerpo monoclonal.

Las proteínas de unión a antígeno aisladas como las descritas en la presente pueden ser de cualquiera de los siguientes tipos: tipo IgG1, IgG2, IgG3 o IgG4. En una modalidad, la proteína de unión a antígeno es del tipo IgG2 o IgG4. Más aún, la proteína de unión a antígeno puede ser acoplada a un grupo marcador. Estos grupos marcadores pueden ser, por ejemplo, un radioisótopo, radionúclido, un grupo fluorescente, un grupo enzimático, un grupo quimioluminiscente, un grupo de biotinilo o un grupo de polipéptidos predeterminado.

En otra modalidad, la proteína de unión a antígeno aislada es acoplada a un grupo efector tal como, por ejemplo, un radioisótopo, un radionúclido, una toxina, un grupo terapéutico o un grupo quimioterapéutico. Los grupos quimioterapéuticos pueden ser, por ejemplo, caliqueamicina, auristatina-PE, geldanamicina, maitansina o derivados de las mismas.

En otra modalidad más, la proteína de unión a antígeno aislada compite por la unión a HB-EGF humano con una proteína de unión a antígeno como la descrita y reclamada en la presente. Esta proteína de unión a antígeno competente puede ser, por ejemplo, un anticuerpo monoclonal, un

anticuerpo policlonal, un anticuerpo recombinante, un anticuerpo humano, un anticuerpo humanizado, un anticuerpo quimérico, un anticuerpo multiespecífico o un fragmento de anticuerpo de los mismos. El fragmento de anticuerpo puede ser, por ejemplo, un fragmento Fab, un fragmento Fab', un fragmento $F(ab')_2$, un fragmento Fv, un dicuerpo o una molécula de anticuerpo de cadena individual. En una modalidad, la proteína de unión aislada es un anticuerpo humano. En otra modalidad, la proteína de unión a antígeno aislada es un anticuerpo monoclonal. En otra modalidad, esta proteína de unión a antígeno aislada es del tipo IgG1, IgG2, IgG3 o IgG4. En una modalidad, la proteína de unión a antígeno es del tipo IgG2 o IgG4. En otra modalidad, las proteínas de unión a antígeno como las descritas en la presente pueden ser acopladas a un grupo marcador. Ejemplos de grupos marcadores son: un radioisótopo, radionúclido, un grupo fluorescente, un grupo enzimático, un grupo quimioluminiscente, un grupo de biotinilo o un grupo de polipéptidos predeterminado. En otra modalidad, la proteína de unión a antígeno aislada es acoplada a un grupo efector tal como, por ejemplo, un radioisótopo, un radionúclido, una toxina, un grupo terapéutico o un grupo quimioterapéutico. Ejemplos de los grupos terapéuticos o quimioterapéuticos incluyen, por ejemplo, caliqueamicina, auristatina-PE, geldanamicina, maitansina o derivados de las mismas.

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En un aspecto, una proteína de unión a antígeno aislada se proporciona que reduce, al menos parcialmente, transducción de señales mediada por HB-EGF.

También se presenta en la presente una molécula de ácido nucleico que codifica para la proteína de unión a antígeno aislada previamente descrita, en donde la molécula de ácido nucleico es enlazada operablemente a una secuencia de control. En un aspecto, se proporciona un vector que comprende la molécula de ácido nucleico mencionada arriba. En otro aspecto, se proporciona una célula hospedera que comprende la molécula de ácido nucleico y/o vector mencionados arriba.

En una modalidad, se proporciona un método para elaborar la proteína de unión a antígeno que incluye la etapa de preparar la proteína de unión a antígeno a partir de una célula hospedera que secrete la proteína de unión a antígeno.

En otra modalidad más, se proporciona una composición farmacéutica que comprende al menos una de las proteínas de unión antígeno mencionadas arriba de la presente invención y un portador, diluyente o adyuvante farmacéuticamente aceptable. En una modalidad, la composición farmacéutica puede comprender un agente activo adicional, tal como un agente antineoplásico. El agente antineoplásico puede ser, por ejemplo, un anticuerpo antitumor. Ejemplos de un anticuerpo antitumor pueden ser,

por ejemplo, anticuerpos dirigidos contra tirosina cinasa receptora o EGFR.

En un aspecto, la composición farmacéutica se usa para diagnóstico, prevención o tratamiento de una enfermedad hiperproliferativa. En un aspecto más, la enfermedad hiperproliferativa está asociada con expresión de HB-EGF. En otro aspecto, la enfermedad hiperproliferativa está asociada con o es acompañada por una activación de receptor de factor de crecimiento alterada (por ejemplo, incrementada patológicamente), en donde la activación de receptor de factor de crecimiento incrementada patológicamente está asociada con o es causada por un incremento patológico en la actividad de una proteína G y/o un receptor acoplado a proteína G.

En una modalidad, la composición farmacéutica comprende al menos una proteína de unión a antígeno y un portador, diluyentes y/o adyuvantes farmacéuticamente aceptables para el diagnóstico, prevención o tratamiento de cáncer, tal como, por ejemplo, cáncer de seno, cáncer gastrointestinal, cáncer de páncreas, cáncer de próstata, cáncer ovárico, cáncer de estómago, cáncer endometrial, cáncer de glándulas salivales, cáncer pulmonar, cáncer de riñón, cáncer de colon, cáncer colorrectal, cáncer de tiroides, cáncer de vejiga, glioma, melanoma, otros cánceres que expresen o sobre-expresen HB-EGF y formación de

metástasis tumorales.

En otra modalidad, las proteínas de unión a antígeno como las descritas en la presente se usan en la elaboración de una composición farmacéutica para el diagnóstico, prevención o tratamiento de una enfermedad hiperproliferativa. En una modalidad más, la enfermedad hiperproliferativa está asociada con expresión de HB-EGF.

Una modalidad describe un método para diagnosticar una afección asociada con la expresión de HB-EGF, el método comprende la etapa de poner en contacto una muestra con las proteínas de unión a antígeno aisladas como las descritas en la presente, y determinar la presencia de HB-EGF en la muestra. En una modalidad más, la afección es una enfermedad hiperproliferativa asociada con expresión de HB-EGF.

Otro aspecto describe un método para prevenir o tratar una afección asociada con la expresión de HB-EGF en un paciente, que comprende administrar a un paciente que lo requiera una cantidad efectiva de una proteína de unión a antígeno como la descrita en la presente. En un aspecto más, la afección es una enfermedad hiperproliferativa asociada con la expresión de HB-EGF. En otro aspecto más, el paciente es un paciente mamífero.

En una modalidad, se proporciona un kit que comprende una proteína de unión a antígeno, una molécula de ácido nucleico o un vector como el descrito arriba. En una

modalidad más, el kit comprende al menos un agente activo adicional, en donde el agente activo adicional es un agente antineoplásico.

Estos y otros aspectos de la invención se describirán en más detalle en la presente. Cada uno de los aspectos de la invención puede abarcar varias modalidades de la presente invención. Se anticipa por lo tanto que cada una de las modalidades de la invención que incluya un elemento o combinaciones de elementos puede ser incluida en cada aspecto de la invención. Otras características, objetivos y ventajas de la presente invención son aparentes en la siguiente descripción detallada.

Breve descripción de las figuras

Las figuras 1A-1P ilustran varias regiones variables de la cadena ligera de las proteínas de unión a antígeno. Las regiones CDR1, CDR2 y CDR3 se indican en cuadros.

Las figuras 2A-2O ilustran varias regiones variables de la cadena pesada de las proteínas de unión a antígeno. Las regiones CDR1, CDR2 y CDR3 se indican en cuadros.

Las figuras 3A-3K ilustran las secuencias de aminoácidos de varias cadenas ligeras de las proteínas de unión a antígeno.

Las figuras 4A-4O ilustran las secuencias de

aminoácidos de varias cadenas pesadas de las proteínas de unión a antígeno.

La figura 5A ilustra la secuencia de aminoácidos de una región constante de la cadena ligera ejemplar de las proteínas de unión a antígeno.

La figura 5B ilustra la secuencia de aminoácidos de una región constante de la cadena pesada ejemplar de las proteínas de unión a antígeno.

Las figuras 6A-6F ilustran las secuencias de aminoácidos para varias regiones CDR de las regiones variables de la cadena ligera de las proteínas de unión a antígeno.

Las figuras 7A-7E ilustran las secuencias de aminoácidos para varias regiones CDR de las regiones variables de la cadena pesada de las proteínas de unión a antígeno.

Las figuras 8A-8H ilustran las secuencias de aminoácidos para varias regiones FR de las regiones variables de la cadena ligera de las proteínas de unión a antígeno.

Las figuras 9A-9F ilustran las secuencias de aminoácidos para varias regiones FR de las regiones variables de la cadena pesada de las proteínas de unión a antígeno.

Las figuras 10A y 10B ilustran una alineación de las secuencias de aminoácidos de las secuencias variables de la cadena ligera de las proteínas de unión a antígeno. Las

regiones CDR1, CDR2 y CDR3 se muestran en cuadros.

Las figuras 11A y 11B ilustran una alineación de las secuencias de aminoácidos de las secuencias variables de la cadena pesada de las proteínas de unión a antígeno. Las regiones CDR1, CDR2 y CDR3 se muestran en cuadros.

La figura 12A ilustra un cladograma que muestra el parentesco de las regiones variables de la cadena ligera de las proteínas de unión a antígeno.

La figura 12B ilustra un cladograma que muestra el parentesco de las regiones CDRL3 de la cadena ligera de las proteínas de unión a antígeno.

La figura 12C ilustra un cladograma que muestra el parentesco de las regiones variables de la cadena pesada de las proteínas de unión a antígeno.

Las figuras 13A-13V ilustran las secuencias de nucleótidos de varias regiones variables de la cadena ligera de las proteínas de unión a antígeno.

Las figuras 14A-14AC ilustran las secuencias de nucleótidos de varias regiones variables de la cadena pesada de las proteínas de unión a antígeno.

Las figuras 15A-15M ilustran las secuencias de nucleótidos de las diferentes cadenas ligeras de las proteínas de unión a antígeno.

Las figuras 16A-16L ilustran las secuencias de nucleótidos de las diferentes cadenas pesadas de las

proteínas de unión a antígeno.

La figura 17A ilustra la secuencia de nucleótidos de la región constante de la cadena ligera de las proteínas de unión a antígeno.

La figura 17B ilustra la secuencia de nucleótidos de la región constante de la cadena pesada de las proteínas de unión a antígeno.

La figuras 18A-18F ilustran las secuencias de nucleótidos para varias regiones CDR de las regiones variables de la cadena ligera de las proteínas de unión a antígeno.

Las figuras 19A-19G ilustran las secuencias de nucleótidos para varias regiones CDR de las regiones variables de la cadena pesada de las proteínas de unión a antígeno.

Las figuras 20A-20K ilustran las secuencias de nucleótidos para varias regiones FR de las regiones variables de la cadena ligera de las proteínas de unión a antígeno.

Las figuras 21A-21K ilustran las secuencias de nucleótidos para varias regiones FR de las regiones variables de la cadena pesada de las proteínas de unión a antígeno.

La figura 22A ilustra gráficamente el grado al cual diferentes preparaciones de anticuerpos anti-HB-EGF IgG2 proporcionadas en la presente inhiben la fosforilación de tirosina receptora de factor de crecimiento epidérmico (EGFR)

inducida por HB-EGF. Se proporcionan los resultados para las preparaciones de anticuerpos U2-1 a U2-68. Como se ilustra, las preparaciones de anticuerpo monoclonal U2-18, U2-24, U2-19 y U2-42 inhiben fuertemente la fosforilación de tirosina EGFR.

La figura 22B ilustra gráficamente el grado al cual diferentes preparaciones de anticuerpo anti-HB-EGF IgG4 proporcionadas en la presente inhiben la fosforilación de tirosina receptora de factor de crecimiento epidérmico (EGFR) inducida por HB-EGF. Se proporcionan los resultados para preparaciones de anticuerpos U2-2 a U2-66. Como se ilustra, las preparaciones de anticuerpo monoclonal U2-39, U2-34, U2-45 y U2-6 inhiben fuertemente la fosforilación de tirosina EGFR.

La figura 23 ilustra que los anticuerpos inhiben la fosforilación de tirosina EGFR inducida por ácido lisofosfatídico (LPA) en células COS-7. LPA es un ligando de GPCR que activa la vía TMPS, dando como resultado la liberación de HB-EGF con consecuente fosforilación de tirosina EGFR. Células COS-7 fueron pre-tratadas con anticuerpos como se indica y estimuladas con LPA, después los lisados celulares se prepararon y las proteínas lisadas fueron separadas mediante electroforesis en gel de poliacrilamida. Después de la preparación del blot, se usó un anticuerpo anti-fosfotirosina para detectar EGFR

fosforilado. Como un control, EGFR total fue detectado como se muestra en el fondo, usando un anticuerpo WB anti-EGFR. Como se ilustra, las preparaciones de anticuerpo anti-HB-EGF U2-24, U2-19 y U2-42 inhiben fuertemente la fosforilación de EGFR inducida por LPA.

La figura 24 ilustra gráficamente la inhibición dependiente de dosis de la fosforilación de tirosina receptora de EGF inducida por HB-EGF por varios anticuerpos proporcionados en la presente. Diferentes concentraciones de las preparaciones de anticuerpo U2-39, U2-42 y U2-45 candidatas fueron preincubadas con HB-EGF antes de la estimulación de células de cáncer escamoso SCC9 y la cantidad de fosforilación de tirosina EGFR fue detectada. Como se muestra, el anticuerpo U2-42 y U2-39 logró hasta 111% de inhibición. Los valores IC50 determinados para los anticuerpos fueron 0.167 nM (U2-39), 1 nM (U2-42) y 2 nM (U2-45), respectivamente.

La figura 25 ilustra gráficamente la inhibición dependiente de dosis de fosforilación de EGFR inducida por trombina mediante TMPS en células MDA-MB231 por preparaciones de anticuerpo anti-HB-EGF. Células MDA-MB231 fueron incubadas con preparaciones de anticuerpo U2-42, U2-39 y U2-45 candidatas en presencia de trombina y la cantidad de fosforilación de tirosina EGFR se detectó usando un procedimiento descrito en el ejemplo 6. Como se muestra, los

anticuerpos U2-42 y U2-39 lograron 100% de inhibición.

La figura 26 ilustra inhibición dependiente de dosis de fosforilación de tirosina EGFR inducida por LPA mediante TMPS en células PPC-1 mediante preparaciones de anticuerpo anti-HB-EGF. Células PPC-1 fueron incubadas con preparaciones de anticuerpo U2-42, U2-39 y U2-45 candidatas y la cantidad de fosforilación de tirosina EGFR después de la estimulación con LPA se detectó usando un procedimiento descrito en el ejemplo 4. Como se muestra, los anticuerpos U2-42, U2-39 y U2-45 lograron 100% de inhibición.

La figura 27 ilustra que preparaciones de anticuerpo anti-HB-EGF inhibieron hasta 100% la inducción de migración de células de cáncer de seno MDA-MB231 mediante esfingosín-1-fosfato. Preparaciones de anticuerpo anti-HB-EGF candidatas U2-42, U2-39 y U2-45 fueron probadas para inhibición de migración celular usando pocillos intermedios recubiertos con colágeno I (BD Falcon, poros de 8 µm). Como se muestra, preparación de anticuerpo anti-HB-EGF U2-42 inhibió la migración de células MDA-MB231 inducida por esfingosín-1-fosfato en alrededor de 70% mientras que las preparaciones de anticuerpo anti-HB-EGF U2-39 y U2-45 inhibieron la migración de células MDA-MB231 en aproximadamente 100%. De esta manera, los anticuerpos anti-HB-EGF provistos en la presente inhiben fuertemente la migración de células MDA-MB231.

La figura 28 ilustra gráficamente que la migración inducida por HB-EGF de células de cáncer de seno MCF-7 es inhibida por tres preparaciones de anticuerpos anti-HB-EGF (las preparaciones de anticuerpo monoclonal U2-42, U2-39 y U2-45).

La figura 29 ilustra la inhibición dependiente de dosis de fosforilación de tirosina inducida por HB-EGF de HER4 por preparaciones de anticuerpos anti-HB-EGF. Las preparaciones de anticuerpos anti-HB-EGF U2-42.1 o U2-39.1 fueron incubadas con HB-EGF antes de la estimulación y detección de la fosforilación de tirosina HER4. Como se muestra, 100% de inhibición de fosforilación de tirosina HER4 fue observada. Nótese que la cantidad de anticuerpo mostrada en el eje x disminuye logarítmicamente.

La figura 30A muestra que preparaciones de anticuerpos monoclonales reaccionan de manera cruzada con HB-EGF de macacos como se evalúa por citometría de flujo (FACS) usando células HEK-293 transfectadas con un vector de ADN que expresa HB-EGF de macaco. Como se muestra, valores medios X muy bajos (1-2) son observados para células de control HEK-293 que fueron transfectadas con un control de vector vacío. En contraste, los valores X-media de 250 o más fueron observados cuando células HEK-293 fueron transfectadas con un casete de expresión que codificaba para HB-EGF de macaco.

La figura 30B muestra que la preparación de

anticuerpo monoclonal U2-45 reacciona en forma cruzada con HB-EGF de ratón según se evalúa mediante citometría de flujo (FACS) usando células HEK-293 transfectadas con un vector de ADN que expresaba HB-EGF de ratón. Los valores X-media de 33.7 fueron observados cuando células HEK-293 fueron transfectadas con un casete de expresión que codificaba para HB-EGF de ratón.

La figura 30C muestra el grado de reactividad cruzada de anticuerpos HB-EGF con anfirregulina.

La figura 31 muestra que HB-EGF es expresado en células endoteliales vasculares humanas (HUVEC), según se detecta por análisis FACS.

Las figuras 32A-32B muestran que aunque HB-EGF estimula la proliferación celular HUVEC, las preparaciones de anticuerpo anti-HB-EGF inhibieron la proliferación basal en aproximadamente 8% a 14%. HB-EGF estimula la proliferación celular HUVEC en alrededor de 38% (figura 32A). Sin embargo, después de la adición de preparaciones de anticuerpo anti-HB-EGF U2-42, U2-39 o U2-45, la proliferación celular basal es inhibida en alrededor de 8% a 14% (figura 32B).

Las figuras 33A-33L ilustran que anticuerpos anti-HB-EGF aceleran la regresión de tubos HUVEC. La formación de tubos HUVEC es un sistema modelo para angiogénesis de células endoteliales. Las figuras 33A-33C proporcionan ensayos de control que fueron llevados a cabo sin anticuerpos anti-HB-

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EGF. Como se muestra, las células HUVEC se unen para formar muchas estructuras circulares o "tubos". Las figuras 33D-33F ilustran los efectos de añadir la preparación de anticuerpo anti-HB-EGF U2-39 después de la formación de tubos. Las figuras 33G-33I ilustran los efectos de añadir la preparación de anticuerpo anti-HB-EGF U2-42 después de la formación de tubos. Las figuras 33J-33L ilustran los efectos de añadir la preparación de anticuerpos anti-HB-EGF U2-45 después de la formación de tubos. Como se muestra, menos tubos HUVEC son visibles y la red es disminuida cuando las preparaciones de anticuerpo anti-HB-EGF U2-42, U2-39 y U2-45 están presentes.

La figura 33M ilustra gráficamente una evaluación cuantitativa de la formación de tubos HUVEC después de añadir las preparaciones de anticuerpo anti-HB-EGF proporcionadas en la presente, soportando la unidad de anticuerpos HB-EGF para inhibir angiogénesis. El número de tubos o estructuras celulares cerradas por campo microscópico es graficado para las preparaciones de anticuerpo U2-42, U2-39 o U2-45 anti-HB-EGF. Como se muestra, aunque aproximadamente 10 tubos HUVEC fueron visibles por campo cuando ningún anticuerpo anti-HB-EGF estuvo presente, sólo aproximadamente 4 tubos HUVEC fueron observados por campo microscópico cuando la preparación de anticuerpos anti-HB-EGF U2-39 fue añadida. En presencia de la preparación de anticuerpo anti-HB-EGF U2-42 sólo aproximadamente 1 tubo HUVEC fue observado. Cuando la

preparación de anticuerpo anti-HB-EGF U2-45 estuvo presente sólo 6 tubos HUVEC se observaron.

La figura 34A ilustra que los anticuerpos anti-HB-EGF inhiben la formación de colonia estimulada por HB-EGF de células de cáncer ovárico OVCAR-8. Como se muestra, células OVCAR-8 estimuladas con HB-EGF forman un tamaño de colonia medio significativamente más grande que las células OVCAR-8 de control sin HB-EGF. Sin embargo, las células OVCAR-8 fueron cultivadas con anticuerpos anti-HB-EGF U2-39 en presencia de HB-EGF, el tamaño de colonia medio fue reducido al tamaño de línea de base observado para células de control sin tratamiento con HB-EGF.

La figura 34B ilustra que anticuerpos anti-HB-EGF inhiben la formación de colonias estimulada por HB-EGF de células de cáncer prostático BM1604 en agar suave. Como se muestra, células BM1604 estimuladas con HB-EGF forman un número más grande de colonias por pocillo que células BM1604 de control cultivadas sin HB-EGF. Sin embargo, cuando células BM1604 fueron cultivadas con anticuerpos anti-HB-EGF U2-39 en presencia de HB-EGF, el tamaño de colonia medio se redujo a un tamaño similar a aquél observado para células de control sin tratamiento con HB-EGF. Los anticuerpos anti-HB-EGF U2-45 y U2-42 inhibieron parcialmente la formación de colonia, en tanto que, en este ensayo, el anticuerpo U2-39 anti-HB-EGF inhibió completamente la formación de colonia.

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La figura 34C ilustra que anticuerpos anti-HB-EGF inhiben la formación de colonia estimulada por HB-EGF de células de carcinoma pulmonar NCI-H226. Como se muestra, células NCI-H226 estimuladas con HB-EGF forman un tamaño de colonia medio significativamente más grande que células NCI-H226 de control cultivadas sin HB-EGF. Sin embargo, cuando células NCI-H226 fueron cultivadas con anticuerpos anti-HB-EGF U2-39 en presencia de HB-EGF, el tamaño de colonia medio se redujo al tamaño de línea de base observado para células de control sin tratamiento con HB-EGF.

La figura 34D ilustra que los anticuerpos anti-HB-EGF inhiben formación de colonias basales de células de clon 71 de SkOV-3 HB-EGF, derivadas de células de cáncer ovárico SkOV-3 transfectadas con un vector de expresión HB-EGF para causar sobre-expresión constitutiva de HB-EGF. Como se muestra, células de clon 71 de SkOV-3 HB-EGF de control formaron grandes números de colonias. Sin embargo, cuando células de clon 71 de SkOV-3 HB-EGF fueron cultivadas ya sea con anticuerpos anti-HB-EGF U2-42 o U2-39, el número de colonias se redujo dramáticamente.

La figura 34E ilustra que anticuerpos anti-HB-EGF inhiben la formación de colonias basales de células de clon 74 de SkOV-3 HB-EGF, derivadas de células de cáncer ovárico SkOV-3 transfectadas con un vector de expresión HB-EGF para causar sobre-expresión constitutiva de HB-EGF. Como se

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muestra, células de clon 74 de SkOV-3 HB-EGF de control formaron grandes números de colonias. Sin embargo, cuando células de clon 74 de SkOV-3 HB-EGF se cultivaron con anticuerpos anti-HB- EGF U2-39, el número de colonias se redujo dramáticamente.

La figura 34F ilustra que anticuerpos anti-HB-EGF inhiben la formación de colonias basales de células de adenocarcinoma pancreático BxPC3 cultivadas en agar suave. Como se muestra, células BxPC3 de control formaron grandes números de colonias. Sin embargo, cuando células BxPC3 fueron cultivadas ya sea con anticuerpos anti-HB-EGF U2-42 o U2-39 en presencia de HB-EGF, el número de colonias se redujo dramáticamente.

La figura 35 ilustra que los anticuerpos anti-HB-EGF inhiben la formación de colonias basales de células de cáncer ovárico de clon 58 de EFO-27 HB-EGF que sobre-expresan HB-EGF cultivado en agar suave. Como se muestra, las células de control formaron grandes números de colonias. Sin embargo, cuando células de clon 58 de EFO-27 HB-EGF se cultivaron ya sea con anticuerpos anti-HB-EGF U2-42, U2-39 o U2-45, el número de colonias se redujo dramáticamente. Más aún, la terapia de combinación de anticuerpos anti-HB-EGF con el anticuerpo anti-EGFR Erbitux inhibió completamente la formación de colonias.

La figura 36 muestra que anticuerpos anti-HB-EGF

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inhiben la angiogénesis inducida por HB-EGF *in vivo*. La formación de una red angiogénica en un ensayo de tapón de matrigel de ratón pudo ser bloqueada de una manera dependiente de dosis por los anticuerpos U2-42, U2-39 y U2-45.

La figura 37 ilustra la inhibición del crecimiento de tumores BxPC3 establecidos en modelos de xenoinjerto de ratón por anticuerpos U2-42 y U2-39.

Las figuras 38A-38C ilustran la inhibición del crecimiento de tumores de clon 58 de EFO-27 HB-EGF establecidos en modelos de xenoinjerto de ratón por anticuerpos U2-42, U2-39 y U2-45 (figura 38A). Como se muestra en la figura 38B, la eficacia de inhibición del crecimiento de tumores de xenoinjerto por anticuerpos U2-42 y U2-39 mostró ser dependiente de dosis. Más aún, el tratamiento en combinación con el anticuerpo anti-EGFR Erbitux lleva a una regresión completa del crecimiento de tumor y muestra la potente actividad sinérgica de los anticuerpos anti-HB-EGF como agentes para terapia de combinación (figura 38C).

Las figuras 39A-39B ilustran el uso de los anticuerpos anti-HB-EGF humanos para la detección de HB-EGF en tejido humano mediante inmunohistoquímica (figura 39A) y mediante ELISA (figura 39B).

La figura 40A ilustra un ensayo de raspadura que

indica la inhibición de migración inducida por HB-EGF de células de carcinoma escamoso epitelial CLS354 (boca).

La figura 40B ilustra un ensayo de transmigración que indica la inhibición de la migración inducida por HB-EGF de células de carcinoma epitelial Detroit 562 (faringe).

Las figuras 41A a 41B ilustran un ensayo de angiogénesis celular a base de esferoides que indica la inhibición de brote de células endoteliales estimulado por VEGF.

La figura 42 ilustra análisis de inmunohistoquímica (IHC) de muestras de xenoinjerto de tumor humano que indica la inhibición de tinción CD31 de tumor *in vivo*.

Las figuras 43A a 43B ilustran el modelo de xenoinjerto de tumor ovárico *in vivo* que indica el tratamiento de combinación de U2-39 con cisplatino y Avastin.

Descripción detallada de la invención

Los encabezados de sección usados en la presente son por propósitos organizacionales únicamente y no se deben considerar como limitativos de la materia descrita.

A menos que se defina lo contrario en la presente, los términos científicos y técnicos usados en relación con la presente solicitud tendrán los significados que se entienden comúnmente por aquellos de capacidad ordinaria en la técnica. Además, a menos que se requiera lo contrario por el contexto, los términos en singular incluirán los plurales y los

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términos en plural incluirán el singular.

Generalmente, las nomenclaturas usadas en relación con, y técnicas de, cultivo de células y tejidos, biología molecular, inmunología, microbiología, genética y química de proteínas y ácido nucleico e hibridación descritas en la presente son aquellas bien conocidas y usadas comúnmente en la técnica. Los métodos y técnicas de la presente solicitud se llevan a cabo generalmente de acuerdo con métodos convencionales bien conocidos en la técnica y como los descritos en varias referencias generales y más específicas que son citadas y descritas a lo largo de la presente descripción a menos que se indique lo contrario. Véase, por ejemplo, Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 3ª edición, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (2001) y Ausubel *et al.*, Current Protocols in Molecular Biology, Greene Publishing Associates (1992), y Harlow y Lane Antibodies: A Laboratory Manual Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1990), los cuales se incorporan en la presente a manera de referencia. Las reacciones enzimáticas y técnicas de purificación se llevan a cabo de acuerdo con las especificaciones del fabricante, como se logra comúnmente en la técnica o como se describe en la presente. La terminología usada en relación con, y los procedimientos y técnicas de laboratorio de, química analítica, química

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orgánica sintética y química medicinal y farmacéutica descritas en la presente son aquellas bien conocidas y usadas comúnmente en la técnica. Pueden usarse técnicas estándares para síntesis químicas, análisis químicos, preparación farmacéutica, formulación y suministro, y tratamiento de pacientes.

Se debe entender que esta invención no está limitada a la metodología, protocolos y reactivos particulares, etc., descritos en la presente y de esta manera pueden variar. La terminología usada en la presente tiene el propósito de describir modalidades particulares únicamente, y no se intenta que limite el alcance de lo descrito, lo cual se define únicamente por las reivindicaciones.

A diferencia de los ejemplos operativos, o en donde se indique lo contrario, todos los números que expresen cantidades de ingredientes o condiciones de reacción usadas en la presente se deben entender como modificados en todos los casos por el término "aproximadamente". El término "aproximadamente" cuando se usa en relación con porcentajes puede significar ± 1%.

A. Perspectiva general

Se proporcionan en la presente proteínas de unión a antígeno que se unen a proteína HB-EGF, en particular proteína HB-EGF humana (hHB-EGF). Las proteínas de unión a antígeno proporcionadas son polipéptidos en los cuales una o

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más regiones de determinación de complementariedad (CDR), como las descritas en la presente, son insertadas y/o unidas. En algunas proteínas de unión a antígeno, las CDR son insertadas en una región "estructural", la cual orienta las CDR de tal manera que las propiedades de unión a antígeno adecuadas de las CDR se logren. En general, las propiedades de unión a antígeno que son proporcionadas pueden interferir con, bloquear, reducir o modular la interacción entre HB-EGF y sus receptores cognados, incluyendo EGF-R y HER4.

Ciertas proteínas de unión a antígeno descritas en la presente son anticuerpos o son derivadas de anticuerpos. En ciertas modalidades, la estructura polipéptida de las proteínas de unión a antígeno se basa en anticuerpos, incluyendo, pero no limitados a, anticuerpos monoclonales, anticuerpos biespecíficos, minicuerpos, anticuerpos de dominio, anticuerpos sintéticos (algunas veces referidos en la presente como "miméticos de anticuerpo"), anticuerpos quiméricos, anticuerpos humanizados, anticuerpos humanos, fusiones de anticuerpos (algunas veces referidas en la presente como "conjugados de anticuerpos"), y fragmentos de los mismos, respectivamente. Las diferentes estructuras se describen en más detalle en la presente abajo.

Las proteínas de unión a antígeno provistas en la presente han demostrado unirse a varios epítopos de HB-EGF, en particular HB-EGF humano. Como se demuestra en los

ejemplos, la capacidad de HB-EGF para unirse a sus receptores cognados se reduce o se inhibe. Como consecuencia, las proteínas de unión a antígeno provistas en la presente son capaces de inhibir la actividad de HB-EGF. En particular, las proteínas de unión a antígeno que se unen a estos epítopos pueden tener una o más de las siguientes actividades: inhibir, entre otros, autofosforilación de EGF-R y HER4, inducción de la vía de transducción de señales de EGF-R y HER4, crecimiento de células inducido por EGF-R y HER4 y otros efectos fisiológicos inducidos por EGF-R y HER4 después de la unión a HB-EGF.

Las proteínas de unión a antígeno que son descritas en la presente tienen una variedad de utilidades. Algunas de las proteínas de unión a antígeno, por ejemplo, son útiles en ensayos de unión específica, purificación por afinidad de HB-EGF, en particular hHB-EGF y en ensayos de tamizado para identificar estos receptores. Además, las proteínas de unión a antígeno descritas pueden usarse para el diagnóstico y/o tratamiento de enfermedades, tales como trastornos proliferativos. Estas incluyen, pero no están limitadas a, varios tipos de cáncer.

B. Factor de crecimiento tipo factor de crecimiento epidérmico de unión a heparina (HB-EGF)

HB-EGF se produce por varias células tumorales y actúa como un factor de crecimiento de tumor autocrino.

Davis-Fleischer *et al.*, 1998, *Front Biosci.* 3:288-299; Iwamoto & Mekada, 2000, *Cytokine Growth Factor Rev.* 11:335-344. HB-EGF tiene una fuerte afinidad para heparina la cual puede incrementar la actividad biológica de HB-EGF. HB-EGF se produce como una proteína de transmembrana que es cortada proteolíticamente por metaloproteinasas para producir la forma soluble madura del factor de crecimiento.

HB-EGF se identificó primero a partir de sobrenadantes de macrófagos humanos cultivados en una forma soluble y secretada. En células humanas, el precursor proHB-EGF, actúa como el receptor de toxina de difteria. Varios tipos de células, incluyendo células epiteliales, queratinocitos, monocitos, células mesangiales, células linfoides y células de músculo esquelético, producen HB-EGF. Es un potente mitógeno y factor quimiotáctico para células epiteliales, fibroblastos, células de músculo liso y varias células de cáncer humano.

La forma de transmembrana de HB-EGF es sintetizada por muchos tipos de células como un precursor de transmembrana de 208 aminoácidos (tm-HB-EGF) que contiene EGF, dominios de unión a heparina, transmembrana y citoplásmicos. El dominio extracelular puede ser liberado como una forma soluble de 12 a 22 kDa de HB-EGF (sol-HB-EGF) a través de la acción de metaloproteinasas, la cual es regulada por diferentes receptores acoplados a proteína G

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(GPCR) o promotores de tumor tales como acetato de tetradecanoil forbol (TPA). Típicamente, una cantidad sustancial de precursor de HB-EGF de transmembrana permanece sin corte sobre la superficie celular.

Tanto tm-HB-EGF como sol-HB-EGF son biológicamente activos. Las funciones biológicas tanto de sol como de tm-HB-EGF son mediadas por el receptor de EGF (EGFR; HER1) y ErbB4 (HER4). La activación de estos tipos de estos receptores se cree que ocurre como una consecuencia de homo- o heterodimerización de receptor inducida por ligandos. Después de la activación, el receptor de EGF ha demostrado que incrementa el crecimiento celular, incrementa motilidad celular, inhibe apoptosis e incrementa transformación celular.

Las vías de señalización dependientes de EGFR pueden ser transactivadas después de la estimulación de receptores acoplados a proteína G (GPCR). La activación del ligando de proteínas G heterotriméricas por interacción con una GPCR da como resultado una señal intracelular que induce la actividad extracelular de una metaloproteinasa de transmembrana. Ligandos que activan la vía GPCR incluyen LPA (ácido lisofosfatídico), trombina, carbacol, bombesina y endotelina. Esta activación lleva a procesamiento extracelular de un precursor de factor de crecimiento de transmembrana y a la liberación del factor maduro que,

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directamente o a través de la matriz de proteoglucano, interactúa con el ectodominio de EGFR y lo activa a través de fosforilación de tirosina. Véase, Prenzel *et al.*, 1999, *Nature* 402:884-888. Así, HB-EGF es un componente de un mecanismo de señal de paso de triple membrana (TMPS) con el cual un GPCR activa una metaloproteinasa unida a membrana, la cual corta proHB-EGF para liberar el factor de crecimiento soluble, el cual activa subsecuentemente el receptor EGFF. La transactivación de EGFR ha estado ligada a varios estados de enfermedad tales como hipertrofia cardiaca (revisado en Shah BH, Catt KJ. Trends Pharmacol Sci. Mayo de 2003; 24(5):239-244), remodelación vascular (revisado en Eguchi *et al.*, 2003, *Biochem Soc Trans.* Diciembre de 2003; 31(*Pt 6*):1198-202) y cáncer (revisado en Fischer *et al.*, 2003, citado arriba).

Las secuencias para proteínas HB-EGF y ácidos nucleicos que codifican para esas proteínas están disponibles para alguien de capacidad en la técnica. Por ejemplo, estas secuencias de HB-EGF pueden encontrarse en la base de datos proporcionada por el Centro Nacional para Información de Biotecnología (NCBI) (véase http://www.ncbi.nim.nih.gov/). Un ejemplo de una secuencia para un HB-EGF es la secuencia de aminoácidos con los números de registro de NCBI NM 001945 y NP_001936 (gi:4503413). Esta secuencia es proporcionada a continuación para fácil referencia (SEQ ID NO: 1072):

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MKLLPSVVLKLFLAAVLSALVTGESLERLRRGLAAGTSNPDPPTVSTDQLL PLGGGRDRKVRDLQEADLDLLRVTLSSKPQALATPNKEEHGKRKKKGKGLGKKRDPCLRKY DKFCIHGECKYVKELRAPSCICHPGYHGERCHGLSLPVENRLYTYDHTTILAVVAVVLSSV CLLVIVGLLMFRYHRRG GYDVENEEKVKLGMTNSH.

Nótese que la secuencia de HB-EGF mostrada arriba (SEQ ID NO: 1072) tiene el péptido de señal de diecinueve aminoácidos (MKLLPSVVLK LFLAAVLSA, SEQ ID NO: 1073).

El dominio extracelular soluble consiste en los aminoácidos 1-149 de la secuencia de HB-EGF anterior. Esta secuencia para el dominio extracelular soluble de HB-EGF es proporcionada abajo como SEQ ID NO: 1074:

MKLLPSVVLKLFLAAVLSALVTGESLERRRGLAAGTSNPDPPTVSTDQLLP LGGGRDRKVRDLQEADLDLLRVTLSSKPQALATPNKEEHGKRKKKGKGLGKKRDPCLRKYK DFCIHGECKYVKELRAPSCICHPGYHGERCHGLSLP.

Después del corte, un HB-EGF maduro se genera que consiste en los aminoácidos 63-149 (87 aminoácidos). Esta secuencia para el HB-EGF es proporcionada a continuación como SEQ ID NO: 1075:

DLQEADLDLLRVTLSSKPQALATPNKEEHGKRKKKGKGLGKKRDPCLRKYK DFCIHGECKYVKELRAPSCICHPGYHGERCHGLSLP.

HB-EGF interactúa con y activa el receptor de factor de crecimiento epidérmico (EGFR). EGFR es una glicoproteína de transmembrana de 170 kDa que consiste en un dominio de unión a ligando extracelular, una región de transmembrana y un dominio intracelular con actividad

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tirosina cinasa. La unión de factores de crecimiento al EGFR da como resultado la internalización del complejo ligando-receptor, autofosforilación de receptor y otros substratos de proteína, llevando finalmente a la síntesis de ADN y división celular. El dominio de unión a ligando externo no sólo es estimulado por HB-EGF, sino también por EGF, TGFα y anfirregulina (AR).

La sobre-expresión del EGFR comúnmente es acompañada por la co-expresión de factores de crecimiento tipo EGF, sugiriendo que una vía autocrina para el control de crecimiento puede jugar un gran papel en la progresión de tumores. Se cree ahora ampliamente que éste es un mecanismo mediante el cual células tumorales pueden escapar de control fisiológico normal.

C. Proteínas de unión a antígeno receptor de HB-EGF

Se proporciona una variedad de agentes de unión selectivos útiles para regular la actividad de HB-EGF. Estos agentes incluyen, por ejemplo, proteínas de unión a antígeno que contienen un dominio de unión a antígeno (por ejemplo, anticuerpos de cadena individual, anticuerpos de dominio, inmunoadhesiones y polipéptidos con una región de unión a antígeno) y se unen específicamente a un polipéptido HB-EGF, en particular HB-EGF humano. Algunos de los agentes, por ejemplo, son útiles para inhibir la unión de HB-EGF a sus receptores, y se pueden entonces usar para inhibir,

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interferir con o modular una o más actividades asociadas con señalización mediada por HB-EGF.

En general, las proteínas de unión a antígeno que son proporcionadas comprenden típicamente uno o más CDR como las descritas en la presente (por ejemplo, 1, 2, 3, 4, 5 ó 6). En algunos casos, la proteína de unión a antígeno comprende (a) una estructura polipéptida y (b) uno o más CDR que son insertadas y/o unidas a la estructura de polipéptido. La estructura de polipéptido puede tener una variedad de formas diferentes. Por ejemplo, puede ser, o comprender, la estructura de un anticuerpo que ocurra naturalmente, o fragmento o variante del mismo, o puede ser de naturaleza completamente sintética. Ejemplos de varias estructuras de polipéptido se describen más abajo.

En ciertas modalidades, la estructura de polipéptido de las proteínas de unión a antígeno es un anticuerpo o se deriva de un anticuerpo, incluyendo, peor no limitado a, anticuerpos monoclonales, anticuerpos biespecíficos, minicuerpos, anticuerpos de dominio, anticuerpos sintéticos (conocidos algunas veces en la presente como "miméticos de anticuerpo"), anticuerpos quiméricos, anticuerpos humanizados, fusiones de anticuerpos (algunas veces referidas como "conjugados de anticuerpos"), y porciones o fragmentos de cada uno, respectivamente. En algunos casos, la proteína de unión a antígeno es un

fragmento inmunológico de un anticuerpo (por ejemplo un Fab, un Fab', un $F(ab')_2$, o un scFv). Las diferentes estructuras se describen más y se definen en la presente.

Ciertas de las proteínas de unión a antígeno proporcionadas en la presente se unen específicamente a HB-EGF humano. En una modalidad específica, la proteína de unión a antígeno se une específicamente a proteína HB-EGF humana que tiene la secuencia de aminoácidos de SEQ ID NO: 1072.

En modalidades en las que la proteína de unión a antígeno se usa para aplicaciones terapéuticas, una proteína de unión a antígeno puede inhibir, interferir con o modular una o más actividades biológicas de HB-EGF. En este caso, una proteína de unión a antígeno se une específicamente a/o inhibe sustancialmente la unión de HB-EGF humano a su receptor cuando un exceso de anticuerpo reduce la cantidad de HB-EGF humano unido a su receptor, o viceversa, en al menos aproximadamente 20%, 40%, 60%, 80%, 85%, o más (por ejemplo al medir la unión en un ensayo de unión competitiva *in vitro*). HB-EGF tiene muchos efectos biológicos distintos, los cuales pueden medirse en muchos ensayos diferentes en tipos de células diferentes; ejemplos de estos ensayos se proporcionan en la presente.

1. Estructura de anticuerpo que ocurre naturalmente

Algunas de las proteínas de unión a antígeno que se

proporcionan tienen la estructura asociada típicamente con anticuerpos que ocurren naturalmente. Las unidades estructurales de estos anticuerpos comprenden típicamente uno o más tetrámeros, cada uno compuesto de dos pares idénticos de cadenas de polipéptidos, aunque algunas especies de mamíferos también producen anticuerpos que sólo tienen una sola cadena pesada. En un anticuerpo típico, cada par o pareja incluye una cadena "ligera" de longitud completa (en ciertas modalidades, aproximadamente 25 kDa) y una cadena "pesada" de longitud completa (en ciertas modalidades, alrededor de 50-70 kDa). Cada cadena de inmunoglobulina individual está compuesta de varios "dominios" de inmunoglobulina, cada uno consistiendo en aproximadamente 90 a 110 aminoácidos y expresando un patrón de dobles característico. Estos dominios son las unidades básicas de las cuales se componen los polipéptidos de anticuerpos. La porción amino-terminal de cada cadena típicamente incluye un dominio variable que es responsable del reconocimiento de antígenos. La porción carboxi-terminal es más conservada evolutivamente que el otro extremo de la cadena y se conoce como la "región constante" o "región C". Las cadenas ligeras humanas generalmente se clasifican como cadenas ligeras kappa y lambda, y cada una de estas contiene un dominio variable y un dominio constante. Las cadenas pesadas se clasifican típicamente como cadenas mu, delta, gama, alfa o épsilon, y

éstas definen el isotipo del anticuerpo como IgM, IgD, IgG, IgA e IgE, respectivamente. IgG tiene varios subtipos, incluyendo, pero no limitados a, IgG1, IgG2, IgG3 e IgG4. Los subtipos de IgM incluyen IgM1 e IgM2. Los subtipos de IgA incluyen IgA1 e IgA2. En humanos, los isotipos IgA e IgD contienen cuatro cadenas pesadas y cuatro cadenas ligeras. Los isotipos IgG e IgE contienen dos cadenas pesadas y dos cadenas ligeras; y el isotipo IgM contiene cinco cadenas pesadas y cinco cadenas ligeras. La región C de la cadena pesada típicamente comprende uno o más dominios que pueden ser responsables de la función efectora. El número de dominios de región constante de la cadena pesada dependerá del isotipo. Las cadenas pesadas de IgG, por ejemplo, contienen tres regiones C conocidas como C_H1, C_H2 y C_H3. Los anticuerpos que se proporcionan pueden tener cualquiera de estos isotipos y subtipos. En ciertas modalidades, el anticuerpo HB-EGF es del subtipo IgG1, IgG2 o IgG4.

En las cadenas ligera y pesada de longitud completa, las regiones variables y constantes son unidas por una región "J" de aproximadamente doce o más aminoácidos, con la cadena pesada incluyendo también una región "D" de aproximadamente diez o más aminoácidos. Véase, por ejemplo, Fundamental Immunology, 2ª edición, Ch. 7 (Paul, W., ed.) 1989, Nueva York: Raven Press (incorporada en la presente a manera de referencia en su totalidad para todos los

propósitos). Las regiones variables de cada par de cadena ligera/pesada forman típicamente el sitio de unión a antígeno.

Un ejemplo de un dominio constante ligero kappa de un anticuerpo monoclonal HB-EGF ejemplar tiene la secuencia de aminoácidos:

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN SQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 187).

Un ejemplo de un dominio constante pesado de IgG2 de un anticuerpo monoclonal HB-EGF ejemplar tiene la estructura de aminoácidos:

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVH TFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAP PVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREE QFNSTFRVVSVLTVVHQDWLNGKEYKCVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRW QQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 188).

Las regiones variables de cadenas de inmunoglobulina exhiben generalmente la misma estructura general, que comprende regiones estructurales (FR) conservadas relativamente unidas por tres regiones hipervariables, muy comúnmente llamadas "regiones de determinación de complementariedad" o CDR. Las CDR de las dos cadenas de cada par de cadena pesada/cadena ligera

mencionadas arriba son alineadas típicamente por las regiones estructurales para formar una estructura que se une específicamente a un epítopo específico en la proteína objetivo (por ejemplo, HB-EGF). De la terminal N a la terminal C, las regiones variables de la cadena ligera y pesada que ocurre naturalmente se conforman típicamente con el siguiente orden de estos elementos: FR1, CDR1, FR2, CDR2, FR3, CDR3 y FR4. Se ha contemplado un sistema de numeración para asignar números a aminoácidos que ocupan posiciones en cada uno de estos dominios. Este sistema de numeración se define en Kabat Sequences of Proteins of Immunological Interest (1987 y 1991, NIH, Bethesda, MD), o Chothia & Lesk, 1987, *J. Mol. Biol.* 196:901-917; Chothia *et al.*, 1989, *Nature* 342:878-883.

Las diferentes regiones variables de la cadena ligera y cadena pesada proporcionadas en la presente se ilustran en las figuras 1A-1P, y las figuras 2A-2O, respectivamente. Cada una de estas regiones variables puede ser fijada a las regiones constantes de la cadena pesada y ligera anteriores para formar una cadena pesada y ligera de anticuerpo completa, respectivamente. Además, cada una de las secuencias de cadena pesada y ligera así generadas puede combinarse para formar una estructura de anticuerpo completa.

Ejemplos específicos de algunas de las cadenas ligera y pesada de longitud completa de los anticuerpos que

se proporcionan y sus secuencias de aminoácidos correspondientes se resumen en las figuras 3A-3K y figuras 4A-4O, respectivamente.

De nuevo, cada una de las cadenas ligeras ejemplares (U_L-1, U_L-2, U_L-3, etc.) listadas en las figuras 3A-3K pueden combinarse con cualquiera de las cadenas pesadas ejemplares mostradas en las figuras 4A-4O para formar un anticuerpo. Ejemplos de estas combinaciones incluyen U_L-1 combinada con cualquiera de U_H-1 a U_H-58; U_L-2 combinada con cualquiera de U_H-1 a U_H-58; o U_L-3 combinada con cualquiera de U_H-1 a U_H-58, y así sucesivamente. En algunos casos, los anticuerpos incluyen al menos una cadena ligera y una cadena pesada de aquellas listadas en las figuras 3A-3K y figuras 4A-4O, respectivamente. En otros casos, los anticuerpos contienen dos cadenas ligeras idénticas y dos cadenas pesadas idénticas. Como un ejemplo, un anticuerpo o fragmento inmunológicamente funcional puede incluir dos cadenas ligeras U_L-1 y dos cadenas pesadas U_H-1, o dos cadenas ligeras U_L-2 y dos cadenas pesadas U_H-2, o dos cadenas ligeras U_L-3 y dos cadenas pesadas U_H-3 y otras combinaciones similares de pares de cadenas ligeras y pares de cadenas pesadas como las listadas en las figuras 3A-3K y figuras 4A-4O, respectivamente.

Otros anticuerpos que se proporcionan son variantes de anticuerpos formadas mediante la combinación de las

cadenas pesada y ligera mostradas en las figuras 3A-3K y figuras 4A-4O, respectivamente, y comprenden cadenas ligeras y/o pesadas que tienen cada una por lo menos 70%, 75%, 80%, 85%, 90%, 95%, 97% o 99% de identidad con las secuencias de aminoácidos de estas cadenas. En algunos casos, estos anticuerpos incluyen al menos una cadena ligera y una cadena pesada, mientras que en otros casos las formas variantes contienen dos cadenas ligeras idénticas y dos cadenas pesadas idénticas.

2. Dominios variables de anticuerpos

También se proporcionan proteínas de unión a antígeno que contienen una región variable de la cadena ligera de anticuerpos seleccionada del grupo que consiste en U-V_L1, U-V_L2, U-V_L3, U-V_L4, U-V_L5, U-V_L6, U-V_L7, U-V_L8, U-V_L9, U-V_L10, U-V_L11, U-V_L12, U-V_L13, U-V_L14, U-V_L15, U-V_L16, U-V_L17, U-V_L18, U-V_L19, U-V_L20, U-V_L21, U-V_L22, U-V_L23, U-V_L24, U-V_L25, U-V_L26, U-V_L27, U-V_L28, U-V_L29, U-V_L30, U-V_L31, U-V_L32, U-V_L33, U-V_L34, U-V_L35, U-V_L36, U-V_L37, U-V_L38, U-V_L39, U-V_L40, U-V_L41, U-V_L42, U-V_L43, U-V_L44, U-V_L45, U-V_L46, U-V_L47, U-V_L48, U-V_L49, U-V_L50, U-V_L51, U-V_L52, U-V_L54, U-V_L55, U-V_L56, U-V_L57, U-V_L58, U-V_L59, U-V_L60, U-V_L61, U-V_L62, U-V_L64, y U-V_L65, y/o una región variable de la cadena ligera de anticuerpo seleccionada del grupo que consiste en U-V_H1, U-V_H2, U-V_H3, U-V_H4, U-V_H5, U-V_H6, U-V_H7, U-V_H8, U-V_H9, U-V_H10, U-V_H11, U-V_H12, U-V_H13, U-V_H14, U-V_H15, U-V_H16, U-V_H17, U-V_H18, U-V_H19, U-V_H20,

U-V_H21, U-V_H22, U-V_H23, U-V_H24, U-V_H25, U-V_H26, U-V_H27, U-V_H28, U-V_H29, U-V_H30, U-V_H31, U-V_H32, U-V_H33, U-V_H34, U-V_H35, U-V_H36, U-V_H37, U-V_H38, U-V_H39, U-V_H40, U-V_H41, U-V_H42, U-V_H43, U-V_H44, U-V_H45, U-VH46, U-V_H47, U-V_H48, U-V_H49, U-V_H50, U-V_H51, U-V_H52, U-V_H53, U-V_H54, U-V_H55, U-V_H56, U-V_H57, y U-V_H58, como se muestra en las figuras 1A-1P, y figuras 2A-2O, respectivamente, y fragmentos inmunológicamente funcionales, derivados, muteínas y variantes de estas regiones variables de la cadena ligera y cadena pesada.

Las alineaciones de secuencia de las diferentes regiones variables de la cadena ligera y pesada, respectivamente, se proporcionan en las figuras 10A y 10B, y figuras 11A y 11B, respectivamente.

Las proteínas de unión a antígeno de este tipo generalmente pueden ser designadas por la fórmula "V_Hx/V_Ly", en donde "x" corresponde al número de regiones variables de la cadena pesada y "y" corresponde al número de regiones variables de la cadena ligera (en general, x y y son cada uno 1 ó 2).

Cada una de las regiones variables de la cadena ligera listadas en las figuras 1A-1P pueden combinarse con cualquiera de las regiones variables de la cadena ligera mostradas en las figuras 2A-2O para formar una proteína de unión a antígeno. Ejemplos de estas combinaciones incluyen U-V_L1 combinada con cualquiera de U-V_H1, U-V_H2, U-V_H3, U-V_H4,

U-V_H5, U-V_H6, U-V_H7, U-V_H8, U-V_H9, U-V_H10, U-V_H11, U-V_H12, U-V_H13, U-V_H14, U-V_H15, U-V_H16, U-V_H17, U-V_H18, U-V_H19, U-V_H20, U-V_H21, U-V_H22, U-V_H23, U-V_H24, U-V_H25, U-V_H26, U-V_H27, U-V_H28, U-V_H29, U-V_H30, U-V_H31, U-V_H32, U-V_H33, U-V_H34, U-V_H35, U-V_H36, U-V_H37, U-V_H38, U-V_H39, U-V_H40, U-V_H41, U-V_H42, U-V_H43, U-V_H44, U-V_H45, U-V_H46, U-V_H47, U-V_H48, U-V_H49, U-V_H50, U-V_H51, U-V_H52, U-V_H53, U-V_H54, U-V_H55, U-V_H56, U-V_H57, o U-V_H58, o U-V_L2 combinada con cualquiera de U-V_H1, U-V_H2, U-V_H3, U-V_H4, U-V_H5, U-V_H6, U-V_H7, U-V_H8, U-V_H9, U-V_H10, U-V_H11, U-V_H12, U-V_H13, U-V_H14, U-V_H15, U-V_H16, U-V_H17, U-V_H18, U-V_H19, U-V_H20, U-V_H21, U-V_H22, U-V_H23, U-V_H24, U-V_H25, U-V_H26, U-V_H27, U-V_H28, U-V_H29, U-V_H30, U-V_H31, U-V_H32, U-V_H33, U-V_H34, U-V_H35, U-V_H36, U-V_H37, U-V_H38, U-V_H39, U-V_H40, U-V_H41, U-V_H42, U-VH43, U-V_H44, U-V_H45, U-V_H46, U-V_H47, U-V_H48, U-V_H49, U-V_H50, U-V_H51, U-V_H52, U-V_H53, U-V_H54, U-V_H55, U-V_H56, U-V_H57, o U-V_H58, etc.

En algunos casos, la proteína de unión a antígeno incluye por lo menos una región variable de la cadena pesada y/o una región variable de la cadena ligera de aquellas listadas en las figuras 1A-1P, y figuras 2A-2O, respectivamente. En algunos casos, la proteína de unión a antígeno incluye por lo menos dos regiones variables de la cadena pesada y/o regiones variables de la cadena ligera diferentes de aquellas listadas en las figuras 1A-1P, y figuras 2A-2O, respectivamente. Un ejemplo de esta proteína de unión a antígeno comprende (a) una U-V_L1, y (b) una de U-

V_L2, U-V_L3, U-V_L4, U-V_L5, U-V_L6, U-V_L7, U-V_L8, U-V_L9, U-V_L10, U-V_L11, U-V_L12, U-V_L13, U-V_L14, U-V_L15, U-V_L16, U-V_L17, U-V_L18, U-V_L19, U-V_L20, U-V_L21, U-V_L22, U-V_L23, U-V_L24, U-V_L25, U-V_L26, U-V_L27, U-V_L28, U-V_L29, U-V_L30, U-V_L31, U-V_L32, U-V_L33, U-V_L34, U-V_L35, U-V_L36, U-V_L37, U-V_L38, U-V_L39, U-V_L40, U-V_L41, U-V_L42, U-V_L43, U-V_L44, U-V_L45, U-V_L46, U-V_L47, U-V_L48, U-V_L49, U-V_L50, U-V_L51, U-V_L52, U-V_L54, U-V_L55, U-V_L56, U-V_L57, U-V_L58, U-V_L59, U-V_L60, U-V_L61, U-V_L62, U-V_L64, y U-V_L65. De nuevo otro ejemplo de esta proteína de unión a antígeno comprende (a) una U-V_L2, y (b) una de U-V_L1, U-V_L3, U-V_L4, U-V_L5, U-V_L6, U-V_L7, U-V_L8, U-V_L9, U-V_L10, U-V_L11, U-V_L12, U-V_L13, U-V_L14, U-V_L15, U-V_L16, U-V_L17, U-V_L18, U-V_L19, U-V_L20, U-V_L21, U-V_L22, U-V_L23, U-V_L24, U-V_L25, U-V_L26, U-V_L27, U-V_L28, U-V_L29, U-V_L30, U-V_L31, U-V_L32, U-V_L33, U-V_L34, U-V_L35, U-V_L36, U-V_L37, U-V_L38, U-V_L39, U-V_L40, U-V_L41, U-V_L42, U-V_L43, U-V_L44, U-V_L45, U-V_L46, U-V_L47, U-V_L48, U-V_L49, U-V_L50, U-V_L51, U-V_L52, U-V_L54, U-V_L55, U-V_L56, U-V_L57, U-V_L58, U-V_L59, U-V_L60, U-V_L61, U-V_L62, U-V_L64, y U-V_L65. De nuevo otro ejemplo más de esta proteína de unión a antígeno comprende (a) una U-V_L3, y (b) una de U-V_L1, U-V_L2, U-V_L4, U-V_L5, U-V_L6, U-V_L7, U-V_L8, U-V_L9, U-V_L10, U-V_L11, U-V_L12, U-V_L13, U-V_L14, U-V_L15, U-V_L16, U-V_L17, U-V_L18, U-V_L19, U-V_L20, U-V_L21, U-V_L22, U-V_L23, U-V_L24, U-V_L25, U-V_L26, U-V_L27, U-V_L28, U-V_L29, U-V_L30, U-V_L31, U-V_L32, U-V_L33, U-V_L34, U-V_L35, U-V_L36, U-V_L37, U-V_L38, U-V_L39, U-V_L40, U-V_L41, U-V_L42, U-V_L43, U-V_L44, U-V_L45, U-V_L46, U-V_L47, U-V_L48, U-V_L49, U-V_L50, U-V_L51, U-V_L52, U-V_L54,

U-V_L55, U-V_L56, U-V_L57, U-V_L58, U-V_L59, U-V_L60, U-V_L61, U-V_L62, U-V_L64, y U-V_L65, etc.

De nuevo otro ejemplo de esta proteína de unión a antígeno comprende (a) una U-V_H1, y (b) una de U-V_H2, U-V_H3, U-V_H4, U-V_H5, U-V_H6, U-V_H7, U-V_H8, U-V_H9, U-V_H10, U-V_H11, U-V_H12, U-V_H13, U-V_H14, U-V_H15, U-V_H16, U-V_H17, U-V_H18, U-V_H19, U-V_H20, U-V_H21, U-V_H22, U-V_H23, U-V_H24, U-V_H25, U-V_H26, U-V_H27, U-V_H28, U-V_H29, U-V_H30, U-V_H31, U-V_H32, U-V_H33, U-V_H34, U-V_H35, U-V_H36, U-V_H37, U-V_H38, U-V_H39, U-V_H40, U-V_H41, U-V_H42, U-V_H43, U-V_H44, U-V_H45, U-V_H46, U-V_H47, U-V_H48, U-V_H49, U-V_H50, U-V_H51, U-V_H52, U-V_H53, U-V_H54, U-V_H55, U-V_H56, U-V_H57, y U-V_H58. Otro ejemplo comprende (a) una U-V_H2, y (b) una de U-V_H1, U-V_H3, U-V_H4, U-V_H5, U-V_H6, U-V_H7, U-V_H8, U-V_H9, U-V_H10, U-V_H11, U-V_H12, U-V_H13, U-V_H14, U-V_H15, U-V_H16, U-V_H17, U-V_H18, U-V_H19, U-V_H20, U-V_H21, U-V_H22, U-V_H23, U-V_H24, U-V_H25, U-V_H26, U-V_H27, U-V_H28, U-V_H29, U-V_H30, U-V_H31, U-V_H32, U-V_H33, U-V_H34, U-V_H35, U-V_H36, U-V_H37, U-V_H38, U-V_H39, U-V_H40, U-V_H41, U-V_H42, U-V_H43, U-V_H44, U-V_H45, U-V_H46, U-V_H47, U-V_H48, U-V_H49, U-V_H50, U-V_H51, U-V_H52, U-V_H53, U-V_H54, U-V_H55, U-V_H56, U-V_H57, y U-V_H58. De nuevo otro ejemplo comprende (a) una U-V_H3, y (b) una de U-V_H1, U-V_H2, U-V_H4, U-V_H5, U-V_H6, U-V_H7, U-V_H8, U-V_H9, U-V_H10, U-V_H11, U-V_H12, U-V_H13, U-V_H14, U-V_H15, U-V_H16, U-V_H17, U-V_H18, U-V_H19, U-V_H20, U-V_H21, U-V_H22, U-V_H23, U-V_H24, U-V_H25, U-V_H26, U-V_H27, U-V_H28, U-V_H29, U-V_H30, U-V_H31, U-V_H32, U-V_H33, U-V_H34, U-V_H35, U-V_H36, U-V_H37, U-V_H38, U-V_H39, U-V_H40, U-V_H41, U-V_H42, U-V_H43,

U-V_H44, U-V_H45, U-V_H46, U-V_H47, U-V_H48, U-V_H49, U-V_H50, U-V_H51, U-V_H52, U-V_H53, U-V_H54, U-V_H55, U-V_H56, U-V_H57, y U-V_H58, etc.

Las diferentes combinaciones de las regiones variables de la cadena pesada pueden combinarse con cualquiera de las diferentes combinaciones de las regiones variables de la cadena ligera.

En otros casos, la proteína de unión a antígeno contiene dos regiones variables de la cadena ligera idénticas y/o dos regiones variables de la cadena pesada idénticas. Como un ejemplo, la proteína de unión a antígeno puede ser un anticuerpo o fragmento inmunológicamente funcional que incluya dos regiones variables de la cadena ligera y dos regiones variables de la cadena pesada en combinaciones de pares de regiones variables de la cadena ligera y pares de regiones variables de la cadena pesada como los listados en las figuras 1A-1P, y figuras 2A-2O, respectivamente.

Algunas proteínas de unión a antígeno que se proporcionan comprenden un dominio variable de la cadena ligera que comprende una secuencia de aminoácidos que difiere de la secuencia de un dominio variable de la cadena ligera seleccionada de U-V_L1, U-V_L2, U-V_L3, U-V_L4, U-V_L5, U-V_L6, U-V_L7, U-V_L8, U-V_L9, U-V_L10, U-V_L11, U-V_L12, U-V_L13, U-V_L14, U-V_L15, U-V_L16, U-V_L17, U-V_L18, U-V_L19, U-V_L20, U-V_L21, U-V_L22, U-V_L23, U-V_L24, U-V_L25, U-V_L26, U-V_L27, U-V_L28, U-V_L29, U-V_L30, U-V_L31, U-V_L32, U-V_L33, U-V_L34, U-V_L35, U-V_L36, U-V_L37, U-V_L38, U-

V_L39, U-V_L40, U-V_L41, U-V_L42, U-V_L43, U-V_L44, U-V_L45, U-V_L46, U-V_L47, U-V_L48, U-V_L49, U-V_L50, U-V_L51, U-V_L52, U-V_L54, U-V_L55, U-V_L56, U-V_L57, U-V_L58, U-V_L59, U-V_L60, U-V_L61, U-V_L62, U-V_L64, o U-V_L65 en sólo 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 ó 15 residuos de aminoácido, en donde cada una de estas diferencias de secuencia es independientemente una supresión, inserción o sustitución de un aminoácido. La región variable de la cadena ligera en algunas proteínas de unión a antígeno comprende una secuencia de aminoácidos que tiene al menos 70%, 75%, 80%, 85%, 90%, 95%, 97% o 99% identidad de secuencia con las secuencias de aminoácidos de la región variable de la cadena ligera de U-V_L1, U-V_L2, U-V_L3, U-V_L4, U-V_L5, U-V_L6, U-V_L7, U-V_L8, U-V_L9, U-V_L10, U-V_L11, U-V_L12, U-V_L13, U-V_L14, U-V_L15, U-V_L16, U-V_L17, U-V_L18, U-V_L19, U-V_L20, U-V_L21, U-V_L22, U-V_L23, U-V_L24, U-V_L25, U-V_L26, U-V_L27, U-V_L28, U-V_L29, U-V_L30, U-V_L31, U-V_L32, U-V_L33, U-V_L34, U-V_L35, U-V_L36, U-V_L37, U-V_L38, U-V_L39, U-V_L40, U-V_L41, U-V_L42, U-V_L43, U-V_L44, U-V_L45, U-V_L46, U-V_L47, U-V_L48, U-V_L49, U-V_L50, U-V_L51, U-V_L52, U-V_L54, U-V_L55, U-V_L56, U-V_L57, U-V_L58, U-V_L59, U-V_L60, U-V_L61, U-V_L62, U-V_L64, o U-V_L65.

Ciertos anticuerpos comprenden un dominio variable de la cadena pesada que comprende una secuencia de aminoácidos que difiere de la secuencia de un dominio variable de la cadena pesada seleccionado de U-V_H1, U-V_H2, U-V_H3, U-V_H4, U-V_H5, U-V_H6, U-V_H7, U-V_H8, U-V_H9, U-V_H10, U-V_H11,

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U-V_H12, U-V_H13, U-V_H14, U-V_H15, U-V_H16, U-V_H17, U-V_H18, U-V_H19, U-V_H20, U-V_H21, U-V_H22, U-V_H23, U-V_H24, U-V_H25, U-V_H26, U-V_H27, U-V_H28, U-V_H29, U-V_H30, U-V_H31, U-V_H32, U-V_H33, U-V_H34, U-V_H35, U-V_H36, U-V_H37, U-V_H38, U-V_H39, U-V_H40, U-V_H41, U-V_H42, U-V_H43, U-V_H44, U-V_H45, U-V_H46, U-V_H47, U-V_H48, U-V_H49, U-V_H50, U-V_H51, U-V_H52, U-V_H53, U-V_H54, U-V_H55, U-V_H56, U-V_H57, o U-V_H58 en sólo 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 o 15 residuos de aminoácido, en donde cada una de estas diferencias de secuencia es independientemente ya sea una supresión, inserción o sustitución de un aminoácido. La región variable de la cadena pesada en algunas proteínas de unión a antígeno comprende una secuencia de aminoácidos que es al menos 70%, 75%, 80%, 85%, 90%, 95%, 97% o 99% de identidad de secuencia con las secuencias de aminoácidos de la región variable de la cadena pesada de U-V_H1, U-V_H2, U-V_H3, U-V_H4, U-V_H5, U-V_H6, U-V_H7, U-V_H8, U-V_H9, U-V_H10, U-V_H11, U-V_H12, U-V_H13, U-V_H14, U-V_H15, U-V_H16, U-V_H17, U-V_H18, U-V_H19, U-V_H20, U-V_H21, U-V_H22, U-V_H23, U-V_H24, U-V_H25, U-V_H26, U-V_H27, U-V_H28, U-V_H29, U-V_H30, U-V_H31, U-V_H32, U-V_H33, U-V_H34, U-V_H35, U-V_H36, U-V_H37, U-V_H38, U-V_H39, U-V_H40, U-V_H41, U-V_H42, U-V_H43, U-V_H44, U-V_H45, U-V_H46, U-V_H47, U-V_H48, U-V_H49, U-V_H50, U-V_H51, U-V_H52, U-V_H53, U-V_H54, U-V_H55, U-V_H56, U-V_H57, o U-V_H58.

Aún otras proteínas de unión a antígeno, por ejemplo, anticuerpos o fragmentos inmunológicamente funcionales incluyen formas variantes de una cadena ligera

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variante y una cadena pesada variante como las recién descritas.

3. CDR

Las proteínas de unión a antígeno descritas en la presente son polipéptidos en los cuales una o más CDR son injertadas, insertadas y/o unidas. Una proteína de unión a antígeno puede tener 1, 2, 3, 4, 5 ó 6 CDR. Una proteína de unión a antígeno puede tener entonces, por ejemplo, una CDR1 de la cadena ligera ("CDRL1"), y/o una CDR2 de la cadena ligera ("CDRL2") y/o una CDR de la cadena ligera ("CDRL3") y/o una CDR1 de la cadena pesada ("CDRH1"), y/o una CDR2 de la cadena pesada ("CDRH2"), y/o una CDR3 de la cadena pesada ("CDRH3"). Algunas proteínas de unión a antígeno incluyen tanto una CDRL3 como una CDRH3. Las CDR específicas se identifican en la figura 6A-6F, y figuras 7A-7E.

Las regiones de determinación de complementariedad (CDR) y regiones estructurales (FR) (ejemplos de secuencias de aminoácidos de FR de la cadena ligera y pesada se dan en las figuras 8A-8H y figuras 9A-9F, respectivamente) de un anticuerpo dado pueden identificarse usando el sistema descrito por Kabat *et al.*, en Sequences of Proteins of Immunological Interest, 5ª edición, US Dept. of Health and Human Services, PHS, NIH, NIH Publication No. 91-3242, 1991. Ciertas modalidades que se describen en la presente comprenden una o más secuencias de aminoácido que son

idénticas o tienen identidad de secuencia sustancial con las secuencias de aminoácidos de una o más de las CDR presentadas en las figuras 6A-6F (CDRL) y figuras 7A-7E (CDRH).

La estructura y propiedades de las CDR dentro de un anticuerpo que ocurre naturalmente han sido descritas, véase arriba. Brevemente, en un anticuerpo tradicional, las CDR son insertadas dentro de una estructura en la región variable de la cadena pesada y ligera en donde constituyen las regiones responsables de la unión y reconocimiento de antígenos. Una región variable comprende al menos tres CDR de la cadena pesada o ligera, véase arriba (Kabat et al., 1991, *Sequences of Proteins of Immunological Interest*, Public Health Services N.I.H., Bethesda, MD; véase también Chothia and Lesk, 1987, *J. Mol. Biol.* 196:901-917; Chothia *et al.*, 1989, *Nature* 342: 877-883), dentro de una región estructural (regiones estructurales designadas 1-4, FR1, FR2, FR3 y FR4, por Kabat *et al.*, 1991, citado arriba, véase también Chothia y Lesk, 1987, citado arriba). Las CDR provistas en la presente, sin embargo, pueden no sólo ser usadas para definir el dominio de unión a antígeno de una estructura de anticuerpo tradicional, sino que pueden ser insertadas en una variedad de otras estructuras de polipéptidos, como se describe en la presente.

En un aspecto, las CDR proporcionadas son (a) una CDRL seleccionada del grupo que consiste en (i) una CDRL1

seleccionada del grupo que consiste en SEQ ID NOs: 189-217; (ii) una CDRL2 seleccionada del grupo que consiste en SEQ ID NO: 218-233; (iii) una CDRL3 seleccionada del grupo que consiste en SEQ ID NO: 234-274, y (iv) una CDRL de (i), (ii) y (iii) que contiene una o más sustituciones, supresiones o inserciones de aminoácido de no más de cinco, cuatro, tres, dos o un aminoácido; (B) una CDRH seleccionada del grupo que consiste en (i) una CDRH1 seleccionada del grupo que consiste en SEQ ID NO: 275-299; (ii) una CDRH2 seleccionada del grupo que consiste en SEQ ID NO: 300-331; (iii) una CDRH3 seleccionada del grupo que consiste en SEQ ID NO: 332-372; y (iv) una CDRLH de (i), (ii) y (iii) que contiene una o más sustituciones, supresiones o inserciones de aminoácido de no más de cinco, cuatro, tres, dos o más aminoácidos.

En otro aspecto más, formas variantes de las CDR se proporcionan que tienen al menos 80%, 85%, 90% o 95% de identidad de secuencia con una secuencia de CDR listada en las figuras 6A-6F y figuras 7A-7E.

En otro aspecto más, las CDR descritas en la presente incluyen secuencias de consenso derivadas de grupos de anticuerpos monoclonales relacionados. Como se describe en la presente, una "secuencia de consenso" se refiere a secuencias de aminoácido que tienen aminoácidos comunes entre un número de secuencias y aminoácidos variables que pueden variar dentro de secuencias de aminoácidos dadas. Las

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secuencias de consenso de CDR proporcionadas incluyen CDR que corresponden a cada una de CDRL1, CDRL2, CDRL3, CDRH1, CDRH2 y CDRH3.

Las secuencias de consenso fueron determinadas usando un enfoque de análisis filogénico estándar de las CDR que corresponden a las U-V_L y U-V_H de anticuerpos anti-HB-EGF. Primero, en este enfoque, secuencias de aminoácidos que corresponden a los dominios variables completos ya sea de U-V_L o U-V_H fueron convertidas en formato FASTA para facilidad de procesamiento de alineaciones comparativas y filogenias interferentes. Con base en esta comparación, cada una de las regiones variables de la cadena ligera y pesada, respectivamente fueron divididas en grupos filogenéticamente emparentados, es decir, las regiones variables de la cadena ligera fueron divididas en seis grupos A, B, C, D, E y F (véase figura 12A y 12B), y las regiones variables de la cadena pesada se dividieron en siete grupos A, B, C, D, E, F y G (véase figura 12C). Después, dentro de cada uno de estos grupos, la comparación de cada una de las regiones CDRL1, CDRL2, CDRL3, CDRH1, CDRH2, CDRH3 se usó para definir colecciones de consenso.

El grupo A de las CDR de la cadena ligera incluye las siguientes colecciones de consenso:

a. una CDRL1 de la fórmula genérica $X_1SSQSLX_2X_3SDGX_4TYLX_5$ (SEQ ID NO: 1035), en donde

X_1 es K o R,

X_2 es L o V,

X_3 es H o Y,

X_4 es K o N,

X_5 es N, S o Y.

b. una CDRL2 de la fórmula genérica $X_1X_2SNX_3X_4S$ (SEQ ID NO: 1041), en donde

X_1 es E o K,

X_2 es I o V,

X_3 es R o W,

X_4 es D o F.

c. una CDRL3 de la fórmula genérica $X_1QX_2X_3X_4X_5PX_6X_7$ (SEQ ID NO: 1046), en donde

X_1 es I o M,

X_2 es A, G o S,

X_3 es I o T,

X_4 es H o Q,

X_5 es F, L o W,

X_6 es C, I, H, L o T,

X_7 es S o T.

El grupo B de las CDR de la cadena ligera incluye las siguientes condiciones de consenso:

a. una CDRL1 de la fórmula genérica $RASQX_1ISX_2YLN$ (SEQ ID NO: 1036), en donde

X_1 ES R, S o T,

X_2 ES R o S.

b. una CDRL2 de la fórmula genérica $X_1X_2SX_4LQS$ (SEQ ID NO: 1042), en donde

X_1 es A o T,

X_2 es A, E o V,

X_3 es S o T.

c. una CDRL3 de la fórmula genérica $QQX_1X_2X_3X_4X_5IT$ (SEQ ID NO: 1047), en donde

X_1 es I o S,

X_2 es F o Y,

X_3 es F, I, S o Y,

X_4 es A, S o T,

X_5 es P o S.

El grupo C de las CDR de la cadena ligera incluye las siguientes colecciones de consenso:

a. una CDRL1 de la fórmula genérica $RASQX_1IX_2X_3X_4LX_5$ (SEQ ID NO: 1037), en donde

X_1 es D, G, S o T,

X_2 es A, R o S,

X_3 es H, I, N, R, S o T,

X_4 es D, W o Y,

X_5 es A, G o N.

b. una CDRL2 de la fórmula genérica X_1ASX_2LQS (SEQ ID NO: 1043), en donde

X_1 es A o V,

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X_2 es S o T.

c. una CDRL3 de la fórmula genérica $X_1X_2X_3X_4X_5X_6X_7X_8T$ (SEQ IDNO: 1048), en donde

X_1 es L o Q,

X_2 es K, N o Q,

X_3 es A, H, S o Y,

X_4 es H, N o Y,

X_5 es N, S o T,

X_6 es A, F, I, T, V o Y,

X_7 es P o ningún aminoácido,

X_8 es F, L o P.

El grupo D de las CDR de la cadena ligera incluye las siguientes colecciones de consenso:

a. una CDRL1 de la fórmula genérica $QASQDIX_1X_2X_3LN$ (SEQ ID NO: 1038), en donde

X_1 es S o T,

X_2 es D o N,

X_3 es S o Y.

b. una CDRL2 de la fórmula genérica $DASX_1LET$ (SEQ ID NO: 1044), en donde

X_1 es I o N.

c. una CDRL3 de la fórmula genérica $QX_1X_2DX_3LPX_4X_5$ (SEQ ID NO: 1049), en donde

X_1 es H o Q,

X_2 es C o Y,

X_3 es D, I, N, S o Y,

X_4 es F, I o L,

X_5 es A, S o T.

El grupo E de las CDR de la cadena ligera incluye las siguientes colecciones de consenso:

a. una CDRL1 de la fórmula genérica $RASQX_1VX_2X_3X_4X_5LA$ (SEQ ID NO: 1039), en donde

X_1 es S o T,

X_2 es I o S,

X_3 es R o S,

X_4 es S, N o ningún aminoácido,

X_5 es Y o ningún aminoácido.

b. una CDRL2 de la fórmula genérica GASSRAT (SEQ ID NO: 223).

c. una CDRL3 de la fórmula genérica $QQX_1X_2X_3X_4PX_5X_6X_7$ (SEQ ID NO: 1050), en donde

X_1 es H o Y,

X_2 es G o N,

X_3 es N o S,

X_4 es S o W,

X_5 es P o ningún aminoácido,

X_6 es R o W,

X_7 es S o T.

El grupo F de las CDR de la cadena ligera incluye las siguientes colecciones de consenso:

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a. una CDRL1 de la fórmula genérica $KSSQX_1X_2LX_3X_4SNNKNYLX_5$ (SEQ ID NO: 1040), en donde

X_1 es N o S,

X_2 es I o V,

X_3 es D o Y,

X_4 es N, R o S,

X_5 es A o V.

b. una CDRL2 de la fórmula genérica $WASX_1RES$ (SEQ ID NO: 1045), en donde

X_1 es A o T.

c. una CDRL3 de la fórmula genérica $X_1QYX_2X_3X_4X_5X_6X_7F$ (SEQ ID NO: 1051), en donde

X_1 es H o Q,

X_2 es F o Y,

X_3 es G, I o S,

X_4 es F, I o T,

X_5 es M, P, S o T,

X_6 es F, L, R o W,

X_7 es S o T.

El grupo A de las CDR de la cadena pesada incluye las siguientes colecciones de consenso:

a. una CDRH1 de la fórmula genérica $GYTX_1TX_2X_3X_4X_5X_6$ (SEQ ID NO: 1052), en donde

X_1 es F o L,

X_2 es E, G o S,

X_3 es H, L o Y,

X_4 es G, S o Y,

X_5 es I o M,

X_6 es H o S.

b. una CDRH2 de la fórmula genérica $X_1X_2X_3X_4X_5X_6GX_7TX_8X_9X_{10}QKX_{11}X_{12}$ (SEQ ID NO: 1058), en donde

X_1 es S o W,

X_2 es F o I,

X_3 es D, N o S,

X_4 es A, P,

X_5 es E, N o S,

X_6 es D, N o S,

X_7 es E, G o N,

X_8 es I o N,

X_9 es C, H o Y,

X_{10} es A o T,

X_{11} es F o L,

X_{12} es D o G.

c. una CDRH3 de la fórmula genérica $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}DX_{12}$ (SEQ ID NO: 1065), en donde

X_1 es E o S,

X_2 es D, G o ningún aminoácido,

X_3 es D, N o ningún aminoácido,

X_4 es G o ningún aminoácido,

X_5 es G o ningún aminoácido,

X_6 es W, Y o ningún aminoácido,

X_7 es I, N o Y,

X_8 es A o Y,

X_9 es g, V o Y,

X_{10} es A, F o G,

X_{11} es F, L o M,

X_{12} es V o Y.

El grupo B de las CDR de la cadena pesada incluyen las siguientes colecciones de consenso:

a. una CDRH1 de la fórmula genérica $GYX_1FTSYWIG$ (SEQ ID NO: 1053), en donde

X_1 es R o S.

b. una CDRH2 de la fórmula genérica $IIYPX_1DSDX_2RYSPSFQG$ (SEQ ID NO: 1059), en donde

X_1 es D o G,

X_2 es A, I o T.

c. una CDRH3 de la fórmula genérica $QX_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_1YX_{12}X_{13}X_{14}DX_{15}$ (SEQ ID NO: 1066), en donde

X_1 es G o ningún aminoácido,

X_2 es K, L o Y,

X_3 es A, g o S,

X_4 es S, V o Y,

X_5 es A o G,

X_6 es G o ningún aminoácido,

X_7 es T o ningún aminoácido,

X_8 es S o ningún aminoácido,

X_9 es Y o ningún aminoácido,

X_{10} es W o Y,

X_{11} es G, S o Y,

X_{12} es F o Y,

X_{13} es G o ningún aminoácido,

X_{14} es M o ningún aminoácido,

X_{15} es V o Y.

El grupo C de las CDR de la cadena pesada incluye las siguientes colecciones de consenso:

a. una CDRH1 de la fórmula genérica $GFTX_1SX_2X_3MH$ (SEQ ID NO: 1054), en donde

X_1 es R o S,

X_2 es H o Y,

X_3 es D o G.

b. una CDRH2 de la fórmula genérica $X_1IX_2X_3DGSX_4X_5X_6YX_7DSVX_8G$ (SEQ ID NO: 1060), en donde

X_1 es F o V,

X_2 es S o W,

X_3 es D, S o Y,

X_4 es I, N o T,

X_5 es K o Q,

X_6 es N, R o Y,

X_7 es A, T o V,

X_8 es K o R.

c. una CDRH3 de la fórmula genérica $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}$ (SEQ ID NO: 1067), en donde

X_1 es D, G, L, S o ningún aminoácido,

X_2 es G, H, W, Y o ningún aminoácido,

X_3 es A, F, W, Y o ningún aminoácido,

X_4 es D, G, Q, T o ningún aminoácido,

X_5 es G, I, Q, S o ningún aminoácido,

X_6 es A, D, N, Q, S o ningún aminoácido,

X_7 es G, Y o ningún aminoácido,

X_8 es D, Y o ningún aminoácido,

X_9 es Y o ningún aminoácido,

X_{10} es A, E, N o Y,

X_{11} es G, P, T, V o Y,

X_{12} es F o I,

X_{13} es D o Q,

X_{14} es C, H, V o Y.

El grupo D de las CDR de la cadena pesada incluyen las siguientes colecciones de consenso:

a. una CDRH1 de la fórmula genérica $GFX_1FSX_2YX_3MX_4$ (SEQ ID NO: 1055), en donde

X_1 es P o T,

X_2 es A, R o S,

X_3 es A o S,

X_4 es N o S.

b. una CDRH2 de la fórmula genérica

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$X_1ISX_2SX_3X_4X_5X_6YYADSVKG$ (SEQ ID NO: 1061), en donde

X_1 es A, H o Y,

X_2 es G, R o S,

X_3 es G o S,

X_4 es G, R o S,

X_5 es S, T o Y,

X_6 es I o T.

c. una CDRH3 de la fórmula genérica $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}DX_{18}$ (SEQ ID NO: 1068), en donde

X_1 es E, D o ningún aminoácido,

X_2 es G, R o ningún aminoácido,

X_3 es I, V, Y o ningún aminoácido,

X_4 es A, G, L o N,

X_5 es A, G, V o W,

X_6 es A, N, R o T,

X_7 es G, N, P o ningún aminoácido,

X_8 es G, T o ningún aminoácido,

X_9 es A o ningún aminoácido,

X_{10} es D, E o ningún aminoácido,

X_{11} es S, Y o ningún aminoácido,

X_{12} es G, Y o ningún aminoácido,

X_{13} es N, Y o ningún aminoácido,

X_{14} es Y o ningún aminoácido,

X_{15} es D, Y o ningún aminoácido,

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X_{16} es A, G o ningún aminoácido,

X_{17} es F o M,

X_{18} es I, V o Y.

El grupo E de las CDR de la cadena pesada incluye las siguientes colecciones de consenso:

a. una CDRH1 de la fórmula genérica $GX_1SX_2SX_3X_4X_5X_6X_7WX_8$ (SEQ ID NO: 1056), en donde

X_1 es D o G,

X_2 es F, I o V,

X_3 es R, S o ningún aminoácido,

X_4 es g, Y o ningún aminoácido,

X_5 es D, G, S o ningún aminoácido,

X_6 es A, S o Y,

X_7 es A o Y,

X_8 es N o S.

b. una CDRH2 de la fórmula genérica $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}YX_{12}X_{13}SX_{14}KS$ (SEQ ID NO: 1062), en donde

X_1 es E, R o Y,

X_2 es I o T,

X_3 es H, N o Y,

X_4 es C, H, S, T o Y,

X_5 es S o r,

X_6 es G o S,

X_7 es G, K, S o T,

X_8 es T o W,

X_9 es N o Y,

X_{10} es N o ningún aminoácido,

X_{11} es D o ningún aminoácido,

X_{12} es A o N,

X_{13} es P o V,

X_{14} es L o V.

c. una CDRH3 de la fórmula genérica

$X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}X_{18}X_{19}X_{20}X_{21}X_{22}X_{23}$

(SEQ ID NO: 1069), en donde

X_1 es A, D, G, S o T,

X_2 es A, E, G, L, N, R, Y o ningún aminoácido,

X_3 es A, G, L, N, R, T, Y o ningún aminoácido,

X_4 es D, G, R, S, V, Y o ningún aminoácido,

X_5 es A, G, I, S, V, Y o ningún aminoácido,

X_6 es F, G, L, R, V o ningún aminoácido,

X_7 es L, T, Y o ningún aminoácido,

X_8 es Y o ningún aminoácido,

X_9 es Y o ningún aminoácido,

X_{10} es D o ningún aminoácido,

X_{11} es S o ningún aminoácido,

X_{12} es S o ningún aminoácido,

X_{13} es g o ningún aminoácido,

X_{14} es D, L, M, S, Y o ningún aminoácido,

X_{15} es H, I, P, V, W o ningún aminoácido,

X_{16} es F, G, L, R, S, Y o ningún aminoácido,

X_{17} es D, F, V, W, Y o ningún aminoácido,

X_{18} es C, F, L, P, S o Y,

X_{19} es D, F, G o Y,

X_{20} es A, C, G, P, R, V o Y,

X_{21} es F, L, M, S o ningún aminoácido,

X_{22} es A, D o ningún aminoácido,

X_{23} es I, L, V, Y o ningún aminoácido.

El grupo F de las CDR de la cadena pesada incluye las siguientes colecciones de consenso:

a. una CDRH1 de la fórmula genérica GFSLSNARMGVS (SEQ ID NO: 279).

b. una CDRH2 de la fórmula genérica X_1IFSNDEKSYSTSLKS (SEQ ID NO: 1063), en donde

X_1 es H o L.

c. una CDRH3 de la fórmula genérica X_1YSSGWX_2X_3YGX_4X_5DX_6 (SEQ ID NO: 1070); en donde

X_1 es M o V,

X_2 es S o ningún aminoácido,

X_3 es F o ningún aminoácido,

X_4 es V o ningún aminoácido,

X_5 es F o M,

X_6 es V o Y.

El grupo G de las CDR de la cadena pesada incluye las siguientes colecciones de consenso:

a. una CDRH1 de la fórmula genérica GFSLX_1TGGVGVG

(SEQ ID NO: 1057), en donde

X_1 es S o N.

b. una CDRH2 de la fórmula genérica $LIYWNX_1X_2KRYSPSLX_3S$ (SEQ ID NO: 1064), en donde

X_1 es D o V,

X_2 es D o E,

X_3 es K o R.

c. una CDRH3 de la fórmula genérica $RX_1X_2X_3PFX_4Y$ (SEQ ID NO: 1071), en donde

X_1 es G, H, L, N o R,

X_2 es E, T o W,

X_3 es L, N, T o V,

X_4 es D o E.

En otro enfoque, las secuencias de consenso pueden determinarse al mantener las CDR contiguas dentro de la misma secuencia que corresponda a un U-V_L o U-V_H. Brevemente, en este enfoque, las secuencias de aminoácidos que corresponden a los dominios variables completos ya sea de U-V_L o U-V_H se convierten en formato FASTA para facilitad de procesamiento de alineaciones comparativas y filogenias de inferencia. Después, regiones estructurales de estas secuencias son reemplazadas con una secuencia enlazadora artificial de tal forma que el examen de las CDR solas se lleve a cabo sin introducir ninguna polarización de ponderación de posiciones de aminoácido debido a eventos coincidentes (por ejemplo,

tales como anticuerpos no emparentados que sin proponérselo compartan una herencia estructural de línea germinal común) manteniendo al mismo tiempo CDR contiguas con la misma secuencia que corresponda a secuencias U-V_L o U-V_H. Secuencias U-V_L o U-V_H de este formato se someten después a interrogación de alineación de similitud de secuencia usando un programa que emplea un algoritmo tipo ClutalW-estándar (véase Thompson *et al.*, 1994, *Nucleic Acids. Res.* 22:4673-4680). Este programa genera asimismo filogramas (ilustraciones de árboles filogénicos) con base en alineaciones de similitud de secuencia usando ya sea UPGMA (método de grupo de pares no ponderados usando promedios aritméticos) o métodos de Unión a Vecinos (véase, Saitou y Nei, 1987, *Molecular Biology and Evolution* 4:406-425) para construir e ilustrar similitud y distinción de grupos de secuencia por medio de comparación de longitud de ramificación y agrupamiento. Ambos métodos producen resultados similares para determinar colecciones de secuencias de consenso dentro de los grupos individuales.

En algunos casos la proteína de unión a antígeno comprende al menos una CDRL1, CDRL2 o CDRL3 que tiene una de las secuencias de consenso anteriores. En algunos casos, la proteína de unión a antígeno comprende al menos una CDRH1, CDRH2 o CDRH3 que tiene una de las secuencias de consenso anteriores. En otros casos, la proteína de unión a antígeno

comprende al menos dos CDRL de acuerdo con las secuencias de consenso anteriores, y/o al menos dos CDRH de acuerdo con las secuencias de consenso anteriores. En un aspecto, las CDRL y/o CDRH se derivan de diferentes grupos. En otros casos, la proteína de unión a antígeno comprende al menos dos CDRL del mismo grupo A, B, C, D, E o F y/o al menos dos CDRH del mismo grupo A, B, C, D, E, F o G. En otros aspectos, la proteína de unión a antígeno comprende todas las tres secuencias CDRL1, CDRL2 y CDRL3 de los mismos grupos anteriores A, B, C, D, E o F y/o todas las tres secuencias CDRH1, CDRH2 y CDRH3 de los mismos grupos anteriores A, B, C, D, E, F o G.

D. Proteínas de unión a antígenos ejemplares

De acuerdo con un aspecto, una proteína de unión a antígeno aislada se proporciona que se une a HB-EGF que comprende (A) una o más regiones de determinación de complementariedad de la cadena ligera (CDRL) seleccionadas del grupo que consiste en: (i) una CDRL1 seleccionada del grupo que consiste en SEQ ID NO: 189-217; (ii) una CDRL2 seleccionada del grupo que consiste en SEQ ID NO: 218-233; (iii) una CDRL4 seleccionada del grupo que consiste en SEQ ID NO: 234-274, y (iv) una CDRL de (i), (ii) y (iii) que contiene una o más sustituciones, supresiones o inserciones de aminoácido de no más de cinco, cuatro, tres, cuatro, dos o un aminoácido; (B) una o más regiones de determinación de complementariedad de la cadena pesada (CDRH) seleccionadas

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del grupo que consiste en: (i) una CDRH1 seleccionada del grupo que consiste en SEQ ID No: 275-299; (ii) una CDRH2 seleccionada del grupo que consiste en SEQ ID NO: 300-331; (iii) una CDRH3 seleccionada del grupo que consiste en SEQ ID NO: 332-372; y (iv) una CDRH de (i), (ii) y (iii) que contiene una o más sustituciones, supresiones o inserciones de aminoácido de no más de cinco, cuatro, tres, cuatro, dos o un aminoácido; o (C) una o más CDRL de la cadena ligera de (A); y (D) una o más CDRH de la cadena pesada de (B).

En otra modalidad más, la proteína de unión a antígeno aislada puede comprender (A) una CDRL seleccionada del grupo que consiste en (i) una CDRL1 seleccionada del grupo que consiste en SEQ ID NO: 189-217; (ii) una CDRL2 seleccionada del grupo que consiste en SEQ ID NO: 218-233; y (iii) una CDRL3 seleccionada del grupo que consiste en SEQ ID No: 234-274; (B) una CDRH seleccionada del grupo que consiste en (i) una CDRH1 seleccionada del grupo que consiste en SEQ ID NO: 275-299; (ii) una CDRH2 seleccionada del grupo que consiste en SEQ ID NO: 300-331; y (iii) una CDRH3 seleccionada del grupo que consiste en SEQ ID NO: 332-372; o (C) una o más CDRL de la cadena ligera de (A); y (D) una o más CDRL de la cadena pesada de (B). En una modalidad, la proteína de unión a antígeno aisladas puede incluir (A) una CDRL1 de SEQ ID NO: 189-217, una CDRL2 de SEQ ID NO: 218-233 y una CDRL3 de SEQ ID NO: 234-274; y (B) una CDRH1 de SEQ ID

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NO: 275-299, una CDRH2 de SEQ ID NO: 300-331, y una CDRH3 de SEQ ID NO: 332-372.

En otra modalidad, la proteína de unión a antígeno comprende una cadena ligera variable (V_L) que tiene al menos 80%, 85%, 90% o 95% de identidad de secuencia con una secuencia de aminoácidos seleccionada del grupo que consiste en SEQ ID NO: 94-141, y/o la cadena pesada variable (V_H) tiene al menos 80%, 85%, 90% o 95% de identidad de secuencia con una secuencia de aminoácidos seleccionada del grupo que consiste en SEQ ID NO: 142-186. En una modalidad más, la V_L se selecciona del grupo que consiste en SEQ ID NO: 94-141, y/o la V_H se selecciona del grupo que consiste en SEQ ID NO: 142-186.

En otro aspecto, también se proporciona una proteína de unión a antígeno aislada que se une específicamente a un epítopo que contiene al menos un epítopo que contiene IHGE y/o epítopo tipo EGF de HB-EGF.

En un aspecto más, está la provisión de una proteína de unión a antígeno aislada que se une a HB-EGF, la proteína de unión a antígeno incluye (A) una región de determinación de complementariedad de la cadena ligera (CDRL) seleccionada del grupo que consiste en (i) una CDRL3 seleccionada del grupo que consiste en SEQ ID NO: 234-274, (iii) una CDRL3 que difiere en secuencia de aminoácidos de la CDRL3 de (i) por una adición, supresión o sustitución de

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aminoácido de no más de dos aminoácidos; (iii) una secuencia de aminoácidos de CDRL3 seleccionada del grupo que consiste en $X_1QX_2X_3X_4X_5PX_6X_7$ (SEQ ID NO: 1046), en donde X_1 se selecciona del grupo que consiste en l y M, X_2 se selecciona del grupo que consiste en A, G y S, X_3 se selecciona del grupo que consiste en I y T, X_4 se selecciona del grupo que consiste en H y Q, X_5 se selecciona del grupo que consiste en F, L y W, X_6 se selecciona del grupo que consiste en C, I, H, L y T, X_7 se selecciona del grupo que consiste en S y T; $QQX_1X_2X_3X_4X_5IT$ (SEQ ID NO: 1047), en donde X_1 se selecciona del grupo que consiste en I y S, X_2 se selecciona del grupo que consiste en F y Y, X_3 se selecciona del grupo que consiste en F, I, S y Y, X_4 se selecciona del grupo que consiste en A, S y T, X_5 se selecciona del grupo que consiste en P y S; $X_1X_2X_3X_4X_5X_6X_7X_8t$ (SEQ ID NO: 1048), en donde X_1 se selecciona del grupo que consiste en L y Q, X_2 se selecciona del grupo que consiste en K, N y Q, X_3 se selecciona del grupo que consiste en A, H, S y Y, X_4 se selecciona del grupo que consiste en H, N y Y, X_5 se selecciona del grupo que consiste en N, S y T, X_6 se selecciona del grupo que consiste en A, F, I, T, V y Y, X_7 se selecciona del grupo que consiste en P y ningún aminoácido, X_8 se selecciona del grupo que consiste en F, L y P; $QX_1X_2DX_3LPX_4X_5$ (SEQ ID NO: 1049), en donde X_1 se selecciona del grupo que consiste en H y Q, X_2 se selecciona del grupo que consiste en C, Y, X_4 se selecciona del grupo que consiste en

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D, I, N, S y Y, X_4 se selecciona del grupo que consiste en F, I y L, X_5 se selecciona del grupo que consiste en A, S y T; $QQX_1X_2X_3X_4PX_5X_6X_7$ (SEQ ID NO: 1050), en donde X_1 se selecciona del grupo que consiste en H y Y, X_2 se selecciona del grupo que consiste en G y N, X_3 se selecciona del grupo que consiste en N y S, X_4 se selecciona del grupo que consiste en S y W, X_5 se selecciona del grupo que consiste en P y ningún aminoácido, X_6 se selecciona del grupo que consiste en R y W, X_7 se selecciona del grupo que consiste en S y T; y $X_1QYX_2X_3X_4X_5X_6X_7F$ (SEQ ID NO: 1051), en donde X_1 se selecciona del grupo que consiste en H y Q, X_2 se selecciona del grupo que consiste en F y Y, X_3 se selecciona del grupo que consiste en G, I y S, X_4 se selecciona del grupo que consiste en F, I y T, X_5 se selecciona del grupo que consiste en M, P, S y T, X_6 se selecciona del grupo que consiste en F, L, R y W, X_7 se selecciona del grupo que consiste en S y T; y/o (B) una región de determinación de complementariedad de la cadena pesada (CDRH) seleccionada del grupo que consiste en (i) una CDRH3 selecciona del grupo que consiste en SEQ ID NOs: 332-372; (ii) una CDRH3 que difiere en secuencia de aminoácidos de la CDRH3 de (i) por una adición, supresión y sustitución de no más de dos aminoácidos; y (iii) una secuencia de aminoácidos de CDRH3 seleccionada del grupo que consiste en $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}DX_{12}$ (SEQ ID NO: 1065), en donde X_1 se selecciona del grupo que consiste en E y S, X_2 se selecciona

del grupo que consiste en D, G y ningún aminoácido, X_3 se selecciona del grupo que consiste en D, N y ningún aminoácido, X_4 se selecciona del grupo que consiste en G y ningún aminoácido, X_5 se selecciona del grupo que consiste en G y ningún aminoácido, X_6 se selecciona del grupo que consiste en W, Y y ningún aminoácido, X_7 se selecciona del grupo que consiste en I, N y Y, X_8 se selecciona del grupo que consiste A y Y, X_9 se selecciona del grupo que consiste en G, V y Y, X_{10} se selecciona del grupo que consiste en A, F y G, X_{11} se selecciona del grupo que consiste en F, L y M, X_{12} se selecciona del grupo que consiste en V y Y; $QX_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}YX_{12}X_{13}X_{14}X_{14}DX_{15}$ (SEQ ID NO: 1066), en donde X_1 se selecciona del grupo que consiste en G y ningún aminoácido, X_2 se selecciona del grupo que consiste en K, L y Y, X_3 se selecciona del grupo que consiste en A, G y S, X_4 se selecciona del grupo que consiste en S, V y Y, X_5 se selecciona del grupo que consiste en A y G, X_6 se selecciona del grupo que consiste en G y ningún aminoácido, X_7 se selecciona del grupo que consiste en T y ningún aminoácido, X_8 se selecciona del grupo que consiste en S y ningún aminoácido, X_9 se selecciona del grupo que consiste en Y y ningún aminoácido, X_{10} se selecciona del grupo que consiste en W y Y, X_{11} se selecciona del grupo que consiste en G, S y Y, X_{12} se selecciona del grupo que consiste en F y Y, X_{13} se selecciona del grupo que consiste en G y ningún aminoácido,

X_{14} se selecciona del grupo que consiste en M y ningún aminoácido, X_{15} se selecciona del grupo que consiste en V y Y; $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}$ (SEQ ID NO: 1067), en donde X_1 selecciona del grupo que consiste en D, G, L, S y ningún aminoácido, X_2 se selecciona del grupo que consiste en G, H, W, Y y ningún aminoácido, X_3 se selecciona del grupo que consiste en A, F, W, Y y ningún aminoácido, X_4 se selecciona del grupo que consiste en D, G, Q, T y ningún aminoácido, X_5 se selecciona del grupo que consiste en G, I, Q, S y ningún aminoácido, X_6 se selecciona del grupo que consiste en A, D, X_8 se selecciona del grupo que consiste en D, Y y ningún aminoácido, X_9 se selecciona del grupo que consiste en Y y ningún aminoácido, X_{10} se selecciona del grupo que consiste en A, E, N y Y, X_{11} se selecciona del grupo que consiste en G, P, T, V y Y, X_{12} es se X_{14} se selecciona del grupo que consiste en C, H, V y Y; $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}DX_{18}$ (SEQ ID NO: 1068), en donde X_1 se selecciona del grupo que consiste en E, D y ningún aminoácido, X_2 se selecciona del grupo que consiste en G, R y ningún aminoácido, X_3 se selecciona del grupo que consiste en I, V, Y y ningún aminoácido, X_4 se selecciona del grupo que consiste en A, G, L y N, X_5 se selecciona del grupo que consiste en A, G, V y W, X_6 se selecciona del grupo que consiste en A, N, R y T, X_7 se selecciona del grupo que consiste en G, N, P y ningún aminoácido, X_8 se selecciona del grupo que consiste en G, T y

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ningún aminoácido, X_9 se selecciona del grupo que consiste en A y ningún aminoácido, X_{10} se selecciona del grupo que consiste en D, E y ningún aminoácido, X_{11} se selecciona del grupo que consiste en S, Y y ningún aminoácido, X_{12} se selecciona del grupo que consiste en G, Y y ningún aminoácido, X_{13} se selecciona del grupo que consiste en N, Y y ningún aminoácido, X_{14} se selecciona del grupo que consiste en Y y ningún aminoácido, X_{15} se selecciona del grupo que consiste en D, Y y ningún aminoácido, X_{16} se selecciona del grupo que consiste en A, G y ningún aminoácido, X_{17} se selecciona del grupo que consiste en F y M, X_{18} se selecciona del grupo que consiste en I, V y Y; $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}X_{18}X_{19}X_{20}X_{21}X_{22}X_{23}$ (SEQ ID NO: 1069), en donde X_1 se selecciona del grupo que consiste en A, D, G, S y T, X_2 se selecciona del grupo que consiste en A, E, G, L, N, R, Y y ningún aminoácido, X_3 se selecciona del grupo que consiste en A, G, L, N, R, T, Y y ningún aminoácido, X_4 se selecciona del grupo que consiste en D, G, R, S, V, Y y ningún aminoácido, X_5 se selecciona del grupo que consiste en A, G, I, S, V, Y, y ningún aminoácido, X_6 se selecciona del grupo que consiste en F, G, L, R, V y ningún aminoácido, X_7 se selecciona del grupo que consiste en L, T, Y y ningún aminoácido, X_8 se selecciona del grupo que consiste en Y y ningún aminoácido, X_9 se selecciona del grupo que consiste en Y y ningún aminoácido, X_{10} se selecciona del grupo que

consiste en D y ningún aminoácido, X_{11} se selecciona del grupo que consiste en S y ningún aminoácido, X_{12} se selecciona del grupo que consiste en S y ningún aminoácido, X_{13} se selecciona del grupo que consiste en G y ningún aminoácido, X_{14} se selecciona del grupo que consiste en D, L, M, S, Y y ningún aminoácido, X_{15} se selecciona del grupo que consiste en H, I, P, V, W y ningún aminoácido, X_{16} se selecciona del grupo que consiste en F, G, L, R, S, Y y ningún aminoácido, X_{17} se selecciona del grupo que consiste en D, F, V, W, Y y ningún aminoácido, X_{18} se selecciona del grupo que consiste en C, F, L, P, S y Y, X_{19} se selecciona del grupo que consiste en D, F, G y Y, X_{20} se selecciona del grupo que consiste en A, C, G, P, R, V y Y, X_{21} se selecciona del grupo que consiste en F, L, M, S y ningún aminoácido, X_{22} se selecciona del grupo que consiste en A, D y ningún aminoácido, X_{23} se selecciona del grupo que consiste en I, L, V, Y y ningún aminoácido; $X_1YSSGWX_2X_3YGX_4X_5DX_6$ (SEQ ID NO: 1070), en donde X_1 se selecciona del grupo que consiste en M y V, X_2 se selecciona del grupo que consiste en S y ningún aminoácido, X_3 se selecciona del grupo que consiste en F y ningún aminoácido, X_4 se selecciona del grupo que consiste en V y ningún aminoácido, X_5 se selecciona del grupo que consiste en F y M, X_6 se selecciona del grupo que consiste en V y Y; y $RX_1X_2X_3PFX_4Y$ (SEQ ID NO: 1071), en donde X_1 se selecciona del grupo que consiste en G, H, L, N y R, X_2 se selecciona del

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grupo que consiste en E, T y W, X_3 se selecciona del grupo que consiste en L, N, T y V, X_4 se selecciona del grupo que consiste en D y E.

En una modalidad, la proteína de unión a antígeno aislada comprende además (A) una CDRL seleccionada del grupo que consiste en: (i) una CDRL1 seleccionada del grupo que consiste en SEQ ID NO: 189-217; (ii) una CDRL1 que difiere en secuencia de aminoácidos de la CDRL1 de (i) por una adición, supresión o sustitución de aminoácido de no más de dos aminoácidos; (iii) una secuencia de aminoácidos de CDRL1 seleccionada del grupo que consiste en $X_2SSQSLX_2X_2SDGX_4TYLX_5$ (SEQ ID NO: 1035), en donde X_1 se selecciona del grupo que consiste en K y R, X_2 se selecciona del grupo que consiste en L y V, X_3 se selecciona del grupo que consiste en H y Y, X_4 se selecciona del grupo que consiste en K y N, X_5 se selecciona del grupo que consiste en N, S y Y; $RASQX_1ISX_2YLN$ (SEQ ID NO: 1036), en donde X_1 se selecciona del grupo que consiste en R, S y t, X_2 se selecciona del grupo que consiste en R y S; $RASQX_1IX_2X_3X_4LX_5$ (SEQ ID NO: 1037), en donde X_1 se selecciona del grupo que consiste en D, G, S y T, X_2 se selecciona del grupo que consiste en A, R y S, X_3 se selecciona del grupo que consiste en H, I, N, R, S y T, X_4 se selecciona del grupo que consiste en D, W y Y, X_5 se selecciona del grupo que consiste en A, G y N; $QASQDIX_1X_2X_3LN$ (SEQ ID NO: 1038), en donde X_1 se selecciona del grupo que consiste en S y T, X_2 se

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selecciona del grupo que consiste en D y N, X_3 se selecciona del grupo que consiste en S y Y; $RASQX_1VX_XX_3X_4X_5LA$ (SEQ ID NO: 1039), en donde X_1 se selecciona del grupo que consiste en S y T, X_2 se selecciona del grupo que consiste en I y S, X_3 se selecciona del grupo que consiste en R y S, X_4 se selecciona del grupo que consiste en S, N y ningún aminoácido, X_5 se selecciona del grupo que consiste en Y y ningún aminoácido; y $KSSQX_1X_2LX_3X_4SNNKNYLX_5$ (SEQ ID NO: 1040), en donde X_1 se selecciona del grupo que consiste en N y S, X_2 se selecciona del grupo que consiste en N, R y S, X_5 se selecciona del grupo que consiste en A y V; o (iv) una CDRL2 se selecciona del grupo que consiste en SEQ ID NO: 218-233; (v) una CDRH2 que difiere en secuencia de aminoácidos de la CDRL2 de (iv) por una adición, supresión o sustitución de aminoácido de uno o más de dos aminoácidos o (vi) una secuencia de aminoácidos de CDRL2 seleccionada del grupo que consiste en $X_1X_2SNX_3X_4S$ (SEQ ID NO: 1041), en donde X_1 se selecciona del grupo que consiste en E y K, X_2 se selecciona del grupo que consiste en I y V, X_3 se selecciona del grupo que consiste en r y W, X_4 se selecciona del grupo que consiste en D y F; $X_1X_2SX_3LQS$ (SEQ ID NO: 1042), en donde X_1 se selecciona del grupo que consiste en A y T, X_2 se selecciona del grupo que consiste en A, E y V, X_3 se selecciona del grupo que consiste en S y T; X_1AS_2LQS (SEQ ID NO: 1043), en donde X_1 se selecciona del grupo que consiste en A y V, X_2 se selecciona del grupo que consiste en

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S y T; DASX$_1$LET (SEQ ID NO: 1044), en donde X$_1$ se selecciona del grupo que consiste en I y N; GASSRAT (SEQ ID NO: 223); y WASX$_1$RES (SEQ ID NO: 1045), en donde X$_1$ se selecciona del grupo que consiste en A y T; o B) una CDRH se selecciona del grupo que consiste en: (i) una CDRH1 se selecciona del grupo que consiste en SEQ ID NO: 275-299; (ii) una CDRH1 que difiere en secuencia de aminoácidos de la CDRH1 de (i) por una adición, supresión o sustitución de aminoácidos de no más de dos aminoácidos; (iii) una secuencia de aminoácidos de CDRH1 seleccionada del grupo que consiste en GYTX$_1$TX$_2$X$_3$X$_4$X$_5$X$_6$ (SEQ ID NO: 1052), en donde X$_1$ se selecciona del grupo que consiste en H, L y Y, X$_4$ se selecciona del grupo que consiste en G, S y Y, X$_5$ se selecciona del grupo que consiste en I y M, X$_6$ se selecciona del grupo que consiste en H y S; GYX$_1$FTSYWIG (SEQ ID NO: 1053), en donde X$_1$ se selecciona del grupo que consiste en R y S; GFTFX$_1$SX$_2$X$_3$MH (SEQ ID NO: 1054), en donde X$_1$ se selecciona del grupo que consiste en R y S, X$_2$ se selecciona del grupo que consiste en H y Y, X$_3$ se selecciona del grupo que consiste en D y G; GFX$_1$FSX$_2$YX$_3$MX$_4$ (SEQ ID NO: 1055), en donde X$_1$ se selecciona del grupo que consiste en P y T, X$_2$ se selecciona del grupo que consiste en A, R y S, X$_3$ se selecciona del grupo que consiste en A y S, X$_4$ se selecciona del grupo que consiste en N y S; GX$_1$SX$_2$SX$_3$X$_4$X$_5$X$_6$X$_7$WX$_8$ (SEQ ID NO: 1056), en donde X$_1$ se selecciona del grupo que consiste en d y G, X$_2$ se selecciona

del grupo que consiste en F, I y V, X_3 se selecciona del grupo que consiste en R, S y ningún aminoácido, X_4 se selecciona del grupo que consiste en G, Y y ningún aminoácido, X_5 se selecciona del grupo que consiste en D, G, S y ningún aminoácido, X_6 se selecciona del grupo que consiste en A, S y Y, X_7 se selecciona del grupo que consiste en A y Y, X_8 se selecciona del grupo que consiste en N y S; GFSLSNARMGVS (SEQ ID NO: 279); y $GFSX_1TGGVGVG$ (SEQ ID NO: 1057), en donde X_1 se selecciona del grupo que consiste en S y N; (iv) una CDRH2 seleccionada del grupo que consiste en SEQ ID NO: 300-331; (v) una CDRH2 que difiere en secuencia de aminoácidos de la CDRH2 de (iv) por una adición, supresión o sustitución de aminoácidos de no más de dos aminoácidos; o (vi) una secuencia de aminoácidos de CDRH2 seleccionada del grupo que consiste en $X_1X_2X_3X_4X_5X_6GX_7TX_8X_9X_{10}QKX_{11}X_{12}$ (SEQ ID NO: 1058), en donde X_1 se selecciona del grupo que consiste en S y W, X_2 se selecciona del grupo que consiste en F e I, X_3 se selecciona del grupo que consiste en D, N y S, X_4 se selecciona del grupo que consiste en A y P, X_5 se selecciona del grupo que consiste en E, N y S, X_6 se selecciona del grupo que consiste en D, N y S, X_7 se selecciona del grupo que consiste en E, G y N, X_8 se selecciona del grupo que consiste en I y N, X_9 se selecciona del grupo que consiste en C, H y Y, X_{10} se selecciona del grupo que consiste en A y T, X_{11} se selecciona del grupo que consiste en F y L, X_{12} se

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selecciona del grupo que consiste en D y G; IIYPX$_1$DSDX$_2$RYSPSFQG (SEQ ID NO: 1059), en donde X$_1$ se selecciona del grupo que consiste en D y G, X$_2$ se selecciona del grupo que consiste en A, I y T; X$_1$IX$_2$X$_3$DGSX$_4$X$_5$X$_6$YX$_7$DSVX$_8$G (SEQ ID NO: 1060), en donde X$_1$ se selecciona del grupo que consiste en F y V, X$_2$ se selecciona del grupo que consiste en S y W, X$_3$ se selecciona del grupo que consiste en D, S y Y, X$_4$ se selecciona del grupo que consiste en I, N y T, X$_5$ se selecciona del grupo que consiste en K y Q, X$_6$ se selecciona del grupo que consiste en N, R y Y, X$_7$ se selecciona del grupo que consiste en A, T y V, X$_8$ se selecciona del grupo que consiste en K y R; X$_1$ISX$_2$SX$_3$X$_4$X$_5$X$_6$YYADSVKG (SEQ ID NO: 1061), en donde X$_1$ se selecciona del grupo que consiste en A, H y Y, X$_2$ se selecciona del grupo que consiste en G, R y S, X$_3$ se selecciona del grupo que consiste en G y S, X$_4$ se selecciona del grupo que consiste en G, R y S, X$_5$ se selecciona del grupo que consiste en S, T y Y, X$_6$ se selecciona del grupo que consiste en I y T; X$_1$X$_2$X$_3$X$_4$X$_5$X$_6$X$_7$X$_8$X$_9$X$_{10}$X$_{11}$YX$_{12}$X$_{13}$SX$_{14}$KS (SEQ ID NO: 1062), en donde X$_1$ se selecciona del grupo que consiste en E, R y Y, X$_2$ se selecciona del grupo que consiste en I y T, X$_3$ se selecciona del grupo que consiste en H, N y Y, X$_4$ se selecciona del grupo que consiste en C, H, S, T y Y, X$_5$ se selecciona del grupo que consiste en S y R, X$_6$ se selecciona del grupo que consiste en G y S, X$_7$ se selecciona del grupo que consiste en

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G, K, S y T, X_8 se selecciona del grupo que consiste en T y W, X_9 se selecciona del grupo que consiste en N y Y, X_{10} se selecciona del grupo que consiste en N y ningún aminoácido, X_{11} se selecciona del grupo que consiste en D y ningún aminoácido, X_{12} se selecciona del grupo que consiste en A y N, X_{13} se selecciona del grupo que consiste en P y V, X_{14} se selecciona del grupo que consiste en L y V; X_1IFSNDEKSYSTSLKS (SEQ ID NO: 1063), en donde X_1 se selecciona del grupo que consiste en H y LI; y LIYWNX_1X_2KRYSPSLX_3S (SEQ ID NO: 1064), en donde X_1 se selecciona del grupo que consiste en D y V, X_2 se selecciona del grupo que consiste en D y E, X_3 se selecciona del grupo que consiste en K y R.

En algunas modalidades, al menos dos, o al menos tres de las secuencias de CDRL1, CDRL2 y CDRL3 se derivan del mismo grupo A, B, C, D, E o F de secuencias de consenso y/o al menos dos, o las tres secuencias CDRH1, CDRH2 y CDRH3 se derivan del mismo grupo A, B, C, D, E, F o G. En otros casos las CDR de diferentes grupos de secuencias de consenso se mezclan e igualan.

En otra modalidad más, la proteína de unión a antígeno aislada descrita anteriormente en la presente comprende la primera secuencia de aminoácidos y la segunda secuencia de aminoácidos, ambas secuencias de las cuales son unidas covalentemente entre sí. En una modalidad más, la primera secuencia de aminoácidos de la proteína de unión a

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antígeno aislada incluye las CDRL3 de SEQ ID NO: 234-274, CDRL2 de SEQ ID NO: 218-233 y CDRL1 de SEQ ID NO: 189-217. Por otro lado, la secuencia de aminoácidos de la proteína de unión a antígeno aislada comprende la CDRH3 de SEQ ID NO: 332-372, CDRH2 de SEQ ID NO: 300-331 y CDRH1 de SEQ ID NO: 275-299.

En un aspecto, las proteínas de unión a antígeno aisladas provistas en la presente pueden ser un anticuerpo monoclonal, un anticuerpo policlonal, un anticuerpo recombinante, un anticuerpo humano, un anticuerpo humanizado, un anticuerpo quimérico, un anticuerpo multiespecífico o un fragmento de anticuerpo de los mismos.

En otra modalidad, el fragmento de anticuerpo de las proteínas de unión a antígeno aisladas provistas en la presente puede ser un fragmento Fab, un fragmento Fab', un fragmento $F(ab')_2$, un fragmento Fv, un dicuerpo o una molécula de anticuerpo de cadena individual.

En una modalidad más, la proteína de unión a antígeno aislada proporcionada en la presente es un anticuerpo humano y puede ser del tipo IgG1, IgG2, IgG3 o IgG4.

En otro aspecto más, la proteína de unión a antígeno aislada provista en la presente puede ser acoplada a un grupo marcador, tal como radioisótopo, radionúclido, un grupo fluorescente, un grupo enzimático, un grupo quimioluminiscente, un grupo biotinilo o un grupo de

polipéptido predeterminado, o un grupo efector, tal como un radioisótopo, un radionúclido, una toxina, un grupo terapéutico o un grupo quimioterapéutico. Ejemplos de un grupo terapéutico o quimioterapéutico son caliqueamicina, auristatina-PE, geldanamicina, maitansina o derivados de las mismas.

En otros aspectos más, la invención incluye proteínas de unión a antígeno que compiten con cualquiera de las proteínas de unión a antígeno descritas arriba.

Como se apreciará por aquellos en la técnica, para cualquier proteína de unión a antígeno con más de una CDR de las secuencias ilustradas, cualquier combinación de CDR seleccionadas independientemente de las secuencias ilustradas es útil. Así, las proteínas de unión a antígeno con uno, dos, tres, cuatro, cinco o seis de las CDR seleccionadas independientemente pueden ser generadas. Sin embargo, como se apreciará por aquellos en la técnica, las modalidades específicas utilizan generalmente combinaciones de CDR que son no repetitivas, por ejemplo, proteínas de unión a antígeno generalmente no se elaboran con dos regiones CDRH2, etc.

Algunas de las proteínas de unión a antígeno proporcionadas se describen en más detalle abajo.

1. Proteínas de unión a antígenos y epítopos de unión

Cuando una proteína de unión a antígeno se dice que

se une a un epítopo con residuos especificados de un polipéptido, tal como HB-EGF, por ejemplo, lo que se intenta decir es que la proteína de unión a antígeno se une específicamente a un polipéptido que consiste en los residuos especificados (por ejemplo, un segmento especificado de HB-EGF). Esta proteína de unión a antígeno típicamente no hace contacto con cada residuo dentro de HB-EGF. Tampoco ninguna sustitución o supresión de aminoácido individual dentro de HB-EGF, o el dominio extracelular de HB-EGF, necesariamente afectan significativamente la afinidad de unión. La especificidad de epítopos de una proteína de unión a antígeno puede determinarse de una variedad de maneras. Un enfoque, por ejemplo, incluye probar una colección de péptidos superpuestos de aproximadamente 15 aminoácidos que abarquen la secuencia del antígeno y difiera en incrementos de un pequeño número de aminoácidos (por ejemplo, tres aminoácidos). Los péptidos son inmovilizados dentro de los pocillos de una caja de microtitulación. La inmovilización se puede llevar a cabo al biotinilar un término de los péptidos. Opcionalmente, diferentes muestras del mismo péptido pueden ser biotiniladas en el término amino y carboxi e inmovilizadas en pocillos separados para propósitos de comparación. Esto es útil para identificar proteínas de unión a antígeno específicas de extremo. Opcionalmente, péptidos adicionales pueden ser incluidos al terminar en un

aminoácido de interés particular. Este enfoque es útil para identificar proteínas de unión a antígeno específicas de extremo a fragmentos internos de HB-EGF. Una proteína de unión a antígeno o fragmento inmunológicamente funcional es tamizado para unión específica a cada uno de los diferentes péptidos. El epítopo se define como ocurriendo dentro de un segmento de aminoácidos que es común a todos los péptidos a los cuales la proteína de unión a antígeno muestra unión específica. Los detalles con respecto a un enfoque específico para definir un epítopo se establecen en el ejemplo 23.

Como se demuestra en el ejemplo 23, las proteínas de unión a antígeno proporcionadas en la presente son capaces de unirse al menos a un epítopo que contenga IHGE y/o un dominio tipo EGF de HB-EGF.

2. Proteínas de unión a antígeno competidoras

En un aspecto, las proteínas de unión a antígeno son provistas que compiten con uno de los anticuerpos o fragmentos de anticuerpo funcionales ejemplificados que se unen al epítopo descrito arriba para unión específica a HB-EGF. Estas proteínas de unión a antígeno también se pueden unir al mismo epítopo que una de las proteínas de unión a antígeno ejemplificadas en la presente, o un epítopo superpuesto. Las proteínas de unión a antígeno y fragmentos que compiten con o se unen al mismo epítopo que las proteínas

de unión a antígeno ejemplificadas se espera que muestren propiedades funcionales similares. Las proteínas de unión a antígeno y fragmentos ejemplificados incluyen aquellas descritas arriba, incluyendo aquellas con las cadenas pesada y ligera, dominios de la región variable y CDR, incluidas en las figuras 1, 2, 3, 4, 6 y 7.

3. Anticuerpos humanos y humanización de anticuerpos

En una modalidad, las proteínas de unión a antígeno HB-EGF son anticuerpos humanos o humanizados. Los anticuerpos humanos evitan muchos de los problemas asociados con anticuerpos que poseen regiones variables y/o constantes de murino o rata. La presencia de estas proteínas derivadas de murino o rata puede llevar a la rápida eliminación de los anticuerpos o puede llevar a la generación de una respuesta inmune contra el anticuerpo por un paciente. Para evitar la utilización de anticuerpos derivados de murino o rata, anticuerpos completamente humanos han sido generados a través de la introducción de locus genéticos de anticuerpos humanos funcionales en un roedor, otro mamífero o animal de tal manera que el roedor, otro mamífero o animal produzca anticuerpos completamente humanos.

Un método para generar anticuerpos completamente humanos es a través del uso de cepas XenoMouse® de ratones que han sido manipuladas para contener fragmentos

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configurados de línea germinal con un tamaño de hasta pero menos de 1000 kb del locus de la cadena pesada humana y locus de cadena ligera kappa. Véase, Méndez *et al.*, 1997, *Nature Genetics* 15: 146-156, y Green y Jakobovits, 1998, *J. Exp. Med.* 188:483-495. Las cepas XenoMouse® están disponibles de Abgenix, Inc. (Fremont, CA).

La producción de las cepas de ratones XenoMouse® se describe y delinea en la solicitud de patente de E.U.A. Nos. de serie 07/466,008, presentada el 12 de enero de 1990, 07/610,515, presentada el 8 de noviembre de 1990, 07/919,297, presentada el 24 de julio de 1992, 07/922,649, presentada el 30 de julio de 1992, 08/031,801, presentada el 15 de marzo de 1993, 08/112,848, presentada el 27 de agosto de 1993, 08/234,145, presentada el 28 de abril de 1994, 08/376,279, presentada el 20 de enero de 1995, 08/430,938, presentada el 27 de abril de 1995, 08/464,584, presentada el 5 de junio de 1995, 08/464,582, presentada el 5 de junio de 1995, 08/463,191, presentada el 5 de junio de 1995, 08/462,837, presentada el 5 de junio de 1995, 08/486,853, presentada el 5 de junio de 1995, 08/486,857, presentada el 5 de junio de 1995, 08/486,859, presentada el 5 de junio de 1995, 08/462,513, presentada el 5 de junio de 1995, 08/724,752, presentada el 2 de octubre de 1996, 08/759,620, presentada el 3 de diciembre de 1996, publicación de E.U.A. 2003/0093820, presentada el 30 de noviembre de 2001 y patentes de E.U.A.

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Nos. 6,162,963, 6,150,584, 6,114,598, 6,075,181 y 5,939,598 y patentes japonesas Nos. 3 068 180 B2, 3 068 506 B2 y 3 068 507 B2. Véase también patente europea No. EP 0 463 151 B1 concesión publicada el 12 de junio de 1996, solicitud de patente internacional No. WO 94/02602, publicada el 3 de febrero de 1994, solicitud de patente internacional No. WO 96/34096, publicada el 31 de octubre de 1996, WO 98/24893, publicada el 11 de junio de 1998, WO 00/76310, publicada el 21 de diciembre de 2000. Las descripciones de cada una de las patentes, solicitudes y referencias citadas arriba se incorporan en la presente a manera de referencia en su totalidad.

En un enfoque alternativo, otros, incluyendo GenPharm International, Inc., han utilizado el enfoque de "minilocus". En el enfoque de minilocus, un locus de Ig exógeno es imitado a través de la inclusión de piezas (genes individuales) del locus de Ig. Así, uno o más genes V_H, uno o más genes D_H, uno o más genes J_H, una región constante mu, y normalmente una segunda región constante (de preferencia una región constante gama) se forman en una construcción para su inserción en un animal. Este enfoque se describe en la patente de E.U.A. No. 5,545,807 a Surani *et al.* y patentes de E.U.A. Nos. 5,545,806, 5,625,825, 5,625,126, 5,633,425, 5,661,016, 5,770,429, 5,789,650, 5,814,318, 5,877,397, 5,874,299 y 6,255,458 cada una a Lonberg and Kay, patente de

E.U.A. No. 5,591,669 y 6,023,010 a Krimpenfort y Berns, patentes de E.U.A. Nos. 5,612,205, 5,721,367 y 5,789,215 a Berns *et al.*, y patente de E.U.A. No. 5,643,763 a Choi y Dunn, y GenPharm International solicitud de patente de E.U.A. Nos de serie 07/574,748, presentada el 29 de agosto de 1990, 07/575,962, presentada el 31 de agosto de 1990, 07/810,279, presentada el 17 de diciembre de 1991, 07/853,408, presentada el 18 de marzo de 1992, 07/904,068,presentada el 23 de junio de 1992, 07/990,860, presentada el 16 de diciembre de 1992, 08/053,131, presentada el 26 de abril de 1993, 08/096,762, presentada el 22 de julio de 1993, 08/155,301, presentada el 18 de noviembre de 1993, 08/161,739, presentada el 3 de diciembre de 1993, 08/165,699, presentada el 10 de diciembre de 1993, 08/209,741, presentada el 9 de marzo de 1994, las descripciones completas de las cuales se incorporan a manera de referencia en su totalidad. Véase también, patente europea No. 0 546 073 B1, solicitudes de patente internacional Nos. WO 92/03918, WO 92/22645, WO 92/22647, WO 92/22670, WO 93/12227, WO 94/00569, WO 94/25585, WO 96/14436, WO 97/13852 y WO 98/24884 y patente de E.U.A. No. 5,981,175, las descripciones de las cuales se incorporan en la presente a manera de referencia en su totalidad.

Kirin también ha demostrado la generación de anticuerpos humanos de ratones en la cual, a través de fusión de microcélulas, grandes piezas de cromosomas, o cromosomas

completos, han sido introducidas. Véase solicitud de patente europea Nos. 773 288 y 843 961, las descripciones de las cuales se incorporan en la presente a manera de referencia. Además, se han generado ratones KM™, los cuales son el resultado del cruzamiento de ratones Tc de Kirin con ratones de minilocus (Humab) de Medarex. Estos ratones poseen el transcromosoma IgH humano de los ratones Kirin y el transgen de la cadena kappa de los ratones Genpharm (Ishida *et al.*, 2002, *Cloning Stem Cells* 4:91-102).

Anticuerpos humanos también pueden derivarse mediante métodos *in vitro*. Ejemplos adecuados incluyen pero no están limitados a despliegue de fagos (CAT, Morphosys, Dyax, Biosite/Medarex, Xoma, Symphogen, Alexion (anteriormente Proliferon), Affimed) despliegue de ribosomas (CAT), despliegue de levaduras y similares.

E. Preparación de anticuerpos

Anticuerpos, como los descritos en la presente, se prepararon a través de la utilización de la tecnología XenoMouse®, como la descrita en la presente. Estos ratones son capaces de producir moléculas de inmunoglobulina humas y anticuerpos y son sustancialmente deficientes en la producción de moléculas de anticuerpos de inmunoglobulina de murino. Las tecnologías utilizadas para lograr la producción de anticuerpos humanos se describen en las patentes, solicitudes y referencias descritas en la presente. En

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algunas modalidades, la producción transgénica de ratones y anticuerpos humanos se lleva a cabo como se describe en la solicitud de patente de E.U.A. No. de serie 08/759,620, presentada el 3 de diciembre de 1996 y solicitud de patente internacional Nos. WO 98/24893, publicada el 11 de junio de 1998 y WO 00/76310, publicada el 21 de diciembre de 2000, las descripciones de las cuales se incorporan en la presente a manera de referencia. Véase también Méndez *et al.*, 1997, *Nature Genetics* 15:146-156, cuya descripción se incorpora en la presente a manera de referencia.

A través del uso de esta tecnología, anticuerpos monoclonales completamente humanos contra una variedad de antígenos han sido producidos. Esencialmente, líneas de ratones XenoMouse® son inmunizadas con un antígeno de interés (por ejemplo, HB-EGF), células linfáticas (tales como células B) se recuperan de los ratones hiper-inmunizados, y los linfocitos recuperados se fusionan con una línea de células tipo mieloide para preparar líneas de células de hibridoma inmortales. Estas líneas de células de hibridoma se tamizan y seleccionan para identificar líneas de células de hibridoma que produzcan anticuerpos específicos para el antígeno de interés. Los sobrenadantes también pueden ser tamizados para inmunorreactividad contra fragmentos de HB-EGF para mapear más los diferentes anticuerpos para su unión a dominios de interés funcional en HB-EGF. Los anticuerpos también pueden

ser tamizados para su unión a otro ligando de EGFR o sus miembros de la familia, otras quimioscinas humanas emparentadas y contra los ortólogos de rata, ratón y primate no humano, tales como mono macaco, de HB-EGF, los últimos para determinar la reactividad cruzada de especies. En la presente se proporcionan métodos para la producción de líneas de célula de hibridoma múltiples que producen anticuerpos específicos para HB-EGF. Además, se proporciona en la presente la caracterización de los anticuerpos producidos por estas líneas de células, incluyendo análisis de secuencias de nucleótidos y aminoácidos de las cadenas pesada y ligeras de estos anticuerpos.

Como alternativa, en lugar de ser fusionados a células de mieloma para generar hibridomas, las células B pueden ser ensayadas directamente. Por ejemplo, las células B pueden ser aisladas ratones XenoMouse® hiperinmunes y dejarse proliferar y diferenciar en células de plasma de secreción de anticuerpos. Los anticuerpos de los sobrenadantes de células son después tamizados mediante ELISA para reactividad contra el inmunógeno HB-EGF. Los sobrenadantes también pueden ser tamizados para inmunorreactividad contra fragmentos de HB-EGF para mapear más los diferentes anticuerpos para su unión a dominios de interés funcional en HB-EGF. Los anticuerpos también se pueden tamizar para su unión a otros ligandos del receptor

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EGF, o sus miembros de la familia, otras quimioscinas humanas relacionadas y contra los ortólogos de HB-EGF de rata, ratón y primate no humano, tales como mono macaco, lo último para determinar la reactividad cruzada de especies. Células B de pocillos que contengan anticuerpos de interés pueden inmortalizarse mediante varios métodos incluyendo fusión para elaborar hibridomas ya sea de pocillos individuales o de pocillos agrupados, o mediante la infección con EBV o transfección mediante genes de inmortalización conocidos y luego plaqueando en medio adecuado. Como alternativa, células de plasma individuales que secreten anticuerpos con las especificidades deseadas son después aisladas usando un ensayo de placa hemolítico específico de HB-EGF (Babcook *et al.*, 1996, *Proc. Natl. Acad. Sci. E.U.A.* 93:7843-48). Las células dirigidas para lisis son de preferencia glóbulos rojos de borrego (SRBCs) recubiertos con el antígeno HB-EGF.

Como se describió, arriba, existe un número de isotipos de anticuerpos incluyendo sin limitación los siguientes: IgG1, IgG2, IgG3 e IgG4 humanas. Se apreciará que los anticuerpos que se generan no tienen que poseer inicialmente este isotipo sino que más bien el anticuerpo que se genere puede poseer cualquier isotipo y que el anticuerpo puede ser cambiado de isotipo usando los genes de la región V clonada molecularmente o genes de la región constante clonada o moléculas de ADNc en vectores de expresión adecuados usando

técnicas convencionales de biología molecular que se conocen bien en la técnica y expresando después los anticuerpos en células hospederas usando técnicas conocidas en la técnica.

En general, anticuerpos producidos mediante los hibridomas fusionados eran ya sea cadenas pesadas de IgG2 humana o cadenas pesadas de IgG4 humana con cadenas kappa completamente humanas. Los anticuerpos también pueden ser de otros isotipos humanos, incluyendo IgG1 o IgG3. Los anticuerpos poseían altas afinidades, poseyendo típicamente una K_D de alrededor de 10^{-6} hasta aproximadamente 10^{-12} M o menos, cuando se mide mediante técnicas de fase sólida y fase de solución. Anticuerpos que poseen una K_D de al menos 10^{-9} M se prefieren para inhibir la actividad de HB-EGF. Se prefieren también anticuerpos que poseen una K_D de al menos 10^{-10} M para inhibir la actividad de HB-EGF. Se prefieren también anticuerpos que poseen una K_D de al menos 10^{-11} M para inhibir la actividad de HB-EGF.

Como se apreciará, los anticuerpos anti-HB-EGF pueden ser expresados en líneas de células que no sean líneas de células de hibridoma. Secuencias que codifican para anticuerpos particulares pueden usarse para transfectar una célula hospedera de mamífero adecuada. Durante la construcción de vectores adecuados para transfección y expresión subsecuente de anticuerpos, el anticuerpo puede ser cambiado en clase de un isotipo a otro, por ejemplo,

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anticuerpos IgG4 pueden ser cambiados en clase a IgG2, mediante técnicas conocidas en la técnica. La transfección puede ser mediante cualquier método conocido para introducir polinucleótidos en una célula hospedera, incluyendo, por ejemplo empaque del polinucleótido en un virus (o en un vector viral) y transducción de una célula hospedera con el virus (o vector) o mediante procedimientos de transfección conocidos en la técnica, como se ejemplifica por las patentes de E.U.A. Nos. 4,399,216, 4.912,040, 4,740,461 y 4,959,455 (patentes que se incorporan en la presente a manera de referencia). El procedimiento de transformación usado depende del hospedero que será transformado. Los métodos para introducir polinucleótidos heterólogos en células de mamífero se conocen bien en la técnica e incluyen transfección mediada por dextrano, precipitación con fosfato de calcio, transfección mediada por polibreno, fusión a protoplastos, electroporación, encapsulación de los polinucleótidos en liposomas y microinyección directa del ADN en núcleos.

Líneas de células de mamífero disponibles como huéspedes para expresión se conocen en la técnica e incluyen muchas líneas de células inmortalizadas disponibles de la Colección Americana de tipos de Cultivos (ATCC), incluyendo pero no limitadas a células de ovario de hámster Chino (CHO), células HeLa, células de riñón de hámster bebé (BHK), células

de riñón de mono (COS), células de carcinoma hepatocelular humano (por ejemplo, Hep G2), células de riñón epitelial humano 293 y un número de otras líneas de células. Las líneas de células de preferencia particular se seleccionan a través de determinar qué líneas de células tienen altos niveles de expresión y producen altas cantidades de anticuerpos anti-HB-EGF.

Como alternativa, estos anticuerpos pueden prepararse a partir de animales manipulados genéticamente para elaborar anticuerpos completamente humanos o a partir de biblioteca de despliegue de anticuerpos hecha en bacteriófagos, levaduras, ribosomas o *E. coli*. Véase, por ejemplo, Clackson et al., 1991, *Nature* 352:624-628, Marks *et al.*, 1991, *J. Mol. Biol.* 222: 581-597, Feldhaus y Siegel, 2004, *J. Immunol Methods*, 290:69-80, Groves y Osbourn, 2005, *Expert Opin Biol Ther*, 5125-135 y Jostock y Dubel, 2005, *Comb Chem High Throughput Screen*. 8:127-133.

Otro aspecto se refiere a una molécula de ácido nucleico aislada que codifica para una proteína de unión a antígeno HB-EGF tal como un anticuerpo. Dentro del presente contexto, el término "molécula de ácido nucleico aislada", según se usa en la presente, significa un polinucleótido de origen genómico, ADNc o sintético o alguna combinación de los mismos, la cual en virtud de su origen, la "molécula de ácido nucleico aislada" (1) no está asociada con toda o una porción

de un polinucleótido en el cual el "polinucleótido aislado" se encuentra en la naturaleza, (2) está enlazado operablemente a un polinucleótido que no está enlazado en la naturaleza, o (3) no ocurre en la naturaleza como parte de una secuencia más grande. Además, el término "molécula de ácido nucleico", según se menciona en la presente, significa una forma polimérica de nucleótidos de al menos 10 bases de largo, ya sea ribonucleótidos o desoxinucleótidos o una forma modificada de cualquier tipo de nucleótido, tal como nucleótidos con grupos de azúcar modificados o sustituidos y similares. El término incluye también formas de una sola o de doble hebra de ADN. Los ácidos nucleicos ejemplares que codifican para proteínas de unión a antígeno o porciones de las mismas se describen en más detalle abajo.

En una modalidad, una molécula de ácido nucleico se enlaza operablemente a una secuencia de control. El término "secuencia de control", según se usa en la presente, se refiere a secuencias de polinucleótidos que son necesarias para llevar a cabo la expresión y procesamiento de secuencias de codificación a las cuales son ligadas. La naturaleza de estas secuencias de control difiere dependiendo del organismo huésped. En procariontes, estas secuencias de control generalmente incluyen promotores, sitios de unión ribosómicos y secuencias de terminación de transcripción. En eucariontes, generalmente, estas secuencias de control

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incluyen promotores y secuencias de terminación de transcripción. El término "secuencia de control" intenta incluir, como mínimo, todos los componentes cuya presencia es esencial para la expresión y procesamiento, y también pueden incluir componentes adicionales cuya presencia sea adecuada, por ejemplo, secuencias líder y secuencias de socios de fusión. Además, el término "enlazado operablemente", según se usa en la presente, se refiere a posiciones de componentes así descritos las cuales están en una relación que les permiten funcionar de la manera deseada. Además, según se proporciona en la presente, una secuencia de control de expresión enlazada operablemente a una secuencia de codificación es ligada de tal manera que la expresión de la secuencia de codificación se logre bajo condiciones compatibles con la secuencia de control de expresión.

Un aspecto más es un vector que comprende una molécula de ácido nucleico que codifica para una proteína de unión a antígeno HB-EGF proporcionada en la presente. La molécula de ácido nucleico puede ser enlazada operablemente a una secuencia de control. Además, el vector puede contener además un origen de replicación o un gen marcador de selección. Ejemplos de vectores que se pueden usar son, por ejemplo, plásmidos, cósmidos, fagos, virus, etc.

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F. Proteínas de unión a antígenos a base de estructura de anticuerpo básica

Como se describió arriba, la unidad estructural de anticuerpo básica se sabe que comprende un tetrámero. Cada tetrámero está compuesto de dos pares idénticos de cadenas de polipéptidos, cada par teniendo una cadena "ligera" (alrededor de 25 kDa) y una "pesada" (aproximadamente 50-70 kDa). La porción amino-terminal de cada cadena incluye una región variable de aproximadamente 100 a 110 o más aminoácidos responsables principalmente del reconocimiento de antígenos. La porción carboxi-terminal de cada cadena define una región constante responsable de la función efectora de dimerización, vida media circulante y otras funciones. Las cadenas ligeras humanas se clasifican como cadenas ligeras kappa y lambda. Las cadenas pesadas se clasifican como mu, delta, gama, alfa o épsilon, y definen el isotipo del anticuerpo como IgM, IgD, IgG, IgA e IgE, respectivamente. Dentro de las cadenas ligeras y pesadas, las regiones variables y constantes son unidas por una región "J" de aproximadamente 12 o más aminoácidos, con la cadena pesada incluyendo también una región "D" de aproximadamente 10 aminoácidos más. Véase, generalmente, Fundamental Immunology Ch. 7 (Paul, W., ed., 2ª edición, Raven Press, N.Y. (1989)) (incorporado a manera de referencia en su totalidad para todos los propósitos). Las regiones variables de cada par de

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cadena ligera/pesada forman el sitio de reconocimiento de antígeno del anticuerpo.

Así, un anticuerpo de IgG intacto tiene dos sitios de unión. Excepto en anticuerpos bifuncionales o biespecíficos, los dos sitios de unión son iguales.

Las regiones variables de las cadenas exhiben todas la misma estructura general de regiones estructurales (FR) conservadas relativamente unidas por tres regiones hipervariables, llamadas también regiones de determinación de complementariedad o CDR. Las CDRSs de las dos regiones variables de cada par son alineadas por las regiones estructurales, haciendo posible la unión a un epítopo específico en el antígeno. De la terminal N a la terminal C, las regiones variables de ambas cadenas ligeras y pesadas comprenden los dominios FR1, CDR1, FR2, CDR2, FR3, CDR3 y FR4. La asignación de aminoácidos a cada dominio es de acuerdo con las definiciones de secuencias de proteínas de interés inmunológico de Kabat Immunological Interest (National Institutes of Health, Bethesda, Md. (1987 y 1991)), o Chothia & Lesk, 1897, *J. Mol. Biol.* 196: 901-917; Chothia *et al.*, 1989, *Nature* 342:878-883.

Así, los anticuerpos proporcionados en la presente pueden incluir al menos una cadena de polipéptidos de la región variable de la fórmula: FR1-CDR1-FR2-CDR2-FR3-CDR3-FR4, en donde FR1 es una primera región estructural humana,

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CDR1 es una primera región de determinación de complementariedad, FR2 es una segunda región estructural humana, CDR2 es una segunda región de determinación de complementariedad, FR3 es una tercera región estructural humana, CDR3 es una tercera región de determinación de complementariedad y FR4 es una cuarta región estructural humana. Las CDR son generalmente la región más diversa de la región variable de anticuerpo.

En algunas modalidades, la región FR1 incluye pero no está limitada a cualquiera de las secuencias de aminoácidos SEQ ID NOs: 373-393 y/o 453-469; la región CDR1 incluye pero no está limitada a cualquiera de las secuencias de aminoácidos SEQ ID NOs: 189-217 y/o 275-299; la región FR2 incluye pero no está limitada a cualquiera de las secuencias de aminoácidos SEQ ID NOs: 394-414 y/o 470-481; la región CDR2 incluye pero no está limitada a cualquiera de las secuencias de aminoácidos SEQ ID NOs: 218-233 y/o 300-331; la región FR3 incluye pero no está limitada a cualquiera de las secuencias de aminoácidos SEQ ID NOs: 415-440 y/o 482-511; la región CDR3 incluye pero no está limitada a cualquiera de las secuencias de aminoácidos SEQ ID NOs: 234-274 y/o 332-372; y la región FR4 incluye pero no está limitada a cualquiera de las secuencias de aminoácidos SEQ ID NOs: 441-452 y/o 512-517. De esta manera, en algunas modalidades, los anticuerpos humanos

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proporcionados en la presente tienen una o más de las secuencias de aminoácidos proporcionadas en la presente.

Se debe entender que la secuencia de aminoácidos de los anticuerpos proporcionados en la presente no está limitada a los 20 aminoácidos convencionales (véase, *Immunology - A Synthesis* (2ª edición, E.S. Golub y D.R. Gren, Eds., Sinauer Associates, Sunderland, Mass (1991)), la cual se incorpora en la presente a manera de referencia). Por ejemplo, los aminoácidos pueden incluir estereoisómeros (por ejemplo, D-aminoácidos) de los veinte aminoácidos convencionales, aminoácidos no naturales tales como aminoácidos α, α-disustituidos, N-alquilaminoácidos, ácido láctico y otros aminoácidos no convencionales. Ejemplos de aminoácidos no convencionales, los cuales pueden ser componentes adecuados para el anticuerpo proporcionado, incluyen: 4-hidroxiprolina, γ-carboxiglutamato, ε-N,N,N-trimetillisina, ε-N-acetillisina, O-fosfoserina, N-acetilserina, N-formilmetionina, 3-metilhistidina, 5-hidroxilisina, σ-N-metilarginina y otros aminoácidos similares e iminoácidos, por ejemplo, 4-hidroxiprolina.

Más aún, variaciones menores en las secuencias de aminoácidos mostradas en SEQ ID NOs: 1-517 y 1035-1071 se contemplan como siendo abarcadas, siempre y cuando las variaciones en la secuencia de aminoácidos mantengan al menos 75%, muy preferiblemente al menos 80%, 90%, 95% y más

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preferiblemente 99% de las secuencias mostradas en SEQ ID NOs: 1-517 y 1035-1071. Las variaciones preferidas en las secuencias de aminoácidos mostradas en SEQ ID NOs: 1-517 y 1035-1071, es decir, supresiones, inserciones y/o reemplazos de al menos un aminoácido, ocurren cerca de los límites de dominios funcionales. Los dominios estructurales y funcionales pueden ser identificados mediante la comparación de los datos de secuencia de nucleótidos y/o aminoácidos con bases de datos de secuencias públicas o privadas. Métodos de comparación computarizados se pueden usar para identificar motivos de secuencia o dominios de conformación de proteína predichos que ocurren en otros anticuerpos de estructura y/o función conocida. Los métodos para identificar secuencias de proteínas que se doblan para crear una estructura tridimensional conocida se conocen. Véase, por ejemplo, Bowie *et al.*, 1991, *Science* 253:164; *Proteinas, Structures and Molecular Principles* (Creighton, Ed., W. H. Freeman and Company, Nueva York (1984)); *Introduction to Protein Structure* (C. Branden and J. Tooze, eds., Garland Publishing, Nueva York, N. Y. (1991)); y Thornton *et al.*, 1991, *Nature* 354: 105, los cuales se incorporan en la presente a manera de referencia. Así, los expertos en la técnica pueden reconocer motivos de secuencia y conformaciones estructurales que se pueden usar para definir dominios estructurales y funcionales.

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Las variaciones especialmente preferidas en las secuencias de aminoácidos mostradas en SEQ ID NOs: 1-517 y 1035-1071 son aquellas que llevan a una susceptibilidad reducida a proteólisis u oxidación, alteran patrones de glicosilación o alteran afinidades de unión o confieren o modifican otras propiedades fisicoquímicas o funcionales del anticuerpo. En particular, los reemplazos de aminoácidos conservadores son contemplados. Los reemplazos conservadores son aquellos que tienen lugar dentro de una familia de aminoácidos que están emparentados en sus cadenas laterales. Las familias de aminoácidos preferidas son las siguientes: familia ácida = aspartato, glutamato; familia básica = lisina, arginina, histidina; familia no polar = alanina, valina, leucina, isoleucina, prolina, fenilalanina, metionina, triptófano y familia polar no cargada = glicina, asparagina, glutamina, cisteína, serina, treonina, tirosina. Las familias que más se prefieren son: familia hidroxialifática = serina y treonina; familia que contiene amida = asparagina y glutamina; familia alifática = alanina, valina, leucina e isoleucina y familia aromática = fenilalanina, triptófano y tirosina. Por ejemplo, es razonable esperar que un reemplazo aislado de una leucina con una isoleucina o valina, un aspartato con un glutamato, una treonina con una serina o un reemplazo similar de un aminoácido con un aminoácido emparentado estructuralmente no

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tenga un gran efecto en la unión o propiedades del anticuerpo resultante, especialmente si el reemplazo no incluye un aminoácido dentro de un sitio estructural. Sin embargo, también se abarcan todos los demás reemplazos de aminoácido posibles. Si un cambio de aminoácido da como resultado un anticuerpo funcional, es decir, un anticuerpo que se una a HB-EGF, y reduzca, neutralice o inhiba sustancialmente la función de HB-EGF, puede determinarse fácilmente al ensayar la actividad específica del anticuerpo resultante en ELISA o FACS para la unión a HB-EGF o ensayo funcional *in vitro* o *in vivo*.

Una reducción, neutralización o inhibición sustancial de la transducción de señales mediada por HB-EGF puede ser causada al influenciar, por ejemplo, reducir o inhibir, la unión de HB-EGF a su receptor, por ejemplo, al EGFR o HER4.

El término "anticuerpo" o "anticuerpo anti-HB-EGF", según se usa en la presente, significa un anticuerpo monoclonal, un anticuerpo policlonal, un anticuerpo recombinante, un anticuerpo humanizado (Jones *et al.*, 1986, *Nature* 321:522:525; Riechmann *et al.*, 1988, *Nature* 332:323-329; y Presta, 1992, *Curr. Op. Struct. Biol.* 2:593-596), un anticuerpo quimérico (Morrison *et al.*, 1984, *Proc. Natl. Acad. Sci. E.U.A.* 81: 6851-6855), un anticuerpo multiespecífico (por ejemplo, un anticuerpo biespecífico)

formado de al menos dos anticuerpos, o un fragmento de anticuerpo del mismo. El término "fragmento de anticuerpo" comprende cualquier porción de los anticuerpos mencionados arriba, de preferencia una de sus regiones de unión a antígeno o variables. Ejemplos de fragmentos de anticuerpo incluyen fragmentos Fab, fragmentos Fab', fragmentos $F(ab')_2$, fragmentos Fv, dicuerpos (Hollinger *et al.*, 1993, *Proc. Natl. Acad. Sci. E.U.A.* 90:6444-6448), moléculas de anticuerpo de cadena individual (Piückthun en The Pharmacology of Monoclonal Antibodies 113, Rosenburg and Moore, EDS, Springer Verlag, N.Y. (1994), 269-315) y otros fragmentos siempre y cuando exhiban la capacidad deseada de unión a HB-EGF.

Además, el término "anticuerpo" o "anticuerpo anti-HB-EGF", según se usa en la presente, puede incluir moléculas tipo anticuerpo que contengan sub-dominios manipulados de anticuerpos o variantes de anticuerpo que ocurren naturalmente. Estas moléculas tipo anticuerpo pueden ser anticuerpos de un solo dominio tales como dominios de sólo VH o sólo VL derivados ya sea de fuentes naturales tales como camélidos (Muyldermans *et al.*, 2001, *Reviews in Molecular biotechnology* 74, 277-302) o a través de despliegue *in vitro* de bibliotecas de humanos, camélidos u otras especies (Holt *et al.*, 2003, *Trends Biotechnol*, 21:484-90).

Un "fragmento Fv" es el fragmento de anticuerpo mínimo que contiene un sitio de reconocimiento y unión a

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antígeno completo. Esta región consiste en un dímero de un dominio variable de la cadena pesada y uno de la ligera en asociación estrecha y no covalente. Es esta configuración en la que los tres CDR de cada dominio variable interactúan para definir un sitio de unión a antígeno sobre la superficie del dímero V_H-V_L. Colectivamente, las seis CDR confieren especificidad de unión a antígeno al anticuerpo. Sin embargo, incluso un solo dominio variable (o la mitad de un Fv que comprenda sólo tres CDR específicas para un antígeno) tienen la capacidad de reconocer y unirse al antígeno, aunque normalmente a una afinidad más baja que el sitio de unión completo. El "fragmento Fab" contiene también el dominio constante de la cadena ligera y el primer dominio constante (C_H1) de la cadena pesada. El "fragmento Fab" difiere del "fragmento Fab" por la adición de pocos residuos en el término carboxi del dominio C_H1 de la cadena pesada incluyendo una o más cisteínas de la región de pivote del anticuerpo. El "fragmento $F(ab')_2$" se produce originalmente como un par de "fragmentos Fab" los cuales tienen cisteínas de pivote entre ellos. Los métodos para preparar estos fragmentos de anticuerpo, tales como digestión con papaína o pepsina, se conocen por aquellos expertos en la técnica.

Un anticuerpo proporcionado en la presente puede fijar complemento (CDC) o activar citotoxicidad celular dependiente de anticuerpo (ADCC), especialmente un anticuerpo

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IgG1, variante de IgG1 cambiada de clase de IgG2 o IgG4 u otro isotipo de origen humano o mamífero, mediante biología molecular o generado de nuevo a partir de ratones productores de IgG1 humana. Otros métodos también pueden usarse. Un anticuerpo provisto en la presente algunas veces puede ser acoplado a un grupo marcador o a un grupo efector, por ejemplo, una toxina, agente quimioterapéutico, molécula reportera o agente de formación de imágenes.

G. Tipos adicionales de proteínas de unión a HB-EGF

En otro aspecto, la proteína de unión a antígeno HB-EGF como la proporcionada en la presente es una proteína estructural que tiene una actividad de unión a tipo anticuerpo, es decir, se une a HB-EGF.

En el contexto de la presente invención, el término "proteína estructural", según se usa en la presente, significa una estructura polipeptídica con una alta tolerancia de su dobles para modificaciones tales como inserciones múltiples, supresiones o sustituciones. Esta estabilidad de conformación intrínseca hace posible la aleatorización dirigida y cambios drásticos dentro de una región definida de la proteína. Así, adquiere ciertas propiedades novedosas, en tanto que su integridad estructural general y comportamiento fisicoquímico original siguen sin cambios. Esta propiedad adoptada de nuevo principalmente, pero no exclusivamente, comprende la especificidad de unión

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para una molécula objetivo predefinida.

Actualmente, una amplia variedad de proteínas estructurales están en uso que imitan el principio de unión de un anticuerpo convencional a diferentes grados (Hey et al., 2005, *Trends in Biotechnol.* 23:514-22). Ejemplos de proteínas estructurales que pueden usarse de acuerdo con la presente invención pueden ser subdivididas en diferentes grupos. Las estructuras relacionadas con anticuerpos, las cuales se definen como derivados de anticuerpos que son ya sea naturalmente más pequeños en tamaño y más simples en estructura, o han sido manipulados de esta manera. Este grupo incluye por ejemplo los llamados nanocuerpos (revisados en Hey et al., Trends in Biotechnol. 2005; 23 (10); 514-522), anticuerpos de dominio (Holt et al., 2003, *Trends in Biotechnol.* 21:484-489) o proteínas reactivas de antígenos de tiburón (Holt et al., Trends in Biotechnol, 2003; 21; 484-489). Un segundo grupo de proteínas estructurales son dobleces de proteínas rígidos que toleran la inserción o aleatorización de péptidos de una sola asa tales como el dominio tipo Kunitz (Dennis *et al.*, 1995; *J. Biol. Cell.* 270:25411-25417), transferrina humana (Ali *et al.*, 1999, *J. Biol. Cell.* 274:24066-24074) o motivos estructurales de nudo de cisteína (Christmann *et al.*, 1999, *Protein Eng.* 12:797-806). Las proteínas que comparten el principio de varias asas hipervariables en una estructura rígida conservada en

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analogía a anticuerpos son representados por CTLA-4 humana (Hufton *et al.*, 2000 *FEBS Lett.* 475:225-231), dominios de fibronectina humana tipo III (Koide *et al.*, 1998; *J. Mol. Biol.* 284:1141-1151), dominios tipo lectina tipo C o lipocalinas (Skerra, 2001, *J. Biotechnol.* 74:257-275). Las estructuras con especificidad de unión lograda a través de residuos de aminoácido que están colocados parcial o completamente dentro de la estructura secundaria rígida de la proteína son por ejemplo proteínas de repetición de anquirina (Binz, 2003, *J. Mol. Biol.* 332:489-503), el dominio Z de proteína A (Nord *et al.*, 1995, *Protein Eng.* 8:601-608) o γ-cristalina (Fiedler y Rudolph, 2001, solicitud de patente internacional WO 01/04144). Las proteínas estructurales y péptidos y aplicaciones de los mismos se revisan en Hey *et al.*, 2005, *Trends en Biotechnol.* 23:514-522; Binz *et al.*, 2005, *Nature Biotechnol.* 23:1257-1268) y Holliger *et al.*, 2005, *Nature Biotechnol.* 23:11261136.

La manipulación de una proteína estructural puede considerarse como injertar o integrar una función de afinidad sobre o dentro de la estructura estructural de una estructura polipeptídica con una alta tolerancia de su dobles para modificaciones. Función de afinidad significa una afinidad de unión a proteína de acuerdo con la presente invención. Una estructura puede ser estructuralmente separable de las secuencias de aminoácidos que confieran especificidad de

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unión. En general, las proteínas que aparecen adecuadas para el desarrollo de estos reactivos de afinidad artificiales pueden obtenerse mediante técnicas de manipulación de proteínas racionales, o más comúnmente combinatorias tales como tamizado contra un antígeno, por ejemplo, HB-EGF, ya sea proteína purificada o proteína desplegada sobre la superficie celular, para agentes de unión en una biblioteca estructural artificial desplegada *in vitro*, usando capacidades que se conocen bien en la técnica (Skerra, 2000, *J. Mol. Recog.* Julio-agosto; 13(4):167-87; Binz y Piückthun, 2005, agosto; 16(4):459-69). Además, una proteína estructural que tenga una actividad de unión tipo anticuerpo puede derivarse de un polipéptido receptor, por ejemplo, una de las proteínas anteriores, que contenga el dominio estructural, la cual puede injertarse con dominios de unión de un polipéptido donador para conferir la especificidad de unión del polipéptido donador sobre el dominio estructural que contenga el polipéptido aceptor. Estos dominios de unión insertados pueden ser, por ejemplo, una o más de la región de determinación de complementariedad (CDR) de un anticuerpo, en particular un anticuerpo HB-EGF. De preferencia, la CDR es un CDR3. La inserción se puede lograr mediante varios métodos conocidos por aquellos expertos en la técnica incluyendo, por ejemplo, síntesis de polipéptidos, síntesis de ácido nucleico de un aminoácido de codificación así como

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mediante varias formas de métodos recombinantes bien conocidos por aquellos expertos en la técnica.

H. Conjugados de proteínas de unión a antígeno HB-EGF

En otra modalidad, una proteína de unión a antígeno HB-EGF, por ejemplo, un anticuerpo proporcionado en la presente se acopla a un grupo marcador. Esta proteína de unión a antígeno marcada es particularmente adecuada para aplicaciones de diagnóstico. Según se usa en la presente, el término "grupo marcador" se refiere a un marcador detectable, por ejemplo, una porción de aminoácido o biotinilo marcada radioactivamente que se puede detectar mediante avidina marcada (por ejemplo, estreptavidina unida a un marcador fluorescente o actividad enzimática puede detectarse mediante métodos ópticos o colorimétricos). Varios métodos para marcar polipéptidos y glicoproteínas, tales como anticuerpos, se conocen en la técnica y pueden ser usados. Ejemplos de grupos marcadores adecuados incluyen, pero no están limitados a, los siguientes: radioisótopos o radionúclidos (por ejemplo, ^{3}H, ^{14}C, ^{15}N, ^{35}S, ^{90}Y, ^{99}Tc, ^{111}In, ^{125}I, ^{131}I), grupos fluorescentes (por ejemplo, FITC, rodamina, fósforos de lantanuro), grupos enzimáticos (por ejemplo, peroxidasa de rábano, β-galactosidasa, luciferasa, fosfatasa alcalina), grupos quimioluminiscentes, grupos biotinilo o epítopos de polipéptido predeterminado reconocidos por un reportero

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secundario (por ejemplo, secuencias de pares de cremalleras de leucina, sitios de unión para anticuerpos secundarios, dominios de unión a metales, marcadores epítopos). En ciertos aspectos, puede ser deseable que los grupos marcadores sean unidos por brazos separadores de varias longitudes para reducir el impedimento estérico potencial.

Como alternativa, una proteína de unión a antígeno HB-EGF proporcionada en la presente, tal como un anticuerpo, puede ser acoplada a un grupo efector. Esta proteína de unión a antígeno modificada por efector es especialmente adecuada para aplicaciones terapéuticas. Según se usa en la presente, el término "grupo efector" se refiere a un grupo citotóxico tal como un radioisótopo o radionúclido, una toxina, un grupo terapéutico u otro grupo efector conocido en la técnica. Ejemplos de grupos efectores adecuados son radioisótopos o radionúclicos (por ejemplo, ^{3}H, ^{14}C, ^{15}N, ^{35}S, ^{90}Y, ^{11}Tc, ^{111}In, ^{125}I, ^{131}I), caliqueamicina, análogos de dolastatina tales como auristatinas y agentes quimoterapéuticos tales como geldanamicina y maitansina derivados, incluyendo DM1. En ciertos aspectos, puede ser deseable que los grupos efectores sean fijados por brazos separadores de varias longitudes para reducir el impedimento estérico potencial.

También como se describe en la presente, muchas de las proteínas de unión a antígeno HB-EGF altamente útiles,

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por ejemplo, preparaciones de anticuerpos proporcionadas en la presente reconocen epítopos dentro del dominio tipo EGF de HB-EGF, el cual incluye los residuos 106-149 de la proteína, por ejemplo, con la siguiente secuencia:

PCLRKYKDFCIHGECKYVKELRAPSCICHPGYHGERCHGLSLP (SEQ ID NO: 1076). En algunas modalidades, el epítopo de factor de crecimiento epidérmico reconocido por las proteínas de unión a antígeno proporcionadas en la presente incluye la secuencia de aminoácidos IHGE. En consecuencia, se proporcionan preparaciones de anticuerpo que se unen a y reconocen un epítopo que contiene IHGE y/o un dominio tipo EGF de HB-EGF, por ejemplo, SEQ ID NO: 1076.

Las proteínas de unión a antígeno anti-HB-EGF son útiles en la detección de HB-EGF en muestras de pacientes y en consecuencia son útiles como diagnósticos para estados de enfermedad como los descritos en la presente. Además, con base en su capacidad para inhibir significativamente la actividad del receptor anti-HB-EGF y/o EGF (como se demuestra en los ejemplos bajo), las proteínas de unión a antígeno HB-EGF tienen efectos terapéuticos para tratar síntomas y afecciones que resultan de la expresión de HB-EGF y/o actividad de HB-EGF. En modalidades específicas, las proteínas de unión a antígeno y métodos de la presente se refieren al tratamiento de síntomas que resultan de enfermedades asociadas con HB-EGF, enfermedades asociadas con

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HER4 o estados de enfermedad asociados con el receptor EGF, por ejemplo, condiciones cancerosas. Modalidades adicionales incluyen el uso de las proteínas de unión a antígeno y métodos descritos en la presente para tratar angiogénesis no deseada, enfermedades neoplásicas tales como melanoma, cáncer pulmonar no microcítico, glioma, carcinoma hepatocelular (hígado), tumor de tiroides, cáncer gástrico (estómago), cáncer de próstata, cáncer de seno, cáncer ovárico, cáncer de vejiga, cáncer pulmonar, glioblastoma, cáncer endometrial, cáncer renal, cáncer de colon y cáncer pancreático.

I. Ácidos nucleicos que codifican para proteínas de unión a antígeno HB-EGF

También se proporcionan ácidos nucleicos que codifican para las proteínas de unión a antígeno descritas en la presente, o porciones de los mismos, incluyendo ácidos nucleicos que codifican para una o ambas cadenas de un anticuerpo, o un fragmento, derivado, muteína o variante del mismo, polinucleótidos que codifican para las regiones variables de la cadena pesada o sólo CDR, polinucleótidos suficientes para usarse como sondas de hibridación, cebadores de PCR o cebadores de secuenciación para identificar, analizar, mutar o amplificar un polinucleótido que codifique para un polipéptido, ácidos nucleicos antisentido para inhibir la expresión de un polinucleótido y secuencias complementarias de los anteriores. Los ácidos nucleicos

pueden tener cualquier longitud. Pueden tener, por ejemplo, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 125, 150, 175, 200, 250, 300, 350, 400, 450, 500, 750, 1,000, 1,500, 3,000, 5,000 o más nucleótidos de largo y/o pueden comprender una o más secuencias adicionales, por ejemplo, secuencias reguladoras y/o ser parte de un ácido nucleico más grande, por ejemplo, un vector. Los ácidos nucleicos pueden ser de una sola hebra o de doble hebra y pueden comprender nucleótidos de ARN y/o ADN, y variantes artificiales de los mismos (por ejemplo, ácidos nucleicos péptidos). Las figuras 15A-15V ilustran las secuencias de nucleótidos para las cadenas ligeras diferentes de las proteínas de unión a antígeno. Las figuras 16A-16AC ilustran las secuencias de nucleótidos de las diferentes cadenas pesadas de las proteínas de unión a antígeno. Las figuras 13A-13M ilustran las secuencias de nucleótidos de varias regiones variables de la cadena ligera de las proteínas de unión a antígeno. Las figuras 14A-14L ilustran las secuencias de nucleótidos de varias regiones variables de la cadena pesada de las proteínas de unión a antígeno. Las figuras 18A-18F ilustran las secuencias de nucleótidos para varias regiones CDR de las regiones variables de la cadena ligera de las proteínas de unión a antígeno. Las figuras 19A-19G ilustran las secuencias de nucleótidos para varias regiones CDR de las regiones variables de la cadena pesada de las proteínas de

unión a antígeno. Las figuras 20A-20K ilustran las secuencias de nucleótidos para varias regiones FR de las regiones variables de la cadena ligera de las proteínas de unión a antígeno. Las figuras 21A-21K ilustran las secuencias de nucleótidos para varias regiones FR de la cadena pesada, regiones variables de las proteínas de unión a antígeno. La figura 17A ilustra la secuencia de nucleótidos de la región constante de la cadena ligera de las proteínas de unión a antígeno. Finalmente, la figura 17B ilustra la secuencia de nucleótidos de la región constante de la cadena pesada de las proteínas de unión a antígeno.

Ácidos nucleicos que codifican para ciertas proteínas de unión a antígeno, o porciones de las mismas (por ejemplo, anticuerpos de longitud completa, dominio variable de la cadena pesada o ligera o CDRH1, CDRH2, CDRH3, CDRL1, CDRL2 o CDRL3) pueden ser aislados de células B de ratones que hayan sido inmunizados con HB-EGF o un fragmento inmunogénico del mismo. El ácido nucleico puede ser aislado mediante procedimientos convencionales tales como reacción en cadena de la polimerasa (PCR). El despliegue de fagos es otro ejemplo de una técnica conocida mediante la cual derivados de anticuerpos y otras proteínas de unión a antígeno pueden ser preparados. En un enfoque, polipéptidos que son componentes de una proteína de unión a antígeno de interés son expresados en cualquier sistema de expresión

recombinante adecuado, y los polipéptidos expresados se dejan ensamblar para formar moléculas de proteínas de unión a antígeno.

Un aspecto proporciona además ácidos nucleicos que hibridan otros ácidos nucleicos (por ejemplo, ácidos nucleicos que comprenden una secuencia de nucleótidos ilustrada en las figuras 13 a 21) bajo condiciones de hibridación particulares. Los métodos para hibridar ácidos nucleicos se conocen bien en la técnica. Véase, por ejemplo, Current Protocols en Molecular Biology, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. Según se define en la presente, la condición de hibridación moderadamente severa usa una solución de prelavado que contiene 5x cloruro de sodio/citrato de sodio (SSC), 0.5% de SDS, 1.0 mM de EDTA (pH 8.0), regulador de pH de hibridación de aproximadamente 50% de formamida, 6x SSC y una temperatura de hibridación de 55°C (u otras soluciones de hibridación similares, tal como la que contiene alrededor de 50% de formamida, con una temperatura de hibridación de 42°C), y condiciones de lavado de 60°C, en 0.5x SSC, 0.1% de SDS. Una condición de hibridación severa hibrida en 6x SSC a 45°C seguida por uno o más lavados en 0.1 x SSC, 0.2% de SDS a 68°C. Además, alguien de capacidad en la técnica puede manipular las condiciones de hibridación y/o lavado para incrementar o reducir la severidad de la hibridación de tal manera que ácidos nucleicos que comprendan

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secuencias de nucleótidos que sean al menos 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% o 99% idénticas entre sí permanezcan típicamente hibridados unos con otros.

Los parámetros básicos que afectan la elección de condiciones de hibridación y la guía para contemplar condiciones adecuadas se muestran, por ejemplo, por Sambrook, Fritsch y Maniatis (2001, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press. Cold Spring Harbor, N.Y., citado arriba y *Current Protocols* en Molecular Biology, 1995, Ausubel *et al.*, ediciones, John Wiley & Sons, Inc., secciones 2.10 y 6.3-6.4), y pueden determinarse fácilmente por aquellos que tengan capacidad ordinaria en la técnica con base en, por ejemplo, la longitud y/o composiciones de base del ácido nucleico.

Pueden introducirse cambios mediante mutación en un ácido nucleico, llevando de esta manera cambios en la secuencia de aminoácidos de un polipéptido (por ejemplo, un anticuerpo o derivado de anticuerpo) para el que codifique. Mutaciones pueden introducirse usando cualquier técnica conocida en la técnica. En una modalidad, uno o más residuos de aminoácido particulares se cambian usando, por ejemplo, un protocolo de mutagénesis dirigido a sitio. En otra modalidad, uno o más residuos seleccionados aleatoriamente se cambia usando, por ejemplo, un protocolo de mutagénesis aleatorio. Sin embargo como se haga, un polipéptido mutante

puede ser expresado y tamizado para una propiedad deseada.

Se pueden introducir mutaciones en un ácido nucleico sin alterar significativamente la actividad biológica de un polipéptido para el que codifique. Por ejemplo, se pueden hacer sustituciones de nucleótidos que lleven a las sustituciones de aminoácido en residuos de aminoácido no esenciales. Como alternativa, pueden introducirse una o más mutaciones en un ácido nucleico que cambien selectivamente la actividad biológica de un polipéptido para el que codifique. Por ejemplo, la mutación puede cambiar cuantitativa o cualitativamente la actividad biológica. Ejemplos de cambios cuantitativos incluyen incrementar, reducir o eliminar la actividad. Ejemplos de cambios cualitativos incluyen cambiar la especificidad de antígeno de un anticuerpo.

Otro aspecto proporciona moléculas de ácido nucleico que son adecuadas para usarse como cebadores o sondas de hibridación para la detección de secuencias de ácido nucleico. Una molécula de ácido nucleico puede comprender sólo una porción de una secuencia de ácido nucleico que codifique para un polipéptido de longitud completa, por ejemplo, un fragmento que se puede usar como una sonda o cebador o un fragmento que codifique para una porción activa (por ejemplo, una porción de unión a HB-EGF) de un polipéptido.

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Las sondas a base de la secuencia de un ácido nucleico se pueden usar para detectar el ácido nucleico o ácidos nucleicos similares, por ejemplo, transcriptos que codifiquen para un polipéptido. La sonda puede comprender un grupo marcador, por ejemplo, un radioisótopo, un compuesto fluorescente, una enzima o un co-factor de enzima. Estas sondas pueden usarse para identificar una célula que exprese el polipéptido.

Otro aspecto proporciona vectores que comprenden un ácido nucleico que codifica para un polipéptido o una porción del mismo (por ejemplo, un fragmento que contiene una o más CDR o uno o más dominios de la región variable). Ejemplos de vectores incluyen, pero no están limitados a, plásmidos, vectores virales, vectores de mamífero no episómicos y vectores de expresión, por ejemplo, vectores de expresión recombinantes. Los vectores de expresión recombinantes pueden comprender un ácido nucleico en una forma adecuada para la expresión del ácido nucleico en una célula hospedera. Los vectores de expresión recombinantes incluyen una o más secuencias reguladoras, seleccionadas con base en las células hospederas que se usarán para expresión, las cuales son enlazadas operablemente a la secuencia de ácido nucleico que será expresada. Las secuencias reguladoras incluyen aquellas que dirigen la expresión constitutiva de una secuencia de nucleótidos en muchos tipos de células hospederas (por

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ejemplo, el promotor del gen temprano de SV40, promotor del virus de sarcoma de Rous y promotor de citomegalovirus), aquellos que dirigen la expresión de la secuencia de nucleótidos sólo en ciertas células hospederas (por ejemplo, secuencias reguladoras específicas de tejidos, véase, Voss *et al.*, 1986 *Trends Biochem. Sci.* 11:287, Maniatis *et al.*, 1987, *Science* 236:1237, incorporada en la presente a manera de referencia en su totalidad), y aquellos que dirigen expresión inducible de una secuencia de nucleótidos en respuesta a un tratamiento o afección particular (por ejemplo, el promotor de metalotioneína en células de mamífero y el promotor que responde a tet y/o sensible a estreptomicina en sistemas tanto procarióticos como eucarióticos (véase arriba). Se apreciará por aquellos expertos en la técnica que el diseño del vector de expresión puede depender de factores tales como la elección de la célula hospedera que será transformada, el nivel de expresión de proteína deseada, etc. Los vectores de expresión pueden introducirse en células hospederas para producir así proteínas o péptidos, incluyendo proteínas o péptidos de fusión, codificados por ácidos nucleicos como se describe en la presente.

Otro aspecto proporciona células hospederas en las cuales se ha introducido un vector de expresión recombinante. Una célula hospedera puede ser cualquier célula procariótica, (por ejemplo, *E. coli*) o célula eucariótica (por ejemplo,

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células de levadura, insecto o mamífero (por ejemplo, células CHO). El ADN de vector puede introducirse en células procarióticas o eucarióticas mediante técnicas convencionales de transformación de transfección. Para la transfección estable de células de mamífero, se conoce que, dependiendo del vector de expresión y técnica de transfección usada, sólo una pequeña fracción de células puede integrar el ADN extraño en su genoma. Para modificar y seleccionar estos integrantes, un gen que codifique para un modificador seleccionable (por ejemplo, para resistencia a antibióticos) se introduce generalmente en las células hospederas junto con el gen de interés. Los marcadores seleccionables que se prefieren incluyen aquellos que confieren resistencia a fármacos, tales como G418, higromicina y metotrexato. Las células establemente transfectadas con el ácido nucleico introducido pueden ser identificadas mediante selección de fármaco (por ejemplo, células que tengan incorporado el gen marcador seleccionable sobrevivirán, en tanto que las otras células morirán), entre otros métodos.

J. Uso de proteínas de unión a antígeno HB-EGF para propósitos de diagnóstico y terapéuticos

1. Indicaciones

Las proteínas de unión a antígeno HB-EGF como las descritas en la presente se pueden usar para detectar o tratar un número de enfermedades y trastornos, incluyendo

aquellos que impliquen una proliferación celular excesiva, migración celular indeseable y/o angiogénesis aberrante. Por ejemplo, estas proteínas de unión a antígeno HB-EGF pueden inhibir la fosforilación de tirosina de EGFR y/o HER4 inducida por HB-EGF en células cancerosas (figuras 22A-29). Esta inhibición puede interrumpir la cascada de los eventos de señalización que conduce a la proliferación y migración celular, y angiogénesis. Además, las proteínas de unión a antígeno HB-EGF pueden interferir con la transactivación del EGF. Además, estas proteínas de unión a antígeno inhiben la proliferación de células HUVEC basales (figura 32B), formación de tubos de células endoteliales (figuras 33A-3M) y formación de vasos inducida por HB-EGF en un ensayo de tapón de matrigel *in vivo* (figura 36). Estos resultados indican que las proteínas de unión a antígeno HB-EGF como las descritas en la presente inhiben angiogénesis *in vitro* e *in vivo*. Además, estas proteínas de unión a antígeno inhiben también el crecimiento celular independiente de anclaje (figuras 34A a 34F y figura 35) y el crecimiento de tumores de xenoinjerto en ratones (figura 37 y figuras 38A a 38C). En forma significativa, las proteínas de unión a antígeno HB-EGF inhiben también la migración de células cancerosas MCF-7 y MDA-MB231 (véase figuras 27 y 28). Así, las proteínas de unión a antígeno HB-EGF como las descritas en a presente atacan varias etapas en el desarrollo de tumores y otras

condiciones cancerosas, incluyendo eventos de señalización que controlan la proliferación celular, angiogénesis y migración celular asociadas con la dispersión y desarrollo de cáncer metastásico. Esta intervención de varias facetas es altamente benéfica para controlar e inhibir el proceso mediante el cual se desarrolla el cáncer. Más aún, los cánceres en cualquier etapa de progresión (por ejemplo, cánceres primarios, metastásicos y recurrente) pueden ser tratados.

Además del uso de las proteínas de unión a antígeno HB-EGF para detectar y tratar cánceres de varias etapas de progresión, estas proteínas de unión a antígeno también pueden ser útiles para detectar un número de tipos de cáncer diferentes. Por ejemplo, HB-EGF es expresado a niveles muy bajos en tejidos de seno y pancreáticos normales. Sin embargo, HB-EGF es expresado a altos niveles en aproximadamente 55% de células de cáncer pancreático y alrededor de 70% de células de cáncer de seno. Más aún, como se describió en los ejemplos, la expresión de HB-EGF fue detectada en varias líneas de células cancerosas, indicando que las proteínas de unión a antígeno HB-EGF descritas en la presente se pueden usar para la detección de una variedad de tipos de cáncer.

Por ejemplo, los cánceres que pueden ser detectados o tratados por las proteínas de unión a antígeno reclamadas

incluyen tumores de mamíferos sólidos así como malignidades hematológicas. Los tumores de mamíferos sólidos incluyen cánceres en niños tales como, por ejemplo tumores de células germinales, sarcomas de tejido blando, tumores cerebrales primarios, neuroblastoma, nefroblastoma y carcinoma, en particular carcinoma escamoso y carcinoma epitelial. Los tumores de mamíferos sólidos también pueden incluir cánceres en adultos tales como, por ejemplo, tumores de origen desconocido, cáncer cerebral primario en adultos, tumores de la glándula pituitaria, labio, cavidad oral, nasofaringe, laringe, sino maxilar, sino etmoide, glándulas salivares, glándula tiroides (incluyendo glándulas paratiroides y carcinoides), esófago, estómago, páncreas, intestino delgado, colon, recto, canal anal, hígado, vesícula biliar, ductos biliares extrahepáticos, ampollas de agua, carcinoides, tumores endocrinos del sistema gastroenterohepático, feocromocitoma y paraganglioma, glándulas adrenales, pulmón, pleura, mediastino, timo, tumores de hueso y tejido blando, tumores dérmicos del labio, párpados, oído externo, otras partes no especificadas del rostro, cuero cabelludo y cuero, tronco, extremidades superiores y hombros, extremidades inferiores y cadera, vulva, pene, escroto, tumores de seno, tumores ginecológicos de vulva, vagina, cérvix, útero, cuello uterino, ovarios, trompas de falopio, tumores gestacionales y trofoblásticos, pene, próstata, testículos, riñón, pelvis

renal y uretra, vejiga urinaria, uretra, tumores oftálmicos de los párpados, conjuntiva, uvea, retina, órbita y glándula lacrimal. Las malignidades hematológicas incluyen en la niñez, por ejemplo, leucemia y linfomas, leucemia aguda y crónica (AML, ANLL, ALL, CML, MDS), enfermedad de Hodgkin, linfomas de células B, células T, células grandes, folicular, indolente/de grado bajo, agresivo/de grado alto de origen linfocítico y cutáneo, neoplasma de células plasmáticas y cánceres asociados con SIDA.

Además, las proteínas de unión a antígeno HB-EGF descritas en la presente se pueden usar también para detectar o tratar afecciones cancerosas o trastornos de neoplasia, las cuales incluyen, por ejemplo, adenoma, adenoma tubulovelloso, adenoma velloso, angiofibroma, neoplasias mucinosas de proliferación atípica, tumor de Brenner, carcinoides, hemangioma cavernoso, leiomioma celular, corangioma, nefroma mesoblástico congénito, cistadenoma mucinoso, cistadenoma seroso, fibroadenoma dermoide, desmoide, fibroma, fibrotecoma, adenoma folicular, ganglioneuroma, tumor de células gigantes, tumor de células granuladas, tumor de células granulosas, hemangioma, papiloma intraductal, tumor de células de las isletas, leiomioma, lipoma, luteoma, meningioma, mole, mielolipoma, mixoma, neurofibroma, nevo, osteocondroma, feocromocitoma, poliposis, schwannoma, cistadenoma seroso, ovarios estrumáticos, condromatosis

sinovial, timoma benigno.

Ejemplos adicionales de los tipos de cánceres que pueden detectarse o tratarse con las proteínas HB-EGF descritas en la presente se pueden encontrar, por ejemplo, de la Sociedad Americana de Cáncer (www.cancer.org), o de Wilson *et al.*, (1991) Harrison's Principles of Internal Medicine, 12ª edición, McGraw-Hill, Inc.

Por lo tanto, las proteínas de unión a antígeno HB-EGF como las descritas en la presente se pueden usar para tratar y/o prevenir cáncer, afecciones cancerosas, crecimiento tumoral, metástasis de células cancerosas, procesos angiogénicos y/o trastornos neoplásicos. Así, estas proteínas de unión a antígeno proporcionan un método para tratar o prevenir cáncer en un sujeto que incluye administrar al sujeto una cantidad efectiva de una composición que comprende una de las preparaciones de unión a antígenos HB-EGF humanas y/o monoclonales como las descritas en la presente, o una combinación de las mismas.

Una alta proporción de enfermedades de tumores sólidos se caracteriza comúnmente por angiogénesis tumoral, el crecimiento excesivo de vasos (anormales) en el tejido tumoral mediado por factores de crecimiento (es decir, VEGF) y otros factores (es decir, HB-EGF). La dirección de HB-EGF a través de una proteína a antígeno específica de HB-EGF podría prevenir la formación de vasos nuevos y por lo tanto

limitar la expansión de tumores existentes y el desarrollo de tumores nuevos (es decir, metástasis).

Aparte de su papel como un ligando mitogénico y pro-invasivo varios estudios han apoyado la imagen de HB-EGF como un regulador importante de procesos angiogénicos en cáncer. Como se ilustra en los ejemplos, una función de HB-EGF en la regulación de angiogénesis *in vivo* fue mostrada. Así, las proteínas de unión a antígeno como las descritas en la presente se pueden usar para tratar enfermedades asociadas con o causadas por angiogénesis, por ejemplo, enfermedades cancerosas o no cancerosas.

Por ejemplo, las proteínas de unión a antígeno HB-EGF como las descritas en la presente pueden interferir con la comunicación entre células de músculo liso (SMC) y células endoteliales, un proceso fundamental en el desarrollo y funcionalidad de vasos sanguíneos en angiogénesis, por ejemplo, angiogénesis tumoral.

Más aún, estas proteínas de unión a antígeno pueden inhibir al menos parcialmente la expresión inducida por HB-EGF y liberación de VEGF a partir de SMC lo cual interactúa subsecuentemente como un mitógeno endotelial poderoso. En forma similar, VEGF incrementa la producción de HB-EGF en células endoteliales lo cual constituye por lo tanto un circuito de retroalimentación pro-angiogénico que consiste en estos dos ligandos importantes que pueden ser interrumpidos

al administrar las proteínas de unión a antígeno HB-EGF como las descritas en la presente. Recientemente, y además de VEGF, varios constituyentes pro-angiogénicos críticos tales como angiopoyetina 1 y 2 (Ang-1 y 2) y su receptor TIE-2 así como la potente angiotensina II (ATII) de estímulo de GPCR de células de músculo liso fueron identificadas. En forma interesante, HB-EGF es un mediador crítico de la transactivación de EGFR inducida por ATII y la subrregulación hacia el extremo 3' de VEGF y Ang-2 en células endoteliales. *In vivo*, ATII induce la angiogénesis de una manera dependiente de HB-EGF e incrementa la actividad angiogénica de VEGF. Estos descubrimientos soportan el hecho de que en paralelo a VEGF, HB-EGF es capaz de activar vías angiogénicas adicionales por medio de Ang-2. Por lo tanto, la angiogénesis aberrante o cáncer en un mamífero puede ser tratada con la administración de una cantidad efectiva de la proteína de unión a antígeno HB-EGF descrita en la presente.

Aparte de su papel como un regulador importante de procesos angiogénicos en cáncer, varias indicaciones no cancerosas con vías angiogénicas activadas y el requerimiento de flujo sanguíneo colateral son áreas de enfermedad putativas para la terapia con proteínas de unión a antígeno HB-EGF.

Enfermedades inflamatorias crónicas (por ejemplo, nefritis, EPOC, enfermedad intestinal inflamatoria)

incluyendo "reacciones inflamatorias mediadas por el sistema inmunitario (por ejemplo, enfermedad de injerto contra huésped, rechazo de transplantes, restenosis), enfermedades metabólicas (por ejemplo, diabetes) o afecciones epóxicas crónicas se caracterizan comúnmente por hiper y/o neovascularización (por ejemplo, úlceras crónicas). Las proteínas de unión a antígeno HB-EGF descritas pueden inhibir al menos parcialmente el proceso esencial de angiogénesis - el reclutamiento de células musculares lisas vasculares por células endoteliales inducido por HB-EGF ya sea producido por células inflamatorias o sobrerregulado por hipoxia - y representan por lo tanto una ruta atractiva para la terapia intervencionista de vascularización excesiva/patológica.

En sujetos obesos, niveles incrementados de HB-EGF derivado de la grasa acumulada que contribuye a la incidencia más alta de enfermedad vascular en obesidad, pueden ser neutralizados por las proteínas de unión a antígeno HB-EGF descritas en la presente. Una intervención terapéutica por una proteína de unión a antígeno HB-EGF puede actuar por lo tanto directamente como un anti-adipocitocina para interrumpir el eje adipovascular.

En fibroblastos, HB-EGF sub-regula significativamente ARNm de elastina mediante la activación del receptor de factor de crecimiento epidérmico. Este efecto proporciona una vía de intervención en el desarrollo

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de fibrosis pulmonar.

Más aún, HB-EGF es un mitógeno de queratinocitos implicados en la patogénesis de enfermedades inflamatorias. Además, la expresión de HB-EGF y la co-localización con el EGFR puede jugar un papel importante en la patogénesis temprana de psoriasis que abre una ventana terapéutica potencial en el tratamiento de enfermedades inflamatorias cutáneas y específicamente en el tratamiento temprano de psoriasis con las proteínas de unión a antígeno reclamadas.

La dirección de HB-EGF con las proteínas de unión a antígeno descritas también puede dar como resultado una opción de tratamiento para pacientes con vitreorretinopatía proliferativa (PVR), toda vez que el desarrollo de PVR es acompañado por una sobrerregulación significativa de HB-EGF en retinas de PVR. Además, la expresión de HB-EGF en tejido fibroproliferativo y su efecto estimulador en la proliferación de células gliales, quimiotaxis y secreción de VEGF sugieren que HB-EGF puede ser un factor que medie las respuestas de células gliales durante PVR. Estos principios también pueden aplicarse a enfermedades oculares dependientes de angiogénesis adicionales tales como degeneración macular relacionada con la edad y no relacionada con la edad, retinopatía diabética, glaucoma rubeótica, queratitis intersticial, retinopatía de prematurez e insuficiencia de injertos corneales.

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GPCR tales como adrenoceptores y receptores de angiotensina han estado ligados con la patogénesis de hipertensión debido a sus capacidades promotoras vasoconstrictoras y de crecimiento. Ya que HB-EGF es un mediador crítico de estas vías, las proteínas de unión a antígeno neutralizantes son adecuadas para la intervención dirigida en trastornos hipertensivos tales como hipertrofia cardiaca e insuficiencia cardiaca congestiva, insuficiencia renal y apoplejía.

HB-EGF, un potente mitógeno y quimioatractor para células de músculo liso (SMC), se detectó en placas ateroescleróticas de arterias coronarias con engrosamiento íntimo y es producido por SMC y macrófagos. Las lipoproteínas restantes son agentes causantes conocidos de aterosclerosis mostraron además inducir proliferación de SMC por medio de transactivación de EGFR mediada por HB-EGF. Por lo tanto, las proteínas de unión antígenos HB-EGF como las descritas en la presente representan agentes selectivos y eficientes que se dirigen a ateroesclerosis al bloquear las funciones de células de músculo liso críticas. Además, la restenosis después de intervención coronaria percutánea que se caracteriza por proliferación de células de músculo liso también podría ser prevenida por la neutralización específica de la función de HB-EGF.

Así, las proteínas de unión a antígeno HB-EGF como

las descritas en la presente se pueden usar para tratar una variedad de enfermedades, incluyendo enfermedades proliferativas no malignas tales como angiogénesis aberrante, leiomioma (fibrosis uterina), tumores de células de músculo liso benignos, glomeruloeslcerosis (hiperproliferación de células mesangiales), hiperplasia de células de músculo liso, aterosclerosis (hiperproliferación de células de músculo liso vasculares), rubeosis; glaucoma neovascular, retinopatía diabética, ceguera diabética, degeneración macular, artritis reumatoide, hipertrofia cardiaca, psoriasis, y similares.

En un aspecto más, estas proteínas de unión a antígeno HB-EGF pueden usarse para tratar trastornos asociados con o acompañados por una activación de receptor de crecimiento incrementada patológicamente por ejemplo alterada.

En otro aspecto, esta activación del receptor de factor de crecimiento incrementada puede estar asociada con o ser causada por un incremento patológico en la actividad de una proteína G y/o un receptor acoplado a proteína G. Se debe notar que los trastornos que están asociados con o están acompañados por una activación alterada, por ejemplo patológicamente incrementada del receptor de factor de crecimiento y los cuales pueden estar asociados con o ser causados por un incremento patológico en la actividad de una proteína G y/o un receptor acoplado a proteína G, se pueden

delimitar a partir de otros trastornos caracterizados por una actividad incrementada de la activación del receptor de factor de crecimiento ya que la transactivación del receptor de factor de crecimiento por medio de receptor acoplado a proteína G tiene lugar.

2. Métodos de diagnóstico

Las moléculas de unión a antígenos HB-EGF como las descritas en la presente se pueden usar en un método para detectar células cancerosas en una muestra de prueba que incluye poner en contacto la muestra de prueba con la molécula de unión a antígeno y detectar si el anticuerpo se une a una célula que exprese protHB-EGF o moléculas HB-EGF en la muestra. El grado al cual ocurre la unión puede evaluarse mediante el uso de una muestra de control. Las muestras de prueba y control pueden, por ejemplo, ser muestras de sangre, suero, ascites, efusión pleural, fluido cerebroespinal, tejido, células, orina, linfa, saliva, leche u otras muestras. Esta muestra de control puede ser una muestra no cancerosa de fluido o tejido o tipo de célula. En algunas modalidades, la muestra de control es una muestra no cancerosa obtenida del mismo sujeto que la muestra de prueba. "Sujeto" o "paciente" se refiere a un mamífero, de preferencia un humano, que requiere de tratamiento de o la detección de una afección, trastorno o enfermedad.

La unión del anticuerpo a componentes de la muestra

de prueba puede detectarse al detectar una molécula reportera, agente de formación de imagen o marcador que se una o pueda ser unido selectivamente a una proteína de unión a antígeno como la descrita en la presente. Estas proteínas de unión a antígeno HB-EGF pueden tener una o más moléculas reporteras, etiquetas o agentes de formación de imágenes. Una molécula reportera se divide como cualquier porción que puede ser detectada usando un ensayo. Ejemplos no limitativos de moléculas reporteras que han sido conjugadas a anticuerpos incluyen enzimas, radiomarcadores, haptenos, marcadores fluorescentes, moléculas fosforescentes, moléculas quimioluminiscentes, cromóforos, moléculas luminiscentes, moléculas de fotoafinidad, partículas coloreadas o ligandos, tales como biotina. La molécula reportera puede proporcionar una señal detectable. Por ejemplo, la señal detectable puede ser un cambio de color o señal enzimática fluorescente, fosforescente, quimioluminiscente, electroquimioluminiscente, electroquímico. Anticuerpos anti-HB-EGF provistos en la presente pueden usarse como anticuerpos de captura para la detección a base de ELISA del análisis de factor de crecimiento o inmunohistoqùímico de muestras de tejido como se muestra en las figuras 39A a 39B.

En algunas modalidades, la molécula reportera se une covalentemente a una proteína de unión a antígeno como la descrita en la presente. En otras modalidades, la molécula

reportera puede unirse selectivamente a la proteína de unión a antígeno HB-EGF como la descrita en la presente. Esta unión selectiva de una molécula reportera a la proteína de unión a antígeno descrita se puede lograr mediante un anticuerpo secundario con el marcador unido covalentemente al mismo, en donde el anticuerpo secundario se una selectivamente a una proteína de unión a antígeno HB-EGF como la descrita en la presente.

3. Métodos de tratamiento: formulaciones farmacéuticas, rutas de administración

El tratamiento de, o tratar el cáncer, intenta incluir el alivio o la reducción de al menos un síntoma asociado típicamente con la enfermedad. El tratamiento también incluye el alivio o reducción de más de uno de los síntomas asociados. El tratamiento puede curar el cáncer, por ejemplo, puede eliminar sustancialmente las células cancerosas y/o detener el crecimiento del tumor canceroso. Como alternativa, el tratamiento puede hacer más lenta la progresión del cáncer.

La actividad anticáncer se puede evaluar contra variedades de cáncer o células cancerosas usando métodos disponibles para alguien de capacidad en la técnica. La actividad anticáncer, por ejemplo, se puede determinar al identificar la LD_{100} o ED_{50} de una preparación de las proteínas de unión a antígeno descritas en la presente que evite el

crecimiento de un cáncer. En una modalidad, la actividad anticáncer es la cantidad de anticuerpo que mata 50% o 100% de las células cancerosas cuando se mide usando métodos de respuesta a dosis estándares.

Las proteínas de unión a antígeno HB-EGF como las descritas en la presente se pueden administrar solas, o en combinación con anticuerpos, fármacos quimioterapéuticos o terapia de radiación. Las composiciones farmacéuticas de acuerdo con la invención se pueden administrar como monoterapia o en combinación con otra composición farmacéutica, que comprende de preferencia otro agente antineoplásico, en particular cisplatino o avastina. Por ejemplo, las proteínas de unión a antígeno HB-EGF descritas pueden ser co-administradas con anticuerpos anti-tumor (por ejemplo, anticuerpos anti-tumor quiméricos, humanizados o humanos), con anticuerpos que se unan específicamente VEGF para inhibir más la angiogénesis tumoral, o con anticuerpos que se unan específicamente a una tirosina cinasa receptora tales como HER2, HER4 o EGFR y por lo tanto inhiban más la proliferación de células tumorales. En las figuras 38A-38C, el efecto sinérgico de un anticuerpo anti-EGFR y anticuerpos anti-HB-EGF puede mostrarse para ambos anticuerpos anti-HB-EGF probados. Además, las proteínas de unión a antígeno HB-EGF descritas en la presente pueden ser co-administradas con otros agentes antitumorales. Ejemplos específicos de agentes

antitumorales que pueden co-administrarse con los anticuerpos proporcionados en la presente incluyen, por ejemplo, gefitinib, lapatinib, sunitinib, permetrexed, bevacisumab, cetuximab, imatinib, trastuzumab, alemtuzumab, rituximab, erlotinib, bortezomib y similares. Cualquier otro agente anticáncer o fármaco que pueda inhibir el cáncer o proliferación de células tumorales se puede usar también en las composiciones descritas y reclamadas aquí. Por ejemplo, las composiciones reclamadas pueden incluir agentes quimioterapéuticos tales como capecitabina, daunorrubicina, daunomicina, dactinomicina, doxorrubicina, epirrubicina, idarrubicina, esorrubicina, bleomicina, mafosfamida, ifosfamida, arabinósido de citosina, bis-cloroetilnitrosurea, busulfano, mitomicina C, actinomicina D, mitramicina, prednisona, hidroxiprogesterona, testosterona, tamoxifen, dacarbacina, procarbacina, hexametilmetlamina, pentametilmelamina, mitoxantrona, amsacrina, clorambucilo, metilciclohexilnitrosurea, mostazas nitrogenadas, melfalan, ciclofosfamida, 6-mercaptopurina, 6-tiocuanina, citarabina, (CA), 5-azacitidina, hidroxiurea, desoxicoformicina, 4-hidroxiperoxiciclofosforamida, 5-fluorouracilo (5-FU), 5-fluorodesoxiuridina (5-FUdR), metotrexato (MTX), colchicina, taxol, vincristina, vinblastina, etopósido, trimetrexato, tenipósido, cisplatino, avastina y dietilestilbestrol (DES). Véase, generalmente, The Merck Manual of Diagnosis and

Therapy, 15ª edición. 1987, pág. 1206-1228, Berkow *et al.*, eds., Rahway, N.J. Cuando se usa las proteínas de unión a antígeno HB-EGF descritas, estos agentes quimioterapéuticos pueden usarse individualmente (por ejemplo, 5-FU y un anticuerpo), secuencialmente (por ejemplo, 5-FU y un anticuerpo durante un periodo de tiempo seguido por MTX y un anticuerpo), o en combinación con uno o más de otros agentes quimioterapéuticos de este tipo (por ejemplo, 5-FU, MTX y un anticuerpo, o 5-FU, radioterapia y un anticuerpo).

También se proporciona un método para evaluar una dosis terapéuticamente efectiva para tratar un cáncer con un anticuerpo que tenga una secuencia de aminoácidos descrita en la presente, que incluye determinar la LD_{100} o ED_{50} de la preparación de proteína de unión a antígeno HB-EGF *in vivo* o *in vitro*. Este método permite el cálculo de la cantidad aproximada de proteína de unión a antígeno necesaria por volumen para inhibir el crecimiento de células cancerosas o metástasis en aproximadamente 10% a 100%, o alrededor de 20% a 100%, o aproximadamente 25% a 100%, o alrededor de 30% a 100%, o aproximadamente 40% a 100%, o alrededor de 50% a 100%. En algunas modalidades, menos de 100% de inhibición de crecimiento de cáncer o metástasis es observado. Por ejemplo, el crecimiento de células cancerosas y/o metástasis es inhibido en alrededor de 90%, 80%, 70%, 60% o 50%. La inhibición porcentual puede determinarse, por ejemplo,

mediante la administración de preparación de proteínas de unión a antígeno a ratones SCID o nu/nu disponibles en la técnica e donde las células tumorales hayan sido introducidas y/o mediante métodos estándares usando células cancerosas cultivadas (véase figura 38B). se describen varios métodos en los ejemplos.

Se incluyen también formulaciones farmacéuticas estériles de las proteínas de unión a antígeno HB-EGF como las descritas en la presente que son útiles para tratamientos para enfermedades incluyendo, por ejemplo, cáncer y/o angiogénesis aberrante. Estas formulaciones inhibirán la unión de HB-EGF a su receptor, por ejemplo, EGFR o a HER4, de esta manera tratando en forma efectiva afecciones patológicas en las que, por ejemplo, el HB-EGF en suero, celular o tejido sea elevado anormalmente o en donde sus receptores, por ejemplo, EGFR o HER4, sean anormalmente activos. Como se ilustran en la presente, las proteínas de unión a antígeno HB-EGF poseen afinidad adecuada para neutralizar potentemente HB-EGF y para modular los eventos de señalización asociados con los receptores de HB-EGF.

Las proteínas de unión a antígeno HB-EGF como las descritas en la presente son de preferencia proteínas de unión a antígeno humanizadas. La administración de estas proteínas de unión a antígeno humanizados reduce la probabilidad de un efecto secundario negativo. Además, esas

proteínas de unión a antígeno son estables *in vivo*, por ejemplo, toda vez que son reconocidas como productos humanos normales, minimizando de esta manera el riesgo de respuestas del sistema inmunitario. Más aún, estas proteínas de unión a antígeno no son propensas a destrucción proteolítica, mejorando sus vidas medias circulantes. Por consiguiente, las preparaciones de HB-EGF como las descritas en la presente tienen una excelente vida media *in vivo* por lo que su administración a humanos es comparativamente infrecuente. Esta duración prolongada de acción puede permitir programas de dosificación menos frecuentes y más convenientes mediante rutas parenterales alternas tales como inyección subcutánea o intramuscular.

Las formulaciones estériles pueden crearse, por ejemplo, mediante filtración a través de membranas de filtración estériles, antes de o después de la liofilización y reconstitución del anticuerpo. Las proteínas de unión a antígeno como las descritas en la presente se almacenan normalmente en forma liofilizada o en solución. Las composiciones de anticuerpos terapéuticos generalmente se ponen en un recipiente que tiene un puerto de acceso estéril, por ejemplo, una bolsa para solución intravenosa o vial que tenga un adaptador que permita el retiro de la formulación, tal como un tapón que pueda ser perforado por una aguja de inyección hipodérmica.

La ruta de administración de las proteínas de unión a antígeno HB-EGF es de acuerdo con métodos conocidos, por ejemplo, inyección o infusión por rutas intravenosa, subcutánea, intradérmica, intraperitoneal, intracerebral, intramuscular, intraocular, intraarterial, intratecal, intravesical, intracavernosa, inhalación, intralesional o por medio de sistemas de liberación prolongada como se indica abajo. En algunas modalidades las proteínas de unión a antígeno descritas en la presente se administran continuamente mediante infusión o inyección de bolo.

Las proteínas de unión a antígeno HB-EGF, como las descritas en la presente, se pueden preparar en una mezcla con un vehículo farmacéuticamente aceptable. Esta composición terapéutica puede ser administrada intravenosamente o a través de la nariz o el pulmón, de preferencia como un aerosol líquido o en polvo (liofilizado). La composición también se puede administrar parenteralmente o subcutáneamente según se desee. Cuando se administra sistémicamente, la composición terapéutica debe ser estéril, libre de pirógenos y en una solución parenteralmente aceptable con consideración de lo cual son los valores de pH fisiológicamente aceptables, isotonicidad y estabilidad. Estas condiciones se conocen por aquellos expertos en la técnica. Brevemente, las formulaciones de dosis de los compuestos descritos en la presente se preparan para

almacenamiento o administración al mostrar el compuesto que tenga el grado de pureza deseado con portadores, excipientes o estabilizadores fisiológicamente aceptables. Estos materiales no son tóxicos para los receptores a las dosis y concentraciones empleadas, e incluyen reguladores de pH tales como HCl TRIS, fosfato, citrato, acetato y otras sales de ácidos orgánicos; antioxidantes tales como ácido ascórbico; péptidos de bajo peso molecular (menos de aproximadamente 10 residuos) tales como poliarginina, proteínas, tales como albúmina de suero, gelatina o inmunoglobulinas; polímeros hidrófilos tales como polivinilpirrolidinona; aminoácidos tales como glicina, ácido glutámico, ácido aspártico o arginina; monosacáridos, disacáridos y otros carbohidratos incluyendo celulosa o sus derivados, glucosa, manosa o dextrinas; agentes quelantes tales como EDTA; alcoholes de azúcar tales como manitol o sorbitol; contraiones tales como agentes tensioactivos de sodio y/o no iónicos tales como TWEEN, PLURONICOS o polietilenglicol.

Composiciones estériles para inyección pueden formularse de acuerdo con práctica farmacéutica convencional como la descrita en *Remington: The Science and Practice of Pharmacy* (20ª edición, Lippincott Williams & Wilkens Publishers (2003)). Por ejemplo, la disolución o suspensión del compuesto activo en un vehículo tal como agua o aceite vegetal que ocurre naturalmente tal como aceite de ajonjolí,

cacahuate o semilla de algodón o un vehículo graso sintético tal como oleato de etilo o similar puede ser deseada. Reguladores de pH, conservadores, antioxidantes y similares pueden ser incorporados de acuerdo con la práctica farmacéutica aceptada.

Ejemplos adecuados de preparaciones de liberación prolongada incluyen matrices semipermeables de polímeros hidrófobos sólidos que contienen el polipéptido, matrices que están en forma de artículos configurados, películas o microcápsulas. Ejemplos de matrices de liberación prolongada incluyen poliésteres, hidrogeles (por ejemplo, metacrilato de poly(2-hidroxietilo) como se describe por Langer *et al.*, 1981, *J. Biomed Mater. Res.* 15:167-277 y Langer, 1982, *Chem. Tech.* 12:98-105, o poly(vinilalcohol)), polilacturos (patente de E.U.A. No. 3,773,919, EP 58,481), copolímeros de ácido L-glutámico y etil-L-glutamato gama (Sidman *et al.*, 1983, *Biopolymers* 22:547-556), acetato de etilenvinilo no degradable (Langer *et al.*, citado arriba), copolímeros de ácido glicólico y ácido láctico degradables tales como el LUPRON Depot™ (microesferas inyectables compuestas de copolímero de ácido láctico-ácido glicólico y acetato de leuprolida), y ácido poly-D-(-)-3-hidroxibutírico (EP 133,988).

Aunque polímeros tales como acetato de etilenvinilo y ácido láctico-ácido glicólico hacen posible la liberación

de moléculas durante más de 100 días, ciertos hidrogeles liberan proteínas durante periodos de tiempo más cortos. Cuando las proteínas encapsuladas permanecen en el cuerpo durante un largo tiempo, pueden desnaturalizarse o agregarse como resultado de su exposición a humedad a 37°C, dando por resultado una pérdida de actividad biológica y posibles cambios en inmunogenicidad. Se pueden contemplar estrategias racionales para la estabilización de proteínas dependiendo del mecanismo implicado. Por ejemplo, si el mecanismo de agregación se descubre que es la formación de enlaces S-S intermoleculares a través de intercambio de disulfuro, la estabilización puede lograrse al modificar residuos de sulfhidrilo, liofilización a partir de soluciones ácidas, control del contenido de humedad, uso de aditivos adecuados y desarrollo de composiciones de matriz polimérica específicas.

Las composiciones de liberación prolongada incluyen también preparaciones de cristales de las proteínas de unión a antígeno suspendidas en formulaciones adecuadas capaces de mantener cristales en suspensión. Estas preparaciones cuando son inyectadas subcutáneamente o intraperitonealmente pueden producir un efecto de liberación prolongado. Otras composiciones incluyen también anticuerpos atrapados liposómicamente. Liposomas que contienen estos anticuerpos se preparan mediante métodos conocidos *per se*: patente de E.U.A. No. DE 3,218,121; Epstein *et al.*, 1985, *proc. Natl.*

Acad. Sci. E.U.A. 82:3688-3692; Hwang *et al.*, 1980, *Proc. Natl. Acad. Sci. E.U.A.* 77:4030-4034; EP 52,322; EP 36,676; EP 88,046; EP 143,949; 142,641; solicitud de patente japonesa 83-118008; patentes de E.U.A. Nos. 4,485,045 y 4,544,545; y EP 102,324.

La dosis de la formulación de proteínas de unión a antígeno para un paciente dado se determinará por el médico que atienda tomando en consideración varios factores que se sepan modifiquen la acción de fármacos incluyendo severidad y tipo de enfermedad, peso corporal, sexo, dieta, hora y ruta de administración, otros medicamentos y otros factores clínicos relevantes. Las dosis terapéuticamente efectivas pueden determinarse mediante métodos ya sea *in vitro* o *in vivo*.

Una cantidad efectiva de las proteínas de unión a antígeno, descrita en la presente, que se empleará terapéuticamente dependerá, por ejemplo, de los objetivos terapéuticos, la ruta de administración y la afección del paciente. En consecuencia, se prefiere que el médico titule la dosis y modifique la ruta de administración según se requiera para obtener el efecto terapéutico óptimo. Una dosis diaria típica puede variar de alrededor de 0.001 mg/kg hasta 100 mg/kg o más, dependiendo de los factores mencionados arriba. Típicamente, el médico administrará la proteína de unión a antígeno terapéutica hasta que se alcance

una dosis que logre el efecto deseado. El progreso de esta terapia se monitoreó fácilmente mediante ensayos convencionales o como se describe en la presente.

Se apreciará que la administración de entidades terapéuticas de acuerdo con las composiciones y métodos de la presente se administrarán con portadores, excipientes y otros agentes adecuados que sean incorporados en formulaciones para proporcionar transferencia, suministro, tolerancia mejorados y similares. Estas formulaciones incluyen, por ejemplo, polvos, pastas, ungüentos, jaleas, ceras, aceites, lípidos, vesículas que contienen lípidos (catiónicas o aniónicas) (tales como Lipofectin™), conjugados de ADN, pastas de absorción anhidras, emulsiones de aceite en agua y agua en aceite, emulsiones carbowax (polietilenglicoles de varios pesos moleculares), geles semisólidos y mezclas semisólidas que contienen carbowax. Cualquiera de las mezclas anteriores puede ser adecuada en tratamientos y terapias que incluyan la proteína de unión a antígeno HB-EGF como la descrita en la presente, siempre y cuando el ingrediente activo en la formulación no sea inactivado por la formulación y la formulación sea fisiológicamente compatible y tolerable con la ruta de administración. Véase, también, Baldrick P. "Pharmaceutical excipient development: the need for preclinical guidance", 2000, *Regul. Toxicol. Pharmacol.* 32:210-2128; Wang, "Lyophilization and development of solid

protein pharmaceuticals", 2000, *Int. J. Pharm.* 203: 1-60; Charman WN "Lipids, lipophilic drugs, and oral drug delivery-some emerging concepts", *J. Pharm. Sci.* 89:967-978; Powell *et al.*, 1998, "Compendium of excipients for parenteral formulations", *PDA J. Pharm. Sci. Technol.* 52:238-311 y las citaciones ahí para información adicional relacionada con formulaciones, excipientes y portadores bien conocidos por los químicos farmacéuticos.

Los siguientes ejemplos, incluyendo los experimentos llevados a cabo y resultados logrados se proporcionan por motivos ilustrativos únicamente y no deben considerarse como limitativos de las enseñanzas de la presente.

Ejemplos

A. Ejemplo 1

Generación de inmunógenos

El dominio tipo EGF que incluye HB-EGF (aminoácidos 1-149) se amplificó a partir de la construcción de expresión pcADN3-VSV-HB-EGF (PrenzeI *et al.*, 1999, citado arriba) y se clonó en un vector de expresión que proporciona un marcador 6His en cuadro en el término carboxilo (pcADN 3.1 myc-his, Invitrogen). Este inmunógeno de HB-EGF con marcador myc(HIS)6 C-terminal fue expresado en células HEK293 y purificado mediante una purificación de dos etapas en Ni-NTA sefarosa (Amersham Pharmacia) y heparina sefarosa (Sigma).

La porción HB-EGF del inmunógeno tuvo la siguiente secuencia (SEQ ID NO: 1077).

1 MKLLPSVVLK LFLAAVLSAL VTGESLERLR RGLAAGTSNP

41 DPPTVSTDQL LPLGGGRDRK VRDLQEADLD LLRVTLSSKP

81 QALATPNKEE HGKRKKKGKG LGKKRDPCLR KYKDFCIHGE

121 CKYVKELRAP SCICHPGYHG ERCHGLSLP

B. Ejemplo 2

Inmunización de ratones Xenomouse y títulos observados

Anticuerpos monoclonales contra HB-EGF fueron desarrollados al inmunizar secuencialmente ratones XenoMouse® (cepas XenoMouse: XMG2 (productoras de IgG2 humana) y XM3C-1 (productora de IgG4 humana), Abgenix, Inc. Fremont, CA).

1. Inmunización

Los animales XenoMouse fueron inmunizados por medio de la pata para todas las inyecciones. El volumen total de cada inyección fue 50 µl por ratón, 25 µl por pata.

Tanto para la cohorte 1 (10 XMG2 ratones) como para la cohorte 2 (10 XM3C-1), la inmunización inicial fue con 10 µg de proteína HB-EGF mezclada 1:1 (v/v) con TITERMAX GOLD® (Sigma, Oakville, ON) por ratón. Los cuatro refuerzos subsecuentes se hicieron con 10 µg de proteína HB-EGF mezclada 1:1 (v/v) con 100 µg de gel de alumbre (Sigma, Oakville, ON) en D-PBS libre de pirógenos. El quinto refuerzo consistió en 10 µg de proteína HB-EGF mezclada 1:1 (v/v) con TITERMAX GOLD®. La sexta y séptima inyecciones

consistieron en 10 µg de proteína HB-EGF mezclada 1:1 v/v con 100 µg de gel de alumbre. Un refuerzo final se hizo con 10 µg de proteína HB-EGF en DPBS libre de pirógenos, sin adyuvante. Los ratones XenoMouse fueron inmunizados los días 0, 4, 8, 14, 18, 21, 25 y 28 para este protocolo y las fusiones se llevaron a cabo el día 32. Los dos sangrados se hicieron a través del procedimiento de Sangrado Retro-Orbital el día 16 después del cuarto refuerzo, el día 23 después del sexto refuerzo.

2. Selección de animales para la cosecha por título

Los títulos de anticuerpos anti-HB-EGF en el suero de ratones XenoMouse inmunizados se determinaron mediante ELISA. Brevemente, la proteína HB-EGF (2 µg/ml) fue recubierta sobre placas de 96 pocillos de Poliestireno de Unión Universal Labcoat Costar (Corning, Acton, MA) durante la noche a 4°C en Regulador de pH de Recubrimiento de Antígenos (regulador de pH de carbonato 0.1 M, pH 9.6 de $NaHCO_3$ (MW 84) 8.4 g/L). Al día siguiente, las placas se lavaron una vez con regulador de pH de lavado (0.05% de Tween 20 en 1x de PBS) usando un lavador de placa Biotek. Las placas fueron después bloqueadas con 200 µl/pocillo de regulador de pH de bloqueo (0.5% de BSA, 0.1% de Tween 20, 0.01% de timerosal en 1x PBS) e incubadas a temperatura ambiente durante 1 hora. Después del bloqueo de 1 hora, las

placas se lavaron una vez con regulador de pH de lavado usando un lavador de placa Biotek. Sueros ya sea de los ratones XenoMouse inmunizados con proteína HB-EGF o animales XenoMouse naives fueron titulados en 0.5% de regulador de pH BSA/PBS a diluciones 1:3 por duplicado a partir de una dilución inicial 1:100. El último pocillo se dejó vacío. Estas placas se incubaron a temperatura ambiente durante 2 horas, y las placas se cosecharon después tres veces con regulador de pH de lavado usando un lavador de placa Biotek. Un anticuerpo conjugado a peroxidasa de rábano específica de Fc de IgG anti-humano de cabra (CALTAG, No. de catálogo H10507) se añadió a una concentración final de 1:2000 en regulador de pH de bloqueo y se incubó durante 1 hora a temperatura ambiente. Las placas se lavaron tres veces con regulador de pH de lavado usando un lavador de placa Biotek. Después del lavado, las placas fueron reveladas con la adición de substrato cromogénico TMB (BioFx BSTP-0100-01) durante 10-20 minutos o hasta que los pocillos de control negativos empezaran a mostrar color. Después se detuvo el ELISA mediante la adición de una solución de paro (650 nM de de reactivo Stop para TMB (BioFx BSTP-0100-01), reconstituido con 100 ml de H_2O por botella). El título específico de cada animal XenoMouse fue determinado a partir de la densidad óptica a 650 nm y se muestra en la tabla 1 abajo. El valor de titulación es el recíproco de la dilución más grande de

sueros con una lectura OD del doble de aquella del fondo. Por lo tanto, entre más alto el número, mayor fue la respuesta inmune humoral a HB-EGF.

Tabla 1

Grupo 1, fp, XMG2, 10 ratones,		
	Después de 4 iny.	Después de 6 iny.
ID de ratón	Reactividad a HB-EGF	
P4721	3,800	59,000
P4722	6,500	68,000
P4723	2,500	43,000
P4724	2,400	22,000
P4725	2,400	71,000
P4726	450	58,000
P4727	1,600	20,000
P4728	2,700	61,000
P4729	800	61,00
P47210	5,700	78,000
NC	<100	<100
PC	<100	<100

Grupo 1, fp, XMG2, 10 ratones,		
	Después de 4 iny.	Después de 6 iny.
ID de ratón	Reactividad a HB-EGF	
P2664	35	2,300
P2666	20	750
P2669	30	850
P26610	75	1,900
P2892	60	550
P2894	60	1,400
P2895	95	2,600
P2896	45	2,500
P3672	50	2,000
P3678	60	1,800
NC	<100	<100
PC	35	20

C. Ejemplo 3

Generación de hibridomas y tamiz primario para aglutinantes

Ratones inmunizados fueron sacrificados y los nódulos linfáticos se cosecharon y agruparon para cada cohorte. Las células linfoides fueron disociadas al moler en

DMEM para liberar las células de los tejidos, y las células fueron suspendidas en DMEM. Las células se contaron, y 0.9 ml de DMEM por 100 millones de linfocitos fueron añadidos al sedimento celular para resuspender las células suavemente pero completamente. Usando 100 µl de esferas magnéticas CD90+ por 100 millones de células, las células fueron marcadas al incubarlas con las esferas magnéticas a 4°C durante 15 minutos. La suspensión de células marcada magnéticamente que contenía hasta 10^8 células positivas (o hasta 2 x 10^9 células totales) se cargó sobre una columna LS+ y la columna se lavó con DMEM. El efluente total se recogió como la fracción negativa a CD90 (se esperaba que la mayoría de estas células fueran células B).

La fusión se llevó a cabo al mezclar células B enriquecidas lavadas de arriba y células P3X63Ag8.653 de mieloma no secretoras compradas de ATCC, # de catálogo CRL 1580 (Kearney *et al.*, 1979, *J. Immunol.* 123: 1548-1550) a una relación de 1:1. La mezcla de células se centrifugó suavemente a 800 g. Después de la remoción completa del sobrenadante, el sedimento celular se trató con 2-4 ml de solución de Pronasa (CalBiochem, # de catálogo 53702; 0.5 mg/ml en PBS) durante no más de 2 minutos. Después, 3-5 ml de FBS fueron añadidos para detener la actividad enzimática y la suspensión se ajustó a 49 ml de volumen total usando una solución de fusión celular electrónica, ECFS (Sucrosa 0.3 M,

Sigma, # de catálogo 57903, 0.1 mM de acetato de magnesio, Sigma, # de catálogo M2545, 0.1 mM de acetato de calcio, Sigma, # de catálogo C4705). El sobrenadante se removió después de centrifugación y las células se resuspendieron en 40 ml de ECFS. Esta etapa de lavado se repitió y las células de nuevo fueron resuspendidas en ECFS hasta una concentración de $2x10^6$ células/ml.

La fusión de electro-celdas se llevó a cabo usando un generador de fusión, modelo ECM2001, Genetronic, Inc., San Diego, CA. El tamaño de la cámara de fusión usado fue 2.0 ml, usando los siguientes ajustes de instrumento: condición de alineación: voltaje: 50 V, tiempo: 50 segundos; ruptura de membrana a: voltaje: 3000 V, tiempo: 30 µseg; tiempo de retención después de fusión: 3 segundos.

Después de la fusión a electro-celdas, las suspensiones de células fueron cuidadosamente retiradas de la cámara de fusión bajo condiciones estériles y transferidas a un tubo estéril que contenía el mismo volumen de Medio de Cultivo de Hibridoma (DMEM (JRH Biosciences), 15% de FBS (Hyclone), complementado con L-glutamina, pen/strep, OPI (oxaloacetato, piruvato, insulina bovina) (todos de Sigma) e IL-6 (Boehringer Mannheim)). Las células se incubaron durante 15-30 minutos a 37°C, y después se centrifugaron a 400 g durante cinco minutos. Las células se resuspendieron suavemente en un pequeño volumen de Medio de Selección de

Hibridomas (Medio de Cultivo de Hibridomas complementado con 0.5x HA (Sigma, # de catálogo A9666)), y el volumen se ajustó aproximadamente con más Medio de Selección de Hibridoma, con base en el plaqueo final de $5x10^6$ células B totales por placa de 96 pocillos y 200 µL por pocillo. Las células se mezclaron suavemente y se pipetearon en placas de 96 pocillos y se les dejó crecer. El día 7 ó 10, la mitad del medio fue removida, y las células se realimentaron con Medio de Selección de Hibridoma.

Después de 14 días de cultivo, sobrenadantes de hibridoma de la cohorte #1 y cohorte #2 fueron tamizados para anticuerpos monoclonales específicos de HB-EGF mediante ELISA. En el tamiz primario, las placas de ELISA (Fisher, No. de catálogo 12-565-136) se cortaron con 50 µL/pocillo de proteína HB-EGF (2 µg/ml) en regulador de pH de recubrimiento (regulador de pH de carbonato 0.1 M, pH 9.6, $NaHCO_3$, 8.4 g/L), luego se incubaron a 4°C durante la noche. Después de la incubación, las placas se lavaron con regulador de pH de lavado (0.05% de Tween 20 en PBS) una vez. Se añadieron 200 µL/pocillo de regulador de pH de bloqueo (0.5% de BSA, 0.1% de Tween 20, 0.01% de timerosal en 1x de PBS) y las placas se incubaron a temperatura ambiente durante 1 hora. Después de la incubación, las placas se lavaron con regulador de pH de lavado una vez. Alícuotas (50 µL/pocillo) de sobrenadantes de hibridoma y controles positivos y negativos fueron

añadidos, y las placas se incubaron a temperatura ambiente durante 2 horas. El control positivo usado a lo largo fue suero de ratones XenoMouse inmunizados con proteína HB-EGF relevantes y el control negativo fue suero de una cepa relevante inmunizada con KLH de ratón XenoMouse. Después de la incubación, las placas se lavaron tres veces con regulador de pH de lavado. Se añadieron 100 µL/pocillo de anticuerpo de detección anti-hulgGFc-HRP de cabra (Caltag Inc., No. de catálogo H10507, la concentración de uso fue una dilución 1:2000) y las placas se incubaron a temperatura ambiente durante 1 hora. Después de la incubación, incubación, las placas se lavaron tres veces con regulador de pH de lavado y 100 µl/pocillo de TMB (BioFX Lab. No. de catálogo TMSK-0100-01) fueron añadidos. Las placas se dejaron después revelar durante aproximadamente 10 minutos (hasta que los pocillos de control negativos deficientemente empezaran a mostrar color). 50 µl/pocillo de solución de paro (TMB Stop Solution (BioFX Lab. No. de catálogo STPR-0100-01) se añadieron después y las placas fueron leídas en un lector de placa ELISA a una longitud de onda de 450 nm.

Los sobrenadantes del cultivo anteriores de los pocillos de crecimiento de células de hibridoma positivas con base en el tamiz primario fueron removidos y las células de hibridoma positivas a HB-EGF fueron suspendidas con medio de cultivo de hibridoma fresco y fueron transferidas a placas de

24 pocillos. Después de 2 días en cultivo, estos sobrenadantes estuvieron listos para un tamiz de confirmación secundario. En el tamiz de confirmación secundario, los positivos en el primer tamiz fueron tamizados mediante ELISA (como el descrito arriba) con dos conjuntos de anticuerpos de detección: anti-hulgGFc-HRP de cabra (Caltag Inc., No. de catálogo H10507, la concentración de uso fue 1:2000 de dilución) para la detección de la cadena gama humana y anti-hlg kappa-HRP de cabra (Southern Biotechnology, No. de catálogo 2060-05) para la detección de la cadena ligera kappa para de esta manera demostrar que la preparación de anticuerpos era específica de HB-EGF y completamente humana en su composición. Los dos conjuntos de procedimientos de ELISA fueron idénticos a las descripciones anteriores excepto que los dos anticuerpos de detección diferentes fueron usados por separado.

En paralelo con el tamiz de confirmación secundario, el tamiz de ELISA contrario se llevó a cabo para excluir los anticuerpos que respondieran al marcador myc(his)6. Los procedimientos de ELISA fueron idénticos a las descripciones anteriores excepto que se recubrió con proteína marcadora myc(his)6 irrelevante (proteína ML-myc(his)6) en lugar de recubrir con proteína HB-EGF myc(his)6.

Después de la confirmación secundaria y del tamiz contra ELISA, 49 anticuerpos monoclonales específicos de HB-EGF IgG/kappa completamente humanos fueron identificados de las cohortes 1 y 2.

D. Ejemplo 4

Escalada ascendente y prueba de anticuerpos en ensayos funcionales

Este ejemplo describe la identificación de líneas de células de hibridoma que producen anticuerpos anti-HB-EGF con afinidad para HB-EGF.

1. Detección FACS de anticuerpos anti-HB-EGF producidos por hibridoma unidos a líneas de células que expresaban HB-EGF

La expresión de HB-EGF en líneas de células se determinó mediante análisis FACS. Para llevar a cabo este análisis, $2x10^5$ células de expresión de HB-EGF seleccionadas se cosecharon con 10 mM de EDTA en PBS, se resuspendieron en regulador de pH FACS (PBS, 3% de FCS, 0.4% de azidas) y se sembraron en una placa de fondo redondo de 96 pocillos. Después de la centrifugación durante 3 minutos a 1000 rpm para remover sobrenadante, las células se resuspendieron en dilución de anticuerpo anti-HB-EGF derivado de hibridoma (100 µl/pocillo) y se incubaron a 4°C durante 45 minutos. Las células fueron lavadas dos veces con regulador de pH FACS y resuspendidas con anticuerpo secundario (100

µl/pocillo) anti-humano-PE de burro (Jackson) diluido 1:100 en regulador de pH FACS. Las suspensiones de células se incubaron a 4°C en la oscuridad durante 30 minutos, se lavaron dos veces con regulador de pH FACS y se analizaron (FACS Beckman Coulter).

Los resultados de estos ensayos se proporcionan en las tablas 2 y 3 abajo, las cuales proporcionan los valores medios de fluorescencia para cada ensayo FACS. Como se ilustra en las tablas 3 y 4, sustancialmente ninguna expresión de HB-EGF se detectó en células de control CHO que no expresan HB-EGF. Sin embargo, cuando HB-EGF es sobre-expresado recombinantemente en células CHO, varias preparaciones de anticuerpos monoclonales que exhiben unión significativa a aquellas células que expresan HB-EGF. La unión a células MDA-MB231, SCC-9 y COS-7 fue un poco variable pero una preparación de anticuerpos que se unió a un tipo de célula que expresaba HB-EGF se unió típicamente al otro. Como se muestra en la tabla 2, varias preparaciones de anticuerpos, incluyendo, por ejemplo, las preparaciones de anticuerpos U2-24, U2-5, U2-19, U2-21, U2-15 y U2-42 exhibieron fuerte unión a células CHO que expresaban HB-EGF. De manera similar, las preparaciones de anticuerpo U2-39, U2-26, U2-44, U2-45 y U2-48 también exhibieron unión adecuada a células CHO que expresaban HB-EGF.

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Tabla 2

Análisis FACS de sobrenadantes de anticuerpos anti-HB-EGF

(cohorte 1)

	Células de control CHO contra células CHO que expresaban HB-EGF		Líneas de células que expresaban HB-EGF endógenamente		
Anticuerpo	CHO-K1	CHO-HB-EGF	MDA-MB231	SCC-9	COS-7
KLH	0.2	0.3	0.4	0.2	0.4
U2-18	0.3	154	3.1	1.2	1.6
U2-68	0.2	238	1.7	0.6	1.1
U2-24	0.2	360	2	0.6	6.7
U2-14	0.3	132	2.8	0.8	1.1
U2-1	0.2	64	1.8	0.7	3.1
U2-32	0.2	76	1.7	1.2	1.8
U2-40	0.2	137	2.1	1.3	1.1
U2-5	0.3	371	6.9	1.7	2.2
U2-8	0.3	148	3.7	1.4	1.4
U2-13	0.2	136	0.4(2.6)	0.5	0.8
U2-17	0.2	170	1.6	0.6	1.4
U2-19	0.4	347	5.5	1.8	6.1
U2-38	0.3	30	3.9	0.9	1.4
U2-21	0.2	344	3.9	3.4	2.1
U2-15	0.2	370	3	0.6	0.9
U2-16	0.2	197	1.5	0.4	0.9
U2-30	0.3	273	3.5	1	3.4
U2-44	0.3	5.6	0.8	0.2	5.2
U2-42	1.2	277	3.3	0.5	6.7
U2-36	0.9	112	1.6	0.3	4.9
U2-22	0.3	221	1.1	0.2	4.9
U2-56	0.2	38	0.5	0.2	1.8
Neg	0.2	0.2	0.3		
Pos (aHB de cabra)	0.2	80	3		

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Tabla 3

Análisis FACS de sobrenadantes de anticuerpos anti-HB-EGF

(cohorte 2)

	Células de control CHO contra células CHO que expresaban HB-EGF		Líneas de células que expresaban HB-EGF endógenamente		
Anticuerpo	CHO-K1	CHO-HB-EGF	MDA-MB231	SCC-9	COS-7
U2-63	0.2	36(0.4)	0.5	0.2	0.6
U2-54	0.3	49	0.6	0.2	2.4
U2-65	0.2	1.9	0.4	0.2	0.3
U2-10	0.2	2.3	0.5	0.2	1.2
U2-53	0.2	144	0.5	0.2	0.6
U2-66	0.2	149	0.5	0.2	0.5
U2-61	0.4	28	0.4	0.2	1.4
U2-67	0.2	82	0.5	0.2	0.6
U2-28	0.3	198	1	0.2	3.2
U2-2	0.2	127	0.5	0.2	0.5
U2-62	0.2	47	0.5	0.2	0.6
U2-39	0.2	205	2.6	0.6	8.3
U2-3	0.2	168	0.9	0.2	2.5
U2-43	0.4	185	0.8	0.2	1.7
U2-34	0.7	125	1.2	0.3	6.4
U2-26	0.2	242	1.5	0.3	4.7
U2-41	0.3	186	1.2	0.2	3.3
U2-44	0.4	248	1.2	0.2	2.2
U2-45	0.6	248	1.4	0.2	6.4
U2-57	0.2	201	0.7	0.2	0.5
U2-12	0.6	1.2	1.2	0.5	1.6
U2-46	0.4	129	1	0.2	2.5
U2-48	0.4	273	1.3	0.3	2.1
U2-6	0.5	108	3.9	1.5	5.9
U2-58	0.2	277	0.9	0.2	0.4
U2-51	0.5	176	1.1	0.2	3.6
U2-60	0.2	3.6	0.4	0.2	0.3
Neg	0.2	0.2	0.3		
Pos (aHB de cabra)	0.2	80	3		

2. Inhibición de la fosforilación de tirosina EGFR inducida por HB-EGF

El siguiente protocolo se usó para identificar qué preparaciones de anticuerpos anti-HB-EGF inhibían la fosforilación de tirosinas del receptor de factor de crecimiento epidérmico inducido por HB-EGF. Estos experimentos caracterizan más los anticuerpos y ayudan a identificar qué líneas de células de hibridoma producen anticuerpos que inhiben la actividad de HB-EGF y entonces deben clonarse y expandirse.

Cuarenta mil células de cáncer escamoso humano SCC9 fueron sembradas en una placa de 96 pocillos en 100 µl de medio. Las células fueron privadas de alimento en 60 µl de medio libre de suero durante 24 horas. Una placa de 96 pocillos Maxisorp negra se recubrió con 100 µl de anticuerpo anti-EGFR (2 µg/ml) durante la noche a 4°C. La solución de recubrimiento se reemplazó por 300 µl de solución de bloqueo (PBS + 0.5% de BSA) sin lavado y se dejó incubar durante 2 horas a temperatura ambiente. Se añadieron 10 µg/ml de IgG2-control (Sigma) o anticuerpos derivados de hibridoma anti-HB-EGF a 20 ng/ml de HB-EGF (R&D Systems) y se pre-incubaron durante 30 minutos a 37°C (volumen: 40 µl). Las células fueron tratadas con medio solo o con la solución de anticuerpo/ligando durante 3 minutos a 37°C. El medio se removió y las células fueron

lisadas en hielo con 100 µl de regulador de pH de lisis a base de Triton-X-100 que contenía 1 mM de PMSF, 10 µg/ml de aprotinina, 10 mM de NaF y 2 mM de Na-ortovanadato. La placa Maxisorp bloqueada fue lavada 6 veces con PBS + 0.05% de Tween 20. 80 µl de lisado de células se transfirieron directamente a la placa Maxisorp lavada y se incubaron durante la noche a 4°C con agitación suave. La placa se lavó 6 veces con PBS + 0.05% de Tween 20, después 100 µl de 4G10-biotina (UBI) diluida 1:4000 en regulador de pH de dilución (PBS+0.5% de BSA+0.05% de Tween-20+5 mM de EDTA) se añadieron a cada pocillo y se incubaron durante 2 horas a temperatura ambiente. La placa se lavó 6 veces con PBS+0.05% de Tween 20 y 100 µl de estreptavidina conjugada a AP (UBI) diluida 1:20000 en regulador de pH de dilución (PBS+0.5% de BSA+0.05% de Tween20+5 mM de EDTA) se añadieron a cada pocillo durante 30 minutos a temperatura ambiente. La placa se lavó 6 veces con PBS+0.05% de Tween 0 y 100 µl de substrato AttoPhos se añadieron a cada pocillo. La placa se incubó durante hasta 3 horas a temperatura ambiente en la oscuridad y la fluorescencia revelada se monitoreó a 30, 90 y 180 minutos (excitación: 430 nm, emisión: 580 nm).

La inhibición porcentual de la fosforilación de tirosina EGFR inducida por HB-EGF se calculó mediante la reducción en la cantidad de fosforilación observada con IgG2-

control (Sigma) por cada preparación de anticuerpo anti-HB-EGF derivado de hibridoma.

Los resultados para las diferentes preparaciones de anticuerpo anti-HB-EGF se proporcionan en las figuras 23A y 23B. Como se ilustra, las preparaciones de anticuerpo monoclonal U2-18, U2-24, U2-19, U2-42, U2-39, U2-34, U2-45 Y U2-6 inhiben fuertemente la fosforilación de tirosina EGFR.

3. Las preparaciones de anticuerpo anti-HB-EGF inhiben la fosforilación de EGFR inducida por LPA

Las vías de señalización dependientes de EGFR pueden ser activadas después de la estimulación de receptores acoplados a proteína G (GPCR). La activación por ligandos de proteínas G heterodiméricas mediante interacción con una GPCR da como resultado una señal intracelular que induce la actividad extracelular de una metaloproteinasa de transmembrana. Los ligandos que pueden activar la vía GPCR incluyen LPA (ácido lifofosfatídico), trombina, carbacol, bombesina y endotelina. Esta activación lleva a procesamiento extracelular de un precursor de factor de crecimiento de transmembrana y a la liberación del factor maduro el cual, directamente o a través de la matriz de proteoglucano, interactúa con el ectodominio de EGFR y lo activa a través de fosforilación. Véase Prenzel *et al.*, 1999, *Nature* 402:884-888.

Las preparaciones de anticuerpo anti-HB-EGF

proporcionadas en la presente se probaron para determinar si podían inhibir la fosforilación de tirosina EGFR inducida por el ligando GPCR LPA en células COS-7, usando el siguiente procedimiento.

250,000 Células COS-7 fueron sembradas en una placa de 6 pocillos en medio 2 ml y se cultivaron durante la noche. Las células fueron ayudadas en 1 ml de medio libre de suero durante 24 horas. Después de la preincubación con anticuerpos (37°C, 1 h), las células fueron estimuladas con 10 µM de LPA (37°C, 3 min) y y lisadas sobre hielo con 400 µl de regulador de pH de lisis a base de Triton-X-100 que contenía 1 mM PMSF, 10 µg/ml de aprotinina, 10 mM de NaF y 2 mM de ortovanadato de sodio. Después de la inmunoprecipitación del EGFR (340 µl de lisado, 340 µl de HNTG, 30 µl de proteína A sefarosa, 1.5 µl de αEGFR (108.1, Prenzel et al., 1999, citado arriba)) durante 4 horas en los precipitados de la habitación fría, se lavaron 3 veces con 500 µl de regulador de pH HNTG y se corrieron en un SDS-PAGE a 7.5%. Luego de la transferencia en una membrana de nitrocelulosa (Schleicher & Schuell) el blot fue sondeado con un anticuerpo que reconocía residuos de fosfotirosina (ab primario 4G10 (1:2000, Upstate Biotechnology); anti-ratón anticuerpo secundario 1:10000, Jackson laboratorios). El reblot con anti-EGFR de borrego (Upstate technology) después de la evaporación mostró que cantidades iguales del receptor

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se precipitaron en cada carril.

La figura 24 proporciona un western blot que ilustra qué preparaciones de anticuerpos anti-HB-EGF inhiben la fosforilación de tirosina EGFR inducida por LPA. Como se muestra en la figura 24, las preparaciones de anticuerpo anti-HB-EGF U2-19 y U2-42 inhibieron fuertemente la fosforilación de EGFR inducida por LPA. La preparación de anticuerpo anti-HB-EGF U2-24 inhibió fosforilación de EGFR inducida por LPA en un grado un poco menor.

E. Ejemplo 5

Clonación de hibridomas para generar anticuerpos monoclonales

Con base en los resultados de prueba observados a partir de experimentos descritos en los ejemplos anteriores, de los 49 aislados originales, 43 líneas de células de hibridoma se seleccionaron para clonación por dilución limitativa y caracterización adicional de su anticuerpo monoclonal. Las líneas seleccionadas para clonación se unieron a líneas de células que expresaban HB-EGF como se exhibió por el análisis FACS e inhibieron la estimulación de HB-EGF de la fosforilación de tirosina del receptor EGF. Para algunos hibridomas, anticuerpo insuficiente se generó para ejecutar todos los ensayos de tamizado primarios. Este subconjunto de hibridomas se pasó a la clonación de hibridomas también.

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F. Ejemplo 6

Caracterización adicional de la inhibición relacionada con anticuerpos de fosforilación de EGFR inducida por tirosina GPCR

Este ejemplo proporciona datos adicionales que muestran que varias preparaciones de anticuerpos anti-HB-EGF provistas en la presente exhiben inhibición dependiente de dosis de la fosforilación de tirosinas del receptor EGF inducida por GPCR.

La inhibición por preparaciones de anticuerpos candidatas U2-42, U2-39 y U2-45 fue examinada usando diferentes concentraciones de estas preparaciones de anticuerpo y el siguiente procedimiento.

150,000 Células (MDA-MB231, PPC1) fueron sembradas en una placa de 12 pocillos en 1 ml de medio. Las células fueron privadas de alimento en 500 µl de medio libre de suero durante 24 horas. Una placa de 96 pocillos Maxisorp negra fue recubierta con 100 µl de anticuerpo anti-EGFR (2 µg/ml) durante la noche a 4°C. La solución de recubrimiento se reemplazó por 300 µl de solución de bloqueo (PBS + 0.5% de BSA) sin lavado y se dejaron incubar 2 horas a temperatura ambiente. Las células fueron pre-incubadas con 10 µg/ml de anticuerpos anti-HB-EGF durante 30 minutos a 37°C y luego se trataron con ligandos GPCR LPA (10 µM, células PPC1) o trombina (1U/ml, células MDA-MB231) durante 3 minutos a 37°C.

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El medio se retiró y las células se lisaron en hielo con 200 µl de regulador de pH de lisis a base de Triton-X-100 que contenía 1 mM de PMSF, 10 µg/ml de aprotinina, 10 mM de NaF y 2 mM de ortovanadato de sodio. La placa Maxisorp bloqueada fue lavada 6x con PBS + 0.05% de Tween 20. El lisado de células se transfirió directamente a una placa Maxisorp lavada y se incubó durante al noche a 4|C con agitación suave.

La placa se lavó 6 veces con PBS + 0.05% de Tween-20, después 100 µl de 4G10-biotina (UBI) diluida 1:4000 en regulador de pH de dilución (PBS+0.5% de BSA- 0.05% de Tween-20 + 5mM de EDTA) se añadió a cada pocillo y se incubó durante 2 horas a temperatura ambiente. La placa se lavó 6 veces con PBS + 0.05% de Tween 20 y 100 µl de estreptavidina conjugada a AP (UBI) diluida 1:20000 en regulador de pH de dilución (PBS + 0.5% de BSA + 0.05% de Tween-20 + 5 mM de EDTA) se añadieron a cada pocillo durante 30 minutos a temperatura ambiente. La placa se lavó 6 veces con PBS + 0.05% de Tween 20 y 100 µl de substrato Atophos se añadieron a cada pocillo. La placa se incubó durante 3 horas a temperatura ambiente en la oscuridad y la fluorescencia de revelado se monitoreó a 30, 90 y 180 minutos (excitación: 430 nm, emisión: 580 nm).

Como se muestra en la figura 26, la inhibición de la fosforilación de tirosina EGFR inducida por LPA fue una

inhibición más grande y dependiente de dosis de la fosforilación de la tirosina EGFR a la observada al incrementarse la cantidad de anticuerpo anti-HB-EGF.

La figura 25 ilustra que preparaciones de anticuerpos candidatas U2-42, U2-39 y U2-45 efectivamente inhiben también la fosforilación de EGFR inducida por trombina en células MDA-MB231. Se observa una inhibición dependiente de dosis, con inhibición incrementada al añadirse más anticuerpo anti-HB-EGF. La figura 26 ilustra que la inhibición de fosforilación de tirosina EGFR inducida por LPA en células PPC-1 por preparaciones de anticuerpo anti-HB-EGF provistas en la presente depende de la dosis. Como se muestra, una mayor inhibición de la fosforilación de tirosina EGFR se detectó al incrementarse la cantidad de anticuerpo anti-HB-EGF.

G. Ejemplo 7

Inhibición de la migración de células MDA-MB231 inducida por GPCR por anticuerpos anti-HB-EGF humanos

Los experimentos de transmigración se llevaron a cabo para investigar si los anticuerpos proporcionados en la presente bloquean la migración celular inducida por el ligando GPCR Esfingosín-1-fosfato.

Células MDA-MB231 de cáncer de seno humano privadas de alimento en suero fueron incubadas con el anticuerpo indicado para la suspensión celular durante 45 minutos a

37°C. Posteriormente, 500 ml de suspensión celular (50,000 células) se colocaron en la cámara superior de pocillos de transferencia recubiertos con colágeno I (BD Falcon, poros de 8 µm). Se usó en la cámara inferior 750 ml de medio (MEM, aminoácidos, piruvato de sodio, Pen.-Strept., 0.1% de BSA) solo o que contenía el ligando GPCR Esfingosin-1-fosfato (R&D Systems). Después de la migración durante 8 horas a 37°C las células se fijaron, se tiñeron con DAPI y los núcleos celulares fueron contados para evaluación estadística.

Los resultados de estos ensayos de migración de células MDA-MB231 usando preparaciones de anticuerpos anti-HB-EGF candidatas U2-42, U2-39 y U2-45 se proporcionan en la figura 27. Como se muestra, la preparación de anticuerpos anti-HB-EGF U2-42 inhibió la migración de células MDA-MB231 en aproximadamente 70%; la preparación de anticuerpo anti-HB-EGF U2-45 inhibió la migración de células MDA-MB231 en aproximadamente 100% y la preparación de anticuerpo anti-HB-EGF U2-39 inhibió la migración de células MDA-MB231 en alrededor de 100%. Por consiguiente, la capacidad de estos anticuerpos anti-HB-EGF para inhibir la migración de células MDA-MB231 es sustancial.

H. Ejemplo 8

Inhibición de la migración inducida por HB-EGF de células MCF-7 por anticuerpos anti-HB-EGF humanos

Se llevaron a cabo experimentos de

transmigración para investigar si los anticuerpos proporcionados en la presente bloqueaban la migración celular que de otra manera podría ser inducida directamente por HB-EGF. Los resultados de estas pruebas resaltan qué preparaciones de anticuerpos pueden usarse para el desarrollo como agentes anticáncer metastásico.

Una suspensión de células de 500 ml de células MCF7 de cáncer de seno humano privadas de alimento en suero (50,000 células) se puso en una cámara superior de pocillos de transferencia recubiertos con colágeno I (BD Falcon, poros de 8 µm). Alícuotas de 700 ml de medio (MEM, aminoácidos, purivato de sodio, Pen.-Strept., 0.1% de BSA) solos o que contenían 20 ng/ml de HB-EGF (R&D Systems) en presencia o ausencia de 10 µg/ml de anticuerpos HB-EGF fueron puestos en la cámara inferior. Después de la incubación y migración durante 8 horas a 37°C, las células fueron fijadas, teñidas con DAPI y los núcleos celulares se contaron para evaluación estadística.

Los resultados de estos ensayos de migración usando preparaciones de anticuerpos anti-HB-EGF candidatos U2-42, U2-39 y U2-45 se proporciona en la figura 28. Como se muestra, la preparación de anticuerpos anti-HB-EGF U2-42 inhibió la migración de

células MCF-7 en alrededor de 55%; la preparación de anticuerpos anti-HB-EGF U2-45 inhibió la migración de células MCF-7 en alrededor de 93% y la preparación de anticuerpos anti-HB-EGF U2-39 inhibió la migración de células MCF-7 en aproximadamente 98%. Por consiguiente, la capacidad de estos anticuerpos anti-HB-EGF para inhibir la migración de células MCF-7 es sustancial.

I. Ejemplo 9

Características de los 10 principales anticuerpos anti-HB-EGF

Un resumen de los resultados se proporciona en la tabla 4 abajo, para las principales 10 preparaciones de anticuerpos derivadas de hibridoma en experimentos de señal de paso de membrana triple inducida por GPCR (TMPS). Los experimentos TMPS implicaron la estimulación con LPA en células SCC9, estimulación de trombina en células MDA-MB231, estimulación LPA de células SkOV-8 y migración de esfingosin-1-fosfato de células MDA-MB231. Los datos proporcionados representan la inhibición porcentual de la señal de transactivación de TMPS que se observó cuando las preparaciones de anticuerpo se usaron en los ensayos en comparación con el mismo ensayo cuando no estuvo presente anticuerpo. Los principales tres anticuerpos de cada experimento se resaltan en negritas.

Tabla 4

Inhibición porcentual de la señal de transactivación de TMPS

	TMPS					Migración
Ab	**SCC9.3**	**MDA-MB-231**	**MDA-MB231**	**SkoV-8**	**SkoV-8**	**MDA-MB231**
U2-39	**56.9**	**126.6**	**131.1**	**130.7**	65.5	**115**
U2-45	**58.5**	**136.8**	**95.7**	99.4	**75.1**	**104**
U2-42	**62.8**	123.2	**125.6**	**110.7**	**73.1**	69.9
U2-34	50.6	109.5	93.6	95.1	73	**99.6**
U2-46	36.6	88.1	77.5	80.5	**76.1**	n.d.
U2-19	n.d.	n.d.	n.d.	N.d.	n.d.	85
U2-26	n.d.	**143**	91.8	**106.1**	31.4	55.9
U2-51	n.d.	n.d.	n.d.	n.d.	n.d.	85.3
U2-15	n.d.	121.7	92.6	87	17.6	45.5
U2-22	n.d.	74.2	94.3	64.4	18.2	n.d.

J. Ejemplo 10

Inhibición de la fosforilación de tirosina HER4 inducida por HB-EGF por anticuerpos anti-HB-EGF

Este ejemplo muestra que las preparaciones de anticuerpos anti-HB-EGF inhiben la fosforilación de tirosina inducida por HB-EGF de HER4. Los siguientes procedimientos se emplearon para evaluar los efectos de anticuerpos anti-HB-EGF en la fosforilación de tirosina HER4.

125,000 Células de cáncer de seno humano T47D fueron sembradas en una placa de 24 pocillos en 500 µl de medio. Las células fueron ayunadas en 200 µl de medio libre de suero durante 24 horas. Se usó un equipo de ELISA Humana Fosfo-ErbB4 de R&D Systems para la detección de la fosforilación de tirosina HER4. Una placa de 96 pocillos Maxisorp transparente se recubrió con 100 µl de anticuerpo anti-humano-ErbB4 de ratón (Anticuerpo de Captura 1 µg/ml) durante la noche a temperatura ambiente. La placa Maxisorp recubierta se lavó 6 veces con PBS+0.05% de Tween-20, la solución de lavado se reemplazó por 300 µl de solución de bloqueo (PBS+0.5% de BSA) y se incubó 2 horas a temperatura ambiente. 50 µl de medio libre de suero con concentración 5x de anticuerpos anti-HB-EGF (10 µg/ml) se incubó con una concentración 5x de HB-EGF (20 ng/ml) durante 30 minutos a 37°C, después se añadió a cada pocillo (por duplicado). El medio se removió y las células se lisaron en hielo con 200 µl de regulador de pH de lisis a base deTriton-X-100 que contenía 1 mM de PMSF, 10 µg/ml de Aprotinina, 10 mM de NaF y 2 mM de ortovanadato de sodio. La placa Maxisorp bloqueada se lavó 3 veces con PBS+0.05% de Tween-20. El lisado celular se transfirió directamente a una placa Maxisorp lavada y se incubó durante la noche a 4°C con agitación suave. La placa se lavó 6 veces con PBS9+0.05% de Tween-20, después 100 µl de anti-fosfo-tirosina-HRP (Anticuerpo de Detección 600 ng/ml)

diluido en regulador de pH de dilución (PBS+0.5% de BSA+0.05% de Tween-20+5 mM de EDTA) se añadió a cada pocillo y se incubó durante 2 horas a temperatura ambiente. La placa se lavó 6 veces con PBS + 0.05% de Tween-20 y 100 µl de tetrametilbencidina (TMB, Calbiochem) se añadieron a cada pocillo durante 20 minutos a temperatura ambiente. La reacción se detuvo mediante la adición de 50 µl de H_2SO_4 1M y la absorbancia se leyó a 450 nm (lector de placa Thermo Lab Systems).

Los resultados se muestran en la figura 29. Como se ilustra, concentraciones cada vez más altas de preparaciones de anticuerpo anti-HB-EGF U2-42.1 o U2-39.1 llevaron a una inhibición incrementada de la fosforilación de HER4 inducida por HB-EGF.

K. Ejemplo 11

Reactividad cruzada de anticuerpos monoclonales

Este ejemplo proporciona datos adicionales que muestran la reactividad cruzada de las preparaciones de anticuerpo anti-HB-EGF para HB-EGF de macaco, HB-EGF de ratón y el factor de crecimiento tipo EGF relacionado Anfirregulina. Después de la clonación de la forma de mono y ratón de HB-EGF, cada construcción de expresión se transfectó en células HEK293 y anticuerpos anti-HB-EGF fueron probados para ver su capacidad de unirse a estas proteínas en un experimento FACS. La reactividad cruzada de Anfirregulina se

probó mediante el ensayo de formato de ELISA.

1. Clonación de HB-EGF de macaco

En el presente estudio, se prepararon plásmidos HB-EG de macaco. El ADNc de HB-EG de macaco se clonó mediante reacción en cadena de la polimerasa (PCR) a partir de ADNc de riñón de macaco con cebadores a base de la secuencia de HB-EG de macaco.

Los cebadores usados para la amplificación de HB-EG de macaco fueron los siguientes:

Cebador hacia adelante: 5'-GGG TTA ACG CCA CCA TGA AGC TGC TGC CGT CG-3' (SEQ ID NO: 1078).

Cebador hacia atrás: 5'-CCG CTC GAG GTG GGA ATT AGT CAT GCC C-3' (SEQ ID NO: 1079).

El producto de PCR fue digerido con Hpa1 y Xho1 y ligado en pCDNA3.1 digerido con Hind3. Después de la purificación, los plásmidos de HB-EG de macaco fueron transformados en células bacterianas DH5α y multiplicados bajo selección con ampicilina. El plásmido se expresó después altamente en medio de selección de ampicilina usando una sola colonia transformada. Después de la purificación usando un kit de purificación de ADN disponible comercialmente, los plásmidos de HB-EG de macaco fueron transfectados transitoriamente en células HEK293T.

2. Clonación de HB-EGF de ratón

En el presente estudio, se prepararon plásmidos HB-

EGF de ratón. El ADNc de HB-EGF de ratón se clonó mediante reacción en cadena de la polimerasa (PCR) a partir de ADNc de pulmón de ratón con cebadores a base de la secuencia de HB-EGF de ratón.

Los cebadores usados para la amplificación de HB-EGF de ratón fueron los siguientes:

Cebador hacia adelante: 5'-GGA AAT CGC CAC CAT GAA GCT GCT GCC GTC G-3' (SEQ ID NO: 1080).

Cebador hacia atrás: 5'CCG CTC GAG GTG GGA GCT AGC AGC CAC GCC-3' (SEQ ID NO: 1081).

El producto de PCR y el ADN del vector pCDNA3.1 fueron digeridos con EcoR1 y Xho1 y ligados. Después de la purificación, plásmidos de HB-EGF de ratón fueron transformados en células bacterianas DH5α y multiplicados bajo selección con ampicilina. El plásmido se expresó después altamente en medio de selección de ampicilina usando una sola colonia transformada. Después de la purificación usando un kit de purificación de ADN disponible comercialmente, plásmidos de HB-EGF de ratón fueron transfectados transitoriamente en células HEK293T.

3. Transfección y expresión de HB-EGF de macaco y ratón

Para tamizar la reactividad cruzada de anticuerpos provistos en la presente células HEK293T fueron transfectadas transitoriamente con plásmidos HB-EGF ya sea de macaco o

ratón usando un método de fosfato de calcio y analizados subsecuentemente mediante análisis FACS.

Por lo tanto, 30 horas antes de la transfección, $3x10^6$ células HEK293T fueron sembradas en 16 ml sobre una placa de cultivo de células de 15 cm e incubadas a 7% de CO_2 y 37°C. 32 µg de ADN de vector de ADN o vació de HB-EGF de macaco o ratón en 720 µl de ddH_2O fueron mezclados con $CaCl_2$ 2.5 M y 2 x BBS (pH6.96) e incubados a temperatura ambiente durante 10 minutos. Después de la incubación, la solución se añadió por goteo sobre las células y se incubó al 3% de CO_2 y 37°C durante 8 horas. Después de sumergir los medios, las células fueron incubadas con medio de cultivo fresco a 7% de CO_2 y 37°C durante 24 horas.

4. Análisis FACS se llevó a cabo para tamizar la reactividad cruzada de los anticuerpos

Por lo tanto, $2x10^5$ células transfectadas fueron cosechadas con 10 mM de EDTA en PBS, resuspendidas en regulador de pH FACS (PBS, 3% de FCS, 0.4% de azida) y sembradas sobre una placa de fondo redondo de 96 pocillos. Después de la centrifugación durante 3 minutos a 1,000 rpm para remover sobrenadante, las células fueron resuspendidas en dilución de anticuerpo anti-HB-EGF (100 µl/pocillo) e incubadas a 4°C durante 45 minutos. Las células se lavaron dos veces con regulador de pH FACS y se resuspendieron con anticuerpo secundario (100 µl/pocillo) anti-humano-PE de

burro (Jackson) diluido 1:100 en regulador de pH FACS. Las suspensiones de células se incubaron a 4°C en la oscuridad durante 30 minutos, se lavaron dos veces con regulador de pH FACS y se analizaron (FACS Backman Coulter).

La figura 30A muestra que las tres preparaciones de mAb reaccionan de manera cruzada con pro-HB-EGF de monos macacos.

La figura 30B muestra que la preparación de mAb U2-45 reacciona de manera cruzada con HB-EGF de ratón según se detecta por análisis FACS. Pruebas adicionales mostraron que los anticuerpos U2-46 y U2-51 también detectaron HB-EGF de ratón. Sin embargo, el anticuerpo U2-45.1 sólo fue muy débilmente (5-10%) neutralizante de la fosforilación de tirosina inducida por HB-EGF de ratón del EGFR.

5. Protocolo para ensayo de ELISA de reactividad cruzada de Anfirregulina

Diferentes concentraciones de Anfirregulina (R&D systems, conc. 1 ng/ml, 10 ng/ml, 100 ng/ml en PBS) se recubrieron durante la noche a 4°C en una placa de 96 pocillos (Nunc, Maxisorp). Después de lavado de la placa (6 veces) con regulador de pH de lavado (PBS + 0.05% de Tween 20; 150 µl por pocillo), la placa se incubó con regulador de pH de bloqueo (PBS + 0.5% de

BSA, 100 µl/pocillo) durante 4 horas a temperatura ambiente. La placa se lavó 6 veces con regulador de pH de lavado. Como anticuerpo primario 5 µg/ml de de anticuerpos anti-HB-EGF humanos purificados en regulador de pH de dilución de anticuerpos (PBS que contenía 0.5% de BSA, 0.05% de Tween 20, 5 mM de EDTA) se usaron y se incubaron durante 90 minutos a temperatura ambiente. La placa se lavó 6 veces con regulador de pH de lavado y anticuerpo anti-humano POD secundario (Dianova) se añadió (1:10 000 en PBS, 0.5% de BSA, 0.05% de Tween 20, 5 mM de EDTA) y se incubó durante 60 minutos a temperatura ambiente.

La placa se lavó 6 veces con regulador de pH de lavado y el substrato de TMB (Merck Biosciences) se añadió durante 15 minutos a temperatura ambiente. Después de detener el desarrollo del color azul al añadir 100 µl de 250 mM de HCl la absorbancia se midió a 450 nm con un lector de placa (Thermo labsystems).

La figura 30C muestra que el anticuerpo U2-45 y débilmente el anticuerpo U2-46 se unen a Anfirregulina como se determina por un ensayo en formato de ELISA. El anticuerpo monoclonal U2-45 se une a Anfirregulina pero la K_D del U2-45.1 para Anfirregulina sólo fue de 8 nM (contra 0.043 nM para HB-EGF). El anticuerpo monoclonal U2-45.1 también fue no neutralizante para AR.

L. Ejemplo 12

Análisis de ensayo de exclusión cinética de los valores K_d para anticuerpos monoclonales anti-HB-EGF U2-42.2, U2-39.1, U2-45.3, U2-26.2 y U2-34.1

Las K_Ds de los anticuerpos monoclonales U2-42.2, U2-39.1, U2-45.3 y U2-26.2 y U2-34.1 que se unen a HB-EGF humana, fueron determinadas usando tecnología KinExA. Para este propósito, un instrumento KinExA 3000 fue utilizado. Para todas las titulaciones de anticuerpos monoclonales, 50 mg de esferas de azlactona fueron acopladas con HB-EGF (~29 µg) en regulador de pH de carbonato de sodio 50 mM, pH 9.0 durante la noche a 4°C. Después de la conjugación de HB-EGF a las esferas, las esferas fueron centrifugadas y se lavaron una vez con regulador de pH de bloqueo (1M regulador de pH Tris, pH 8.3, 10 mg/ml de BSA) y se centrifugaron de nuevo, y luego se incubaron en regulador de pH de bloqueo durante una a dos horas a ~23°C para de esta manera bloquear cualquier grupo de azlactona reactivo restante presente sobre la superficie de las esferas. Después de bloqueo, las esferas fueron transferidas a un vial de esferas KinExA estándar y se pusieron sobre el instrumento.

MAb U2-42.2: Se llevó a cabo un análisis de curva doble para determinar la K_D. Doce soluciones que contenían una concentración de sitio de unión a mAb nominal de 37 pM fueron tituladas con concentraciones cada vez más altas de

HB-EGF para la titulación controlada por K_D, y 1,110 pM de sitio de unión se tituló en la curva de titulación controlada por mAb. Cada solución tuvo un volumen total de 10 ml (controlado por K_D) o 2 ml (controlado por mAb) y se dejó equilibrar durante 30-36 horas (controlado por K_d) o 6 horas (controlado por mAb) a ~23°C. Todas las soluciones para la titulación se prepararon usando artículos de vidrio volumétricos y las concentraciones de HB-EGF variaron de 10.5 nM a 205 fM. El método de instrumento usado para el análisis de estas soluciones consistió en una etapa de empaque de esferas en la cual las esferas son encapadas en capilares de vidrio, y las soluciones equilibradas fueron hechas fluir a través de la columna de esferas a 0.25 ml/min durante 10 minutos (2.5 ml, controlado por K_D) o 1 minuto (0.25 ml, controlado por mAb) por triplicado. Posteriormente, un anticuerpo policlonal anti-humano de cabra cy-5 marcado fluorescentemente (específico para Fc) a 3.4 nM (controlado por K_D) o 1.1 nM (controlado por mAb) fue hecho fluir a través del empaque de esferas durante 2 minutos a 0.5 ml/min para marcar el sitio de unión a mAb libre capturado sobre las esferas. La emisión de fluorescencia del empaque de esferas se midió a 670 nm con excitación a 620 nm.

Las mediciones de fluorescencia resultantes fueron convertidas en % de sitio de unión a mAb libre contra concentración de antígenos total como se hace normalmente con

el paquete de software KinExA acompañante (versión 1.0.3). Las curvas de titulación doble fueron ajustadas con el software KinExA a una isotermia en equilibrio de 1:1 con factores de corrección de desplazamiento incluidos.

El valor de la K_D que ajustó los datos óptimamente fue 53 pM con altos y bajos límites de confianza de 95% a 34 pM y 81 pM, respectivamente.

MAb U2-39.1: Se llevó a cabo una curva de titulación controlada por K_D para determinar la K_D. Doce soluciones que contenían una concentración de sitio de unión de mAb nominal de 55 pM fueron tituladas con concentraciones cada vez más altas de HB-EGF. Cada solución tuvo un volumen total de 10 ml y se dejó equilibrar durante 30-36 horas a ~23°C. Todas las soluciones para la titulación se prepararon usando artículos de vidrio volumétricos y las concentraciones de HB-EGF variaron de 10.5 nM a 205 fM. El método de instrumento usado para el análisis de estas soluciones consistió en una etapa de empaque de esferas en la cual las esferas fueron empacadas en un capilar de vidrio, y las soluciones equilibradas se hicieron fluir a través de la columna de esferas a 0.25 ml/min durante 10 minutos (2.5 ml) por triplicado. Posteriormente, un anticuerpo policlonal anti-humano de cabra cy-5 marcado fluorescentemente (Fc específico) a 3.4 nM se hizo fluir a través del empaque de esferas durante 2 minutos a 0.5 ml/min para marcar el sitio

de unión a mAb libre capturado sobre las esferas. La emisión de fluorescencia del empaque de esferas se midió a 670 nm con excitación a 620 nm. Las mediciones de fluorescencia resultantes se convirtieron en % de sitio de unión a mAb libre contra concentración de antígeno total en sitio de unión usando el paquete de software KinExA acompañante (versión 1.0.3). Debido a la unión no específica de ligando al empaque de esferas, la curva de titulación se ajustó con software KinExA a una isotermia de equilibrio de 1:1 con una termia para unión no específica a ligando incluida.

El valor de la K_D que se ajustó los datos óptimamente fue 7.8 pM con altos y bajos límites de confianza de 95% a 5.6 pM y 11 pM, respectivamente.

MAb U2-45.3: Se llevó a cabo un análisis de curva doble para determinar la K_D. Doce soluciones que contenían concentración de sitio de unión a mAb nominal de 40 pM fueron tituladas con concentraciones cada vez más altas de HB-EGF para la titulación controlada por K_D, y 1060 pM de unión se titularon en la curva de titulación controlada por mAb. Cada solución tuvo un volumen total de 10 ml (controlado por K_D) o 2 ml (controlado por mAb) y se dejó equilibrar durante 30-36 horas (controlado por K_D) o 6 horas (controlado por mAb) a ~23°C. Todas las soluciones para la titulación se prepararon usando artículos de vidrio volumétricos y las concentraciones de HB-EGF variaron de 5.25 nM a 102 fM. El método

instrumental usado para el análisis de estas soluciones consistió en una etapa de empaque de esferas en la cual las esferas fueron empacadas en un capilar de vidrio, y las soluciones equilibradas se hicieron fluir a través de la columna de esferas a 0.25 ml/min durante 10 minutos (2.5 ml, controlado por K_D) o 1 min (0.25 ml, controlado por mAb) por triplicado. Posteriormente, un anticuerpo policlonal anti-humano de cabra cy-5 marcado fluorescentemente (específico de Fc) a 3.4 nM (controlado por K_D) o 1.1 nM (controlado por mAb) se hizo fluir a través del empaque de esferas durante 2 minutos a 0.5 ml/min para marcar el sitio de unión a mAb libre capturado en las esferas. La emisión de fluorescencia del empaque de esferas se midió a 670 nm con excitación a 620 nm. Las mediciones de fluorescencia resultantes se convirtieron en % de sitio de unión a mAb contra concentración de antígeno total como se hace normalmente con el paquete de software KinExA acompañante (versión 1.0.3). Las curvas de titulación doble se ajustaron con el software KinExA a una isotermia de equilibrio de 1:1 con factores de corrección de desplazamiento incluidos.

El valor de la K_D que se ajustó a los datos óptimamente fue 43 pM con bajo y altos límites de confianza de 95% a 27 pM y 65 pM, respectivamente.

MAb U2-26.2: Se llevó a cabo un análisis de curva doble para determinar la K_D. Doce soluciones que contenían

una concentración de sitios de unión a mAb nominal de 41 pM se titularon con concentraciones cada vez más altas de HB-EGF para la titulación controlada por K_D, y 1060 pM de sitio de unión se titularon en la curva de titulación controlada por mAb. Cada solución tuvo un volumen total de 10 ml (controlado por K_D) o 2 ml (controlado por mAb) y se dejó equilibrar durante 30-36 horas (controlado por K_D) o 6 horas (controlado por mAb) a ~23°C. Todas las soluciones para la titulación se prepararon usando artículos de vidrio volumétricos y las concentraciones de HB-EGF variaron de 2.63 nM-51.4 fM (controlado por K_D) y 5.26 nM-103 fM (controlado por mAb). El método instrumental usado para el análisis de estas soluciones consistió en una etapa de empaque de esferas en la cual las esferas fueron empacadas en un capilar de vidrio, y las soluciones equilibradas se hicieron fluir a través de la columna de esferas a 0.25 ml/min durante 10 min (2.5 ml, controlado por K_D) o 1 min (0.25 ml, controlado por mAb) por triplicado. Posteriormente, un anticuerpo policlonal anti-humano de cabra cy-5 marcado fluorescentemente (específico de Fc) a 3.4 nM (controlado por K_D) o 1.1 nM (controlado por mAb) se hizo fluir a través del empaque de esferas durante 2 minutos a 0.5 ml/min para marcar el sitio de unión a mAb libre capturado en las esferas. La emisión de fluorescencia desde el

empaque de esferas se midió a 670 nm con excitación a 620 nm. Las mediciones de fluorescencia resultantes se convirtieron en % de sitios de unión a mAb libre contra concentración de antígeno total como se hace normalmente con el paquete de software KinExA acompañante (versión 1.0.3). Las curvas de titulación dobles fueron ajustadas con el software KinExA a una isotermia de equilibrio de 1:1 con factores de corrección de desplazamiento incluidos.

El valor de la K_D que se ajustó a los datos óptimamente fue 61 pM con altos y bajos límites de confianza de 95% a 37 pM y 100 pM, respectivamente.

MAb U2-34.1: Se llevó a cabo una curva de titulación controlada por K_D para determinar la K_D. Todas las soluciones que contenían concentración de sitio de unión a mAb nominal de 40 pM fueron tituladas con concentraciones cada vez más altas de HB-EGF. Cada solución tuvo un volumen total de 10 ml y se dejó equilibrar durante 30-36 horas a ~23°C. Todas las soluciones para la titulación se prepararon usando artículos de vidrio volumétricos y las concentraciones de HB-EGF variaron de 5.26 nM-103 fM. El método instrumental usado para el análisis de estas soluciones consistió en una etapa de empaque de esferas en la cual las esferas fueron empacadas en un capilar de vidrio, y las soluciones

equilibradas se hicieron fluir a través de la columna de esferas a 0.25 ml/min durante 10 minutos (2.5 ml) por triplicado. Posteriormente, un anticuerpos policlonal anti-humano de cabra cy-5 marcado fluorescentemente (específico de Fc) a 5.1 nM se hizo fluir a través del empaque de esferas durante 2 minutos a 0.5 ml/min para marcar el sitio de unión a mAb libre capturado sobre las esferas. La emisión de fluorescencia a partir del empaque de esferas se midió en 670 nm con excitación a 620 nm. Las mediciones de fluorescencia resultantes se convirtieron en % de sitio de unión a mAb libre contra concentración de antígeno total como se lleva a cabo normalmente con el paquete de software KinExA acompañante (versión 1.0.3). Debido a la unión no específica a ligando al empaque de esferas, la curva de titulación se ajustó con el software KinExA a una isotermia de equilibrio 1:1 con una termia para unión no específica a ligando incluida.

El valor de la K_D que ajustó los datos óptimamente fue 59 pM con bajos y altos límites de confianza de 95% a 32 pM y 87 pM, respectivamente.

M. Ejemplo 13

Determinación de análisis Scatchard de afinidad a anticuerpos

Las mediciones de afinidad de anticuerpos

proporcionados en la presente se llevaron a cabo mediante análisis FACS Scatchard indirecto. Para llevar a cabo este análisis $2x10^5$ células de interés fueron cosechadas con 10 mM de EDTA en PBS, resuspendidas en regulador de pH FACS (PBS, 3% de FCS, 0.4% de azida) y sembradas sobre una placa de fondo redondo de 96 pocillos. Después de la centrifugación durante 3 minutos a 1,000 rpm para remover sobrenadante, las células fueron resuspendidas en dilución de anticuerpo anti-HB-EGF (100 µl/pocillo) iniciando con 20 µg/ml, diluido en 1:2 etapas de dilución. Las suspensiones celulares se incubaron a 4°C durante 45 minutos, se lavaron dos veces con regulador de pH FACS y se resuspendieron con anticuerpo secundario (100 µl/pocillo) PE anti-humano de burro (Jackson) diluido 1:100 en regulador de pH FACS. Las suspensiones de células se incubaron a 4°C en la oscuridad durante 30 minutos, se lavaron dos veces con regulador de pH FACS y se analizaron (FACS, Beckman Coulter).

De acuerdo con el análisis FACS Scatchard, la media de fluorescencia se calculó para cada medición. La fluorescencia de fondo de las células sin anticuerpos HB-EGF se restó de cada media de fluorescencia. La gráfica de Scatchard con valor x = media de fluorescencia y valor y = media de fluorescencia/concentración de mAb (nM) fue generada. La K_D se tomó como el valor absoluto de 1/m de ecuación lineal.

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Tabla 5

Afinidades determinadas por FACS Scatchard de anticuerpos U2-42 y U2-39 en tres líneas de células de cáncer humano diferentes

Línea celular / Anticuerpo	DLD-1	NCI-ADR	MDA-MB231
U2-42	4.88	5.98	0.41
U2-39	9.05	7.63	6.21

N. Ejemplo 14

Análisis de ensayo de exclusión cinética de valores K_d para la unión de Mab anti-HB-EGF U2-45.3 a Anfirregulina

Una curva de titulación controlada por K_D se llevó a cabo para determinar la K_D. Doce soluciones que contenían una concentración de sitios de unión a mAb nominal de 4.4 nM fueron tituladas con concentraciones cada vez más altas de Anfirregulina. Cada solución tuvo un volumen total de 10 ml y se dejó equilibrar durante 30-36 horas a ~23°C. Todas las soluciones para la titulación se prepararon usando artículos de vidrio volumétricos y las concentraciones de Anfirregulina variaron de 1.23 µM a 24 pM. El método instrumental usado para el análisis de estas soluciones consistió en una etapa de empaque de esferas en la cual esas esferas fueron empacadas en un capital de vidrio, y las soluciones equilibradas se hicieron fluir a través de la columna de esferas a 0.25 ml/min durante 1 minuto (0.25 ml) por triplicado. Posteriormente, un anticuerpo policlonal anti-

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humano de cabra cy-5 marcado fluorescentemente (específico de Fc) a 684 pM se hizo fluir a través del empaque de esferas durante 2 minutos a 0.5 ml/min para marcar el sitio de unión a mAb libre capturado sobre las esferas. La emisión de fluorescencia a partir del empaque de esferas se midió a 670 nm con excitación a 620 nm. Las mediciones de fluorescencia resultante se convirtieron en porcentaje del sitio de unión a mAb libre contra concentración de antígeno total como se hace normalmente con el paquete de software KinExA acompañante (versión 1.0.3). Debido a la unión no específica del ligando al empaque de esferas, sólo un replicado de los tres recogidos a cada concentración (las tres concentraciones de Anfirregulina dobles más altas fueron excluidas del análisis) pudo ser analizado y ajustado con el software KinExA a una isotermia de equilibrio de 1:1.

El valor de la K_D que ajustó los datos óptimamente fue 5.0 nM con bajos y altos límites de confianza de 95% a 3.1 nM y 7.7 nM, respectivamente.

Q. Ejemplo 15

Criterio de selección para preparaciones de anticuerpos principales

Los siguientes criterios se usaron para identificar las preparaciones de anticuerpos principales: potencia para inhibir TMPS, potencia para inhibir directamente HB-EGF medida al observar el grado al cual los anticuerpos

inhibieron fosforilación de tirosina del receptor EGF, y HER4, la afinidad de los anticuerpos para HB-EGF, la reactividad cruzada de los anticuerpos para otras moléculas y las características de los epítopos.

P. Ejemplo 16

Anticuerpos anti-HB-EGF inhiben la estimulación por HB-EGF de proliferación celular Huvec y formación de tubos

Este ejemplo ilustra que aunque HB-EGF estimula la proliferación de células endoteliales vasculares humanas (HUVEC), los anticuerpos anti-HB-EGF proporcionados en la presente inhiben la proliferación de células HUVEC basal. Asimismo, como se muestra por este ejemplo, anticuerpos anti-HB-EGF inhiben la formación de tubos HUVEC, lo cual es un modelo *in vitro* para neo-angiogénesis. Preparaciones de anticuerpos que inhibían la proliferación y/o angiogénesis HUVEC son útiles no sólo para tratar cáncer sino también para tratar afecciones no cancerosas que incluyan angiogénesis no deseada (por ejemplo, retinopatía diabética).

1. Procedimientos: Determinación de la expresión de HB-EGF en células HUVEC mediante citometría de flujo

La expresión de HB-EGF en células endoteliales humanas se determinó mediante análisis FACS. Por lo tanto, $2x10^5$ células de interés fueron cosechadas con 10 mM de EDTA en PBS, resuspendidas en regulador de pH FACS (PBS, 3% de

FCS, 0.4% de azida) y plaqueadas en una placa de fondo redondo de 96 pocillos. Después de la centrifugación durante 3 minutos a 1,000rpm, el sobrenadante se removió, las células fueron resuspendidas en dilución de anticuerpo anti-HB-EGF (100 µl/pocillo, 10 µg/ml de anticuerpo anti-HB-EGF) y se incubaron a 4°C durante 45 minutos. Las células se lavaron dos veces con regulador de pH FACAS y se resuspendieron con anticuerpo secundario (100 µl/pocillo) anti-humano-PE (Jackson) diluido 1:100 en regulador de pH FACS. Las suspensiones de células se incubaron a 4°C en la oscuridad durante 30 minutos, se lavaron dos veces con regulador de pH FACS y se analizaron (FACS, Beckman Coulter).

Para probar los efectos de los anticuerpos anti-HB-EGF en la proliferación de HUVEC, aproximadamente 5,000 células HUVEC fueron sembradas en cada uno de los 48 pocillos que contenían medio con EGM-2, hidrocortisona, ácido ascórbico, gentamicina-anfotericina y 2% de FCS que contenía bFGF, VEGF, EGF e IGF-1 (Cambrex). Después de incubar las células durante la noche a 37°C, las células se lavaron dos veces con PBS que contenía 0.5% de FCS. Las células fueron después ayunadas 8 horas en EGF-2, 0.5% de FCS sin complementación de factores de crecimiento. HB-EGF o anticuerpo anti-HB-EGF y sus preparaciones se añadieron en 500 µl de medio de privación de alimento.

Las células se cultivaron después durante 60 horas

más, se tripsinizaron y se contaron.

Para probar los efectos de los anticuerpos anti-HB-EGF en la formación de tubos HUVEC, 200 µl de factor de crecimiento reducido en matrigel (BD biosciences) se pusieron en 48 pocillos. 250 µl de medio HUVEC se añadieron por 48 pocillos (EBM-2 + hidrocortisona + ácido ascórbico fentamicina-anfotericina + 0.25% de FCS de Cambrex). Después de la pre-incubación durante 20 minutos, se añadieron 20,000 células HUVEC en 50 µl de medio + 0.25% de FCS que contenía HB-EGF (10 ng/ml) o anticuerpos anti-HB-EGF U2-42, U2-39 o U2-45 (10 µg/ml). La formación de tubos se monitoreó al obtener fotomicrografías de áreas representativas de los pocillos de cultivo. Para un análisis cuantitativo áreas cerradas de tubos HUVEC fueron contadas.

2. Resultados

Como se muestra por el análisis FACS en las figuras 30A-30C, HB-EGF se expresan en HUVEC. Los resultados en las pruebas de proliferación celular se proporcionan en las figuras 32A-32B. Como se muestra en la figura 32A, HB-EGF estimula la proliferación celular HUVEC en alrededor de 38%. Sin embargo, después de la adición de preparaciones de anticuerpo anti-HB-EGF U2-42, U2-39 o U2-45, esta estimulación de la proliferación celular es inhibida en aproximadamente 8% a 14% (figura 31B). En este ensayo, la preparación de anticuerpo anti-HB-EGF U2-39 proporcionó el

nivel más alto de inhibición.

Los resultados de las pruebas de formación de tubos se proporcionan en las figuras 33A-33M. Análisis de control, sin anticuerpos anti-HB-EGF mostrados en las figuras 34A-C, muestra que las células HUVEC se unen para formar estructuras circulares o "tubos". Sin embargo, después de la adición de las preparaciones de anticuerpo anti-HB-EGF U2-42, U2-39 o U2-45, esta formación de tubos es inhibida. Un resumen del número de tubos observado se proporciona en la figura 33M. Como se muestra en la figura 33M, la preparación de anticuerpos anti-HB-EGF U2-42 proporcionó la aceleración más alta de regresión de tubos, seguida por la preparación de anticuerpo anti-HB-EGF U2-39.

Q. Ejemplo 17

Anticuerpos anti-HB-EGF inhiben la formación de colonias estimulada por HB-EGF y basal

Ensayos en agar suave se llevaron a cabo para investigar la capacidad de los anticuerpos proporcionados en la presente para inhibir crecimiento celular independiente de anclaje. El ensayo de formación de colonia en agar suave es un ensayo *in vitro* estándar para probar células transformadas, ya que sólo estas células transformadas pueden crecer en agar suave.

Para llevar a cabo este ensayo, células OVCAR-8, BM-1640 y NCI-H226 se incubaron con 10 ng/ml de HB-EGF y con

anticuerpos anti-HB-EGF o IgG2 (SIGMA) como control negativo, a 20 µg/ml en medio IMDM (Gibco) y se resuspendieron en 0.2% de agar noble Difco. La suspensión de células se plaqueó sobre una capa inferior de agar al 0.4% por cuadruplicado en una placa de 96 pocillos y se cubrió con medio IMDM. Las colonias se dejaron formar durante alrededor de 14 días y después fueron teñidas con 40 µl de MTT (Sigma, 1 mg/ml en PBS) durante 4 horas. La estimulación de HB-EGF y los efectos inhibitorios de los anticuerpos anti-HB-EGF fueron cuantificados mediante software de formación de colonia HTSBonit (Lemma Tec).

En otro ensayo, 750 ó 1,000 células (dependiendo del clon 71 ó 74 de KsOV-3, figuras 34D y 34E) fueron preincubados con anticuerpos anti-HB-EGF o IgG2 (SIGMA) como control negativo, a 20 µg/ml en medio IMDM (Gibco) durante 30 minutos a 37°C y se resuspendieron en 0.4% de agar noble Difco (o 0.2% para clon 74). La suspensión celular se plaqueó sobre una capa inferior de agar 0.75% (0.4% para clon 74) por cuadriplicado en una placa de 96 pocillos y se cubrieron con medio IMDM. En un ensayo similar, 2,000 células BxPC-3 (figura 34F) fueron pre-incubadas con 20 µg/ml de anticuerpos anti-HB-EGF o 20 µg/ml de IgG2 (SIGMA) como control negativo, en medio IMDM (Gibco) que contenía 20% de FCS durante 30 minutos a 37°C. Las células se resuspendieron en 0.4% de agar noble Difco y la suspensión celular se

plaqueó sobre una placa inferior de agar al 0.75% por cuadruplicado en una placa de 96 pocillos. Los pocillos fueron cubiertos con medio IMDM. Ambas capas contenían 20% de FCS.

Las colonias se dejaron formar durante alrededor de 14 días y después fueron teñidas con 40 µl de MTT (Sigma, 1 mg/ml en PBS) durante 4 horas. Los resultados se muestran en las figuras 34A-34F, las cuales ilustran que HB-EGF estimuló la formación de colonias (figura 34A-34C) y la formación de colonias basales (figuras 34D-34F) se reducen significativamente por los anticuerpos anti-HB-EGF. Como se muestra, por ejemplo, en la figura 34A, células OVCAR-8 estimuladas con HB-EGF forman un tamaño de colonia medio significativamente más grande que las células OVCER-8 de control cultivadas sin HB-EGF. Sin embargo, cuando células OVCAR-8 fueron cultivadas con anticuerpos anti-HB-EGF U2-39 en presencia de HB-EGF, el tamaño de colonia medio se redujo a un tamaño similar a aquél observado para células de control sin tratamiento con HB-EGF (figura 34A). Resultados similares se observaron para células BM1604 (derivadas de tejido de cáncer de próstata) (véase figura 34B). Los anticuerpos anti-HB-EGF U2-45 y U2-42 inhibieron también la formación de colonia BM1604.

Los anticuerpos anti-HB-EGF también inhiben la formación de colonia estimulada por HB-EGF de células de

carcinoma pulmonar NCI-H226 (figura 34C). Como se muestra en la figura 36C, cuando células NCI-H226 fueron cultivadas con anticuerpos anti-HB-EGF U2-39 en presencia de HB-EGF, el tamaño de colonia medio se redujo a un tamaño similar a aquél observado para células de control sin tratamiento con HB-EGF.

Los números de colonias, así como el tamaño de la colonia, se redujeron por el tratamiento con los presentes anticuerpos anti-HB-EGF (figuras 34D-F). Así, la figura 34D ilustra que los anticuerpos anti-HB-EGF reducen el número de colonias basales formadas por células de clon 71 de SkOV-3 HB-EGF (derivadas de células de cáncer ovárico SkOV-3 transfectadas establemente con una construcción de expresión proHB-EGF). Como se muestra, células SkOV-3 de control que sobre-expresaban HB-EGF formaron grandes números de colonias. Sin embargo, cuando células KsOV-3 HB-EGF clon 71 fueron cultivadas ya sea con anticuerpos anti-HB-EGF U2-42 o U2-39 en presencia de HB-EGF, el número de colonias se redujo dramáticamente. De manera similar, los anticuerpos anti-HB-EGF inhiben la formación de colonias de células SkOV-3 (clon 74), derivadas de tejido de cáncer ovárico, y células BxPC3, derivadas de tejido de adenocarcinoma pancreático (figuras 34E-34F).

Estos datos indican que la formación de colonia y tumores por una gran variedad de tipos de células cancerosas puede ser inhibida por los presentes anticuerpos anti-HB-EGF,

incluyendo las preparaciones de anticuerpos U2-42, U2-39 y U2-45 proporcionadas en la presente.

R. Ejemplo 18

Los anticuerpos anti-HB-EGF inhiben el crecimiento de tumores *in vivo*

La figura 37 ilustra el volumen medio de tumores BxPC3 pancreáticos formados en experimentos de xenoinjerto con ratones SCID. Como se muestra, el crecimiento de tumor establecido se inhibió significativamente en presencia de preparaciones de anticuerpo U2-42 y/o U2-39 cuando se comparan con el control de vehículo. En la figura 38A, se muestra que los anticuerpos anti-HB-EGF U2-42, U2-39 y U2-45 inhiben el crecimiento establecido de células de clon 58 de HB-EGF EFO-27 *in vivo*. El efecto de la inhibición de crecimiento de tumor pudo ser mostrado que dependía de dosis, con 25 mg/kg como un tratamiento altamente efectivo aunque dosis más bajas tales como 1 ó 5 mg/kg fueron menos eficientes (figura 38B).

S. Ejemplo 19

Anticuerpos anti-HB-EGF en terapia de combinación con el anticuerpo anti-EGFR Erbitux

La figura 35 muestra que la inhibición de un solo agente de las células de clon 58 de EFO-27 HB-EGF con anticuerpos anti-HB-EGF es moderada a fuerte. Sin embargo, en una combinación controlada por dosis de anticuerpos anti-

HB-EGF y anti-EGFR, la inhibición de formación de colonias es extremadamente efectiva. Además, el crecimiento de xenoinjertos *in vivo* es inhibido fuertemente por la combinación de anticuerpos anti-EGF y anti-EGFR llevando a una regresión completa de crecimiento de tumor de cáncer ovárico (figura 38C).

T. Ejemplo 20

Expresión de HB-EGF en una variedad de tipos de células cancerosas

La expresión de HB-EGF en líneas de células cancerosas humanas se determinó mediante análisis FACS. Para llevar a cabo este análisis $2x10^5$ células fueron cosechadas con 10 mM de EDTA en PBS, resuspendidas en regulador de pH FACS (PBS, 3% de FCS, 0.4% de azida) y trasferidas a una placa de fondo redondo de 96 pocillos. Después de la centrifugación durante 3 minutos a 1,000 rpm para remover sobrenadante, las células fueron resuspendidas en dilución de anticuerpo anti-HB-EGF (100 µl/pocillo) e incubadas a 4°C durante 45 minutos. Las células fueron lavadas dos veces con regulador de pH FACS y resuspendidas con anticuerpo secundario (100 µl/pocillo) anti-humano-PE de burro (Jackson) diluido 1:100 en regulador de pH FACS. Las suspensiones celulares se incubaron a 4°C en la oscuridad durante 30 minutos, se lavaron dos veces con regulador de pH FACS y se analizaron (FACS, Beckman Coulter).

Los resultados de estos ensayos se muestran en la siguiente tabla 6.

Tabla 6

Expresión de HB-EGF en células cancerosas

Línea celular	Tejido	Nivel de expresión
MDA-MB231	Seno	++
NCI-ADR	Seno	+++
ZR75-1	Seno	-/+
MKN-1	Gástrico	+
MKN-28	Gástrico	+++
PPC1	Próstata	++
PC3	Próstata	++
HT144	Melanoma	-/+
MelGerlach	Melanoma	+++
IGROV-1	Ovario	+
ES2	Ovario	++
SkOV-3	Ovario	+
SkOV-8	Ovario	+
TOV21G	Ovario	++
OVCAR-8	Ovario	+++
Calu-6	Pulmón	+
NCI-H460	Pulmón	++
MS-751	Cérvix	++
SIHA	Cérvix	+
HelaS3	Cérvix	+
U266	Mieloma	-
SCABER	Vejiga	++
HCT-116	Colon	++
HCT-15	Colon	+
SW620	Colon	++

U. Ejemplo 21

Anticuerpos anti-HB-EGF para la detección de HB-EGF en tejido y fluidos corporales mediante inmunohistoquímica y ELISA

Los anticuerpos anti-HB-EGF U2-42 y U2-39 se probaron para su capacidad para teñir HB-EGF expresado en

muestras fijas humanas. Como se muestra en la figura 39A ambos anticuerpos muestran una tinción de membrana y citoplásmica prominente de células tubulares de riñón humano mientras que el control no muestra ninguna tinción. Además de la detección inmunohistoquímica de HB-EGF en muestras de tejido de pacientes HB-EGF es liberado como un factor de crecimiento en varios fluidos corporales. Con base en anticuerpos anti-HB-EGF humanos como reactivos de recubrimiento se estableció un ELISA el cual detecta HB-EGF en muestras líquidas hasta niveles debajo de 40 pg/ml (figura 39B).

V. Ejemplo 22

Clases canónicas de anticuerpos

Los genes que codifican para anticuerpos principales fueron sentenciados como se describió en el último ejemplo. Estos datos de secuencia se usaron para asignar los anticuerpos a clases canónicas.

Chothia *et al.* han descrito la estructura de anticuerpos en términos de "clases canónicas" para las regiones hipervariables de cada cadena de inmunoglobulina (Chothia, *et al.*, 1987, *J. Mol. Biol.*, 196(4):901-17). Las estructuras atómicas de los fragmentos Fab y VL de una variedad de inmunuglobulinas fueron analizadas para determinar la relación entre sus secuencias de aminoácidos y las estructuras tridimensionales de sus sitios de unión a

antígeno. Chothia *et al.*, encontraron que había relativamente pocos residuos que, a través de su empaque, enlace a hidrógeno o la capacidad de asumir conformaciones phi, psi u omega inusuales, eran principalmente responsables de las conformaciones de cadena principal de las regiones hipervariables. Se encontró que estos residuos ocurrían en sitios dentro de las regiones hipervariables y en el armazón de lámina α conservado. Al examinar secuencias de inmunoglobulinas que tenían estructura desconocida, Chothia, *et al.*, muestran que muchas inmunoglublinas tienen regiones hipervariables que son similares en tamaño a una de las estructuras conocidas y residuos idénticos contenidos adicionalmente en los sitios responsables de la conformación observada.

Su descubrimiento indicó que estas regiones hipervariables tienen conformaciones cercanas a aquellas en las estructuras conocidas. Para cinco de las regiones hipervariables, el repertorio de conformaciones pareció estar limitado a un número relativamente pequeño de clases estructurales individuales. Estas conformaciones de cadena principal que ocurren comúnmente de las regiones hipervariables fueron llamadas "estructuras canónicas". Trabajo adicional por Chothia, *et al.*, 1989; *Nature* 342:877-83) y otros (Martín *et al.*, 1996; *J. Mol. Biol.* 263:800-15) confirmó que hay un pequeño repertorio de conformaciones

de cadena principal para al menos cinco de las seis regiones hipervariables de anticuerpos.

Las regiones de determinación de complementariedad (CDR) de cada preparación de anticuerpo se analizaron para determinar su clase canónica. Como se conoce, las clases canónicas sólo han sido asignadas para CDR1 y CDR2 de la cadena pesada de anticuerpos, junto con CDR1, CDR2 y CDR3 de la cadena ligera de anticuerpos. Las siguientes tablas resumen los resultados del análisis. Los datos de clase canónica están en forma de HCDR1-HCDR2-LCDR1-LCDR2-LCDR3 (H1-H2-L1-L2-L3), en donde "HCDR" se refiere a la CDR de la cadena pesada y "LCDR" se refiere a la CDR de la cadena ligera. Así, por ejemplo, una clase canónica de 1-3-2-1-1 se refiere a un anticuerpo que tiene una HCDR1 que está en la clase canónica 1, una HCDR2 que está en la clase canónica 3, una LCDR1 que está en la clase canónica 2, una LCDR2 que está dentro de la clase canónica 1 y una LCDR3 que está dentro de la clase canónica 1.

Las asignaciones se hicieron a una clase canónica particular en donde los aminoácidos en el anticuerpo coinciden con los aminoácidos definidos para cada clase canónica. Los aminoácidos definidos para cada clase canónica pueden encontrarse, por ejemplo, en

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los artículos por Chothia, *et al.*, referidos arriba. La tabla 7 y tabla 8 reportan las asignaciones de clases canónicas para cada uno de los anticuerpos HB-EGF. Aunque no hubo clase canónica coincidente, la asignación de clases canónicas es marcada con una letra s y un número, tal como "s18", significando que la CDR tiene el tamaño 18.

Tabla 7

Anticuerpo (clasificado)	**H1-H2-L1-L2-L3**	**H3longitud**
U2-18.1	3-1-2-1-1	17
U2-13.1	1-3-4-1-1	14
U2-19.1	3-1-3-1-1	13
U2-38.1	3-1-12-1-1	23
U2-21.1	3-1-3-1-s9	8
U2-15.1	1-3-4-1-1	14
U2-16.1	1-2-8-1-1	11
U2-30.1	1-2-3-1-1	13
U2-42.1	1-3-2-1-s9	8
U2-36.1	3-s18-2-1-s10	13
U2-22.1	1-3-3-1-1	11
U2-56.1	3-1-2-1-1	8
U2-24.1	3-s16-3-1-s9	12
U2-24.2.1	3-s16-3-1-s9	12
U2-14.1	1-3-4-1-1	14
U2-1.1	1-3-4-1-1	5
U2-32.1	1-1-3-1-1	15
U2-40.1	1-3-2-1-3	8
U2-5.1	1-3-4-1-1	6
U2-8.1	3-1-4-1-1	17
U2-39.1	1-3-2-1-1	6
U2-3.1	3-1-4-1-1	16
U2-43.1	1-1-2-1-1	12
U2-34.1	1-3-2-1-1	16
U2-26.1	3-1-3-1-s9	9

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U2-41.1	1-3-2-1-1	12
U2-45.1	1-3-2-1-1	19
U2-54.1	3-1-2-1-1	15
U2-57.1	3-1-2-1-1	8
U2-12.1	1-3-2-1-s9	9
U2-46.1	1-3-2-1-1	16
U2-48.2	1-1-2-1-1	12
U2-6.1.1	1-3-4-1-1	11
U2-6.1.2	1-3-2-1-1	16
U2-58.1	3-s16-2-1-1	8
U2-51.1	1-3-2-1-1	16
U2-65.2	3-1-2-1-1	8
U2-53.1	1-1-2-1-1	12
U2-61.1	1-3-2-1-1	9
U2-28.1	3-1-3-1-s9	12

Tabla 8

Anticuerpo	**H1-H2-L1-L2-L3 (clasificado)**	**H3longitud**
U2-43.1	1-1-2-1-1	12
U2-48.2	1-1-2-1-1	12
U2-53.1	1-1-2-1-1	12
U2-32.1	1-1-3-1-1	15
U2-30.1	1-2-3-1-1	13
U2-16.1	1-2-8-1-1	11
U2-39.1	1-3-2-1-1	6
U2-61.1	1-3-2-1-1	9
U2-41.1	1-3-2-1-1	12
U2-34.1	1-3-2-1-1	16
U2-46.1	1-3-2-1-1	16
U2-6.1.2	1-3-2-1-1	16
U2-51.1	1-3-2-1-1	16
U2-45.1	1-3-2-1-1	19
U2-40.1	1-3-2-1-3	8
U2-42.1	1-3-2-1-s9	8
U2-12.1	1-3-2-1-s9	9
U2-22.1	1-3-3-1-1	11
U2-1.1	1-3-4-1-1	5
U2-5.1	1-3-4-1-1	6
U2-6.1.1	1-3-4-1-1	11
U2-13.1	1-3-4-1-1	14
U2-15.1	1-3-4-1-1	14
U2-14.1	1-3-4-1-1	14
U2-56.1	3-1-2-1-1	8

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U2-57.1	3-1-2-1-1	8
U2-65.2	3-1-2-1-1	8
U2-54.1	3-1-2-1-1	15
U2-18.1	3-1-2-1-1	17
U2-19.1	3-1-3-1-1	13
U2-21.1	3-1-3-1-s9	8
U2-26.1	3-1-3-1-s9	9
U2-28.1	3-1-3-1-s9	12
U2-3.1	3-1-4-1-1	16
U2-8.1	3-1-4-1-1	17
U2-58.1	3-s16-2-1-1	8
U2-24.1	3-s16-3-1-s9	12
U2-24.2.1	3-s16-3-1-s9	12
U2-36.1	3-s18-2-1-s10	13
U2-38.1	3-1-2-1-1	23

La tabla 9 es un análisis del número de anticuerpos por clase. El número de anticuerpos que tienen la clase canónica particular designada en la columna izquierda se muestra en la columna derecha.

La estructura más comúnmente vista es 1-3-2-1-1. Ocho de un total de 40 mAbs tuvieron esta combinación.

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Tabla 9

Número de anticuerpos anti-HB-EGF en cada combinación de clases canónicas

H1-H2-L1-L2-L3	Conteo
1-1-2-1-1	3
1-1-3-1-1	1
1-2-3-1-1	1
1-2-8-1-1	1
1-3-2-1-1	8
1-3-2-1-3	1
1-3-2-1-s9	2
1-3-3-1-1	1
1-3-4-1-1	6
3-1-2-1-1	5
3-1-3-1-1	1
3-1-3-1-s9	3
3-1-4-1-1	2
3-s16-2-1-1	1
3-s16-3-1-s9	2
3-s18-2-1-s10	1
3-1-2-1-1	1

W. Ejemplo 23

Mapeo de epítopos de anticuerpos anti-HB-EGF

Este ejemplo describe el mapeo de epítopos reconocidos por preparaciones de anticuerpos.

Anticuerpos probados: Cinco preparaciones de anticuerpo monoclonales humanos derivados de XenoMouse capaces de neutralizar la actividad de HB-EGF fueron analizados: U2-39;

U2-42; U2-45; U2-26 y U2-19. Cuatro de estas preparaciones de anticuerpo monoclonales mostraron ser específicas para HB-EGF humano en tanto que la preparación de anticurpos U2-45 exhibió cierta reactividad cruzada con HB-EGF de ratón y anfurregulina humana. Todas estas preparaciones de anticuerpos neutralizantes mapean los compartimientos 6 y 8 de MCAB (véase abajo).

1. Mapeo de epítopos

El ADNc de HB-EGF humano se aisló del ARNm de HeLa mediante amplificación por PCR y la secuencia de HB-EGF madura se clonó en un vector pSecTAg como una proteína de fusión myc-His, usando la secuencia de péptidos de señal kappa de Ig. El polipéptido HB-EGF maduro fue expresado en células 293T, con secreción en los medios.

El sitio de unión a toxina de difteria de HB-EGF fue mutado así como el sitio de unión al receptor EGF mediante mutagénesis dirigida a sitio.

La forma corta de HB-EGF (Loukianov *et al.*, *Gene* 195:81-86), que no tiene el tercer enlace de disulfuro del dominio tipo EGF, también fue clonada.

El dominio tipo HB-EGF que tiene SEQ ID NO: 1082 (DPCLRKYKDFCIHGECKYVKELRAPSCICHPGYHGERCHGLSLP) se clonó en pSecTag y fue expresado y secretado como una proteína de fusión Myc-His.

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2. Resultados

Todas las preparaciones de anticuerpos U2-39; U2-42; U2-45; U2-26 y U2-19 reconocen un epítopo discontinuo. Ninguno de los anticuerpos reconoce la forma corta del HB-EGF.

El sitio de unión para las cinco preparaciones de anticuerpos están dentro del dominio tipo EGF, el cual incluye los residuos 44-86 de la proteína madura que tiene la siguiente secuencia: CPCLRKYKDFCIHGECKYVKELRAPSCICHPGYHGER CHGLSLP (SEQ ID NO: 1082). El tercer enlace de disulfuro en el dominio tipo EGF se requiere para la unión de todas las preparaciones de anticuerpos U2-39; U2-42; U2-45; U2-26 y U2-19.

3. Análisis de la estructura-función de sitio de unión a anticuerpos mediante mutagénesis dirigida a sitio

Doce mutaciones independientes fueron creadas en HB-EGF al reemplazar uno a cuatro residuos dentro del dominio tipo EGF de pro-HB-EGF humana con el residuo de aminoácido correspondiente encontrado normalmente en el pro-HB-EGF de ratón.

Dado que muchas de las presentes preparaciones de anticuerpos fueron selectivas de especie, la mutagénesis dirigida a sitio con el propósito de identificar epítopos EGF se llevó a cabo a una

diferencia conocida entre la proteína HB-EGF humana y proteínas relacionadas de diferentes especies. En particular, las diferencias de aminoácidos entre HB-EGF de humano y ratón son las siguientes: K122R; V124L; K125Q; I133K y H135L.

Una lista completa de secuencias de polipéptidos mutantes de HB-EGF para el mapeo de epítopos es proporcionada en la tabla 10. Ácidos nucleicos de HB-EGF mutantes que codifican para la proteína mutante deseada se expresaron transitoriamente en células 293T, y la unión al anticuerpo monoclonal fue medida por ELISA.

Así, se hicieron polipéptidos mutantes de HB-EGF con estas mutaciones y estos polipéptidos mutantes fueron probados para evaluar si las presentes preparaciones de anticuerpos aún se unían al polipéptido mutante HB-EGF. Si no, entonces el aminoácido mutado era probablemente importante para la unión a anticuerpo, y por consiguiente formaba una parte importante de un epítopo.

La tabla 11 resume los resultados de unión obtenidos, en donde "Sí" indica que la unión tuvo lugar a pesar de la mutación indicada, "No" indica que la unión fue eliminada sustancialmente por la mutación indicada y "Reducida" indica que ocurrió una unión

LS86

reducida cuando la mutación estuvo presente.

Tabla 10

Tipo silvestre	LGKKRDPCLRKYKDFCIHGE-CKYVKELRAPSCICHPGYHGERCHGLSLP	SEQ ID NO:
F115y	----------Y----------	1083
L127f	----------F----------	1084
E141H	----------H---------	1085
K122R; V124L; K125Q	----------R-LQ----------	1086
F115Y; K122R; V124L; K125Q	----------R-LQ----------H---------	1088
I133K; H135L	----------K-L----------	1089
F115Y; I133K; H135L	----------Y----------K-L----------	1090
L127F; I133K; H135L	----------F-----K-L----------	1091
L148T	----------T-	1092
E141H; L148T	----------H------T-	1093
117-120 IHGE Cambiado a LHDGV	----------LHDGV----------	1094

Tabla 11

Resultados de unión

	Construcción/Mab	U2-42.3	U2-39.1	U2-19.3	U2-26.1	U2-45
1	proHB-EGF (WT) humano	Sí	Sí	Sí	Sí	Sí
2	F115Y	**No**	**No**	Sí	Sí	**Reducida**
3	L127F	Sí	**No**	Sí	Sí	Sí
4	E141H	**No**	Sí	Sí	Sí	Sí
5	K122R, V124L, K125Q	Sí	Sí	Sí	Sí	Sí
6	F115Y, K122R, V124L, K125Q	**No**	**No**	Sí	Sí	**Reducida**
7	K122R, V124L, K125Q, E141H	**No**	Sí	Sí	Sí	Sí
8	I133K, H135L	Sí	Sí	**No**	**No**	Sí
9	F115Y, I133K, H135L	**No**	**No**	**No**	**No**	**Reducida**
10	L127F, I133K, H135L	Sí	**No**	**No**	**No**	Sí
11	S147T	Sí	Sí	Sí	Sí	Sí
12	E141H, S147T	**No**	Sí	Sí	Sí	Sí
13	IHGE (117-120) a LHDGV	Sí	Sí	**No**	**No**	**No**
	Residuos críticos	F115 y E141	F115 y L127	I133 o H135	I133 o H135	F115?

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Estos estudios de unión indican que las preparaciones de anticuerpos U2-42 y U2-39 reconocen el dominio de unión a toxina de difteria y los residuos F115, L127 y E141 son importantes para la unión a toxina de difteria.

Además, cuando las mutaciones F115Y o E141H están presentes en HB-EGF, la unión es eliminada sustancialmente para las preparaciones de anticuerpo U2-42. Así, Phe-115 y Glu-141 son importantes para la unión al anticuerpo U2-42. La preparación de anticuerpo U2-45 también parece requerir Phe-115 toda vez que la unión por esta preparación de anticuerpo se reduce cuando Phe-115 es mutada.

La preparación de anticuerpo U2-39 requiere Phe-115 y Leu-127 para la unión a HB-EGF ya que la mutación de cualquiera de estos residuos elimina sustancialmente la unión a anticuerpo.

Las preparaciones de anticuerpo U2-19, U2-26 y U2-45 se unen a la región conservada entre los residuos 117-120 (IHGE). Como se muestra en la tabla 11, las preparaciones de anticuerpo U2-19 y U2-26 reconocen también un epítopo en Ile-133 y/o His-135, porque al menos uno de estos residuos es crítico para su unión.

Con base en sus propiedades de unión, de los anticuerpos fueron puestos en la relación

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"compartimientos" listada en la tabla 12.

La compartimentalización es un método para agrupar anticuerpos con base en su competencia para unión al antígeno (véase Jia *et al.*, 2004, *J. Immunol. Methods* 288:91-98).

La asignación de compartimientos depende de qué tan diferentes patrones de unión observados para todos los anticuerpos probados sean. Por lo tanto, los compartimientos no siempre se correlacionan con epítopos determinados por otros medios y se pueden usar para sólo definir aproximadamente epítopos.

Tabla 12

Compartimientos de relación de anticuerpos

Compartimiento #1	Compartimiento #2	Compartimiento #3	Compartimiento #4	Compartimiento #5	Compartimiento #6	Compartimiento #7	Compartimiento #8
U2-24.2	U2-1.3	U2-15.3	U2-13.3	U2-16.3	U2-18.3	U2-19.2	U2-3.2
U2-32.3		U2-30.2	U2-14.3		U2-38.1	U2-21.3	
U2-5.3			U2-2.1		1.19.2	U2-34.1	
U2-17.1			U2-57.1		U2-36.3	U2-26.2	
U2-56.3			U2-58.3		U2-40.3	U2-41.3	
			U2-61.1		U2-8.3	U2-45.3	
					U2-22.3	U2-46.3	
						U2-48.2.1	
					U2-39.1	U2-6.1	
					U2-54.2	U2-51.2	
						U2-53.3	
						U2-28.2	

En general, el mapeo de epítopos de la preparación de anticuerpo U2-45 indica que las preparaciones de anticuerpos del compartimiento 7 reaccionan de manera cruzada con HB-EGF de ratón y Anfirregulina humana.

Las mutaciones de F115 a Ala o Tyr afectan la afinidad de unión de anticuerpos U2-45. Sin embargo, la unión al anticuerpo U2-45 no fue afectada por las mutaciones I133 y H135, las cuales sí afectan alguns otras preparaciones de anticuerpo del compartimiento 7. Cuando la secuencia HB-EGF humana de IHGE fue cambiada por LHDGV, la cual está presente en HB-EGF de ratón y Anfirregulina humana, todas las preparaciones de anticuerpo del compartimiento 7 no pudieron unirse. Por lo tanto, los residuos IHGE (117-120) probablemente forman el epítopo para las preparaciones de anticuerpo de compartimiento 7.

Estudios de mutagénesis dirigida a sitio adicionales que incluyen la unión de mutantes HB-EGF a EGFR, indican que residuos que incluyen Asp-106 y Pro-107 son tanto necesarios para la unión óptima de HB-EGF al receptor de EGF. Más aún, Leu-148, el cual es necesario para la unión de HB-EGF al receptor de EGF, no pareció estar implicado en la unión de cualquiera de las preparaciones de anticuerpo anti-HB-EGF.

HH. Ejemplo 24

Secuencias de elementos clave de anticuerpo anti-HB-EGF

Este ejemplo proporciona las secuencias de preparaciones de anticuerpos en las figuras 1-21.

Ejemplo 25A

Ensayo de rayado - Inhibición de la migración inducida por HB-EGF de células de carcinoma escamosa epitelial CLS354 (boca)

Se llevaron a cabo experimentos de rayado para investigar si los anticuerpos de la invención bloqueaban la migración celular que de otra manera podría ser inducida directamente por HB-EGF.

$1x10^6$ Células CLS354 fueron sembradas en medio (medio RPMI con 10% de FCS) en 1 ml de una placa de 12 pocillos y ayunadas de suero (medio con 0.5% de FCS) durante la noche. Después de que las células alcanzaron una capa confluente, se llevó a cabo un rayado en medio del pocillo usando una punta de plástico estéril. Las células fueron lavadas con PBS y las células CLS354 rayadas fueron tratadas solas o conteniendo 20 mg/ml de HB-EGF en presencia o ausencia de 10 µg/ml de U2-39, Erbitux o IgG humana. El experimento se detuvo después de la incubación de 12 horas a 37°C. Se retiró medio, las células se lavaron con PBS y se fijaron con 100% de metanol helado a -20°C, se tiñeron con violeta cristal, se lavaron y se secaron durante la noche. Se tomaron fotografías para documentación.

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La figura 40A muestra que el tratamiento con HB-EGF estimula el cierre del rayado y que el anticuerpo de la invención, U2-39, inhibe la migración mediada por HB-EGF de células de carcinoma escamoso epitelial CLS354 en el rayado.

Ejemplo 25B

Ensayo de transmigración - Inhibición de la migración inducida por HB-EGF de células de carcinoma epitelial Detroit 562 (faringe)

Se llevaron a cabo experimentos de transmigración para investigar si los anticuerpos de la invención bloquean la migración celular que de otra manera podría ser inducida directamente por HB-EGF.

Una suspensión de células de 500 ml de células de carcinoma epitelial humano ayunadas en suero (50,000 células) se puso en la cámara superior de pocillos de transferencia recubiertos con fibronectina (BD Falcon, poros de 8 µm). Alícuotas de 750 ml de medio (medio esencial mínimo (Eagle) en BSS de Earle con aminoácidos no esenciales, piruvato de sodio (1 mM) e hidrolizado de lactalbúmina (0.1%), 90%; suero bovino fetal 10%, Pen.-Strept., 0.1% de BSA) solo o que contenía 02 ng/ml de HB-EGF (R&D Systems) en presencia o ausencia de 10 µg/ml de anticuerpos humanos IgG, U-39 o Erbitux fueron puestos en la cámara inferior después de 30 minutos de pre-incubación a 37°C. Después de la incubación y migración durante 6 horas a 37°C, las células fueron fijadas,

teñidas con DAPI y los pocillos de transferencia se fotografiaron para evaluación.

El resultado demuestra que el anticuerpo HB-EGF U2-39 inhibe efectivamente la migración de células de carcinoma epitelial Detroit 562 inducida por HB-EGF comparable con la inhibición de migración celular mediada por HB-EGF por el tratamiento con Erbitux.

Ejemplo 26

Ensayo de angiogénesis celular a base de esferoides - Inhibición del brote celular endotelial estimulado por VEGF

Se llevaron a cabo ensayos de angiogénesis celular a base de esferoides para investigar si los anticuerpos de la invención son capaces de inhibir el brote de células endoteliales (EC) inducido por VEGF en una matriz de colágeno. Células endoteliales de vena umbilical humana primaria (HUVEC) fueron sembradas a 500 células en una gota colgante sobre cajas de plástico para permitir la agregación de esferoides durante la noche. 50 esferoides EC fueron sembrados en 0.9 ml de solución de colágeno (2 mg/ml) y pipeteadas en pocillos individuales de una placa de 24 pocillos para permitir la polimerización. El anticuerpo de la invención U2-39 se mezcló directamente en la solución de colágeno antes de la polimerización (concentraciones diferentes) y el factor de crecimiento VEGF-A (25 ng/ml) se añadió

después de 30 minutos por pipeteo de 100 µl de una dilución de trabajo concentrada 10 veces en la parte superior del gel polimerizado. Las placas fueron incubadas a 37°C durante 24 horas y fijadas al añadir 4% de paraformaldehído. La intensidad de brote de esferoides EC fue cuantificada mediante un sistema de análisis de imágenes que determinaba la longitud de brote acumulativa por esferoide usando un microscopio invertido y el software de formación de imágenes digitales Analysis 3.2.

La figura 41A ilustra la media de la longitud de brote acumulativa de 10 esferoides seleccionados aleatoriamente por punto de datos. La figura 41B muestra la inhibición relativa de la longitud de brote acumulativa de 10 esferoides seleccionados aleatoriamente por punto de datos por U2-39. El ajuste de curvas IC50 y cálculo de valores IC50 se llevó a cabo con GraphPad Prism 4.03.

Los resultados del ejemplo 26 demuestran que el anticuerpo de la invención U2-39 inhibe el brote de células endoteliales de vena umbilical humana estimulado por VEGF-A de una manera dependiente de dosis en el ensayo a base de esferoides usando una matriz de colágeno. El brote de HUVEC fue inhibido con un valor IC50 de 5.2×10^{-8} molar.

Ejemplo 27

Análisis de inmunohistoquímica (IHC) de muestras de xenoinjerto de tumor humano - inhibición de la tinción con CD31 de tumores *in vivo*

Para investigar la eficacia del anticuerpo de la invención, U2-39, en la inhibición de angiogénesis *in vivo*, xenoinjertos de tumor humano tratados con U2-39 o Erbitux fueron analizados mediante análisis de inmunohistoquímica.

La línea de células de adenocarcinoma ovárico humano EFO27 se manipuló genéticamente para sobre-expresar HB-EGF y el clon EFO27-C158 fue seleccionado para estudios de xenoinjerto en ratones SCID. $3x10^6$ Células EFO27-CI58 en 100 µl de PBS/Matrigel (1:1) fueron inyectadas subcutáneamente en el flanco izquierdo de ratones C.B-17 SCID hembra de 7 semanas de edad. Los ratones que portaban tumor con volúmenes de tumor medios de 250 mm^3 fueron aleatorizados en grupos que contenían 10 animales. Los animales se trataron intraperitonealmente con dosis semanales de 25 µg/kg de U2-39 o 25 mg/kg de Erbitux o vehículo de control, PBS, durante 3 semanas. Después de 28 días los ratones fueron sacrificados, los tejidos de tumor primarios fueron recogidos y una mitad del tumor se congeló rápidamente en nitrógeno líquido y se almacenó a -80°C.

Secciones de 5 a 8 µm del tumor preparado sobre portaobjetos de cámaras de video fueron fijados en 100% de

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acetona durante 10 minutos a 4°C y secados completamente. Para bloquear los sitios de unión no específica portaobjetos con secciones de tumor fijas fueron tratados con bloque de Avidin D (15 minutos), bloque de biotina (15 minutos) y una solución de BSA al 1.25% (1 hora). Entre cada etapa del tratamiento los portaobjetos se lavaron dos veces con PBS. Para el examen inmunohistoquímico de la vasculatura del tumor la expresión del marcador de células endoteliales clásico CD31, también conocido como PECAM-1 (Molécula de Adhesión a Células Endoteliales de Plaquetas-1) se analizó mediante tratamiento de los portaobjetos con 2 µg/ml de anticuerpo anti-CD31 (diluido en solución de BSA al 1.25% e incubado durante 2 horas a temperatura ambiente en una cámara humidificada). La detección se llevó a cabo al aplicar un anticuerpo IgG anti-rata de cabra biotinilado (30 min a temperatura ambiente) y Alexa 546 de estreptavidina (15 min en la oscuridad). Las etapas de lavado con PBS se llevaron a cabo entre cada etapa de tratamiento. Las secciones se montaron con el medio de montaje VECTASHIELD con DAPI en la oscuridad, se fotografiaron (microscopia de fluorescencia) para documentación y se almacenaron a 4°C.

La figura 42 demuestra que los xenoinjertos de tumor humano tratados con U2-39 muestran una tinción de marcador de células endoteliales reducida (tinción CD31) en comparación con los xenoinjertos de tumor tratados con

control o tratados con Erbitux. Este resultado demuestra la eficacia anti-angiogénica del anticuerpo de la invención *in vivo*.

Ejemplo 28

Modelo de xenoinjerto de tumor ovárico *in vivo*- tratamiento de combinación de U2-39 con cisplatino y Avastin

Para evaluar la eficacia antitumoral del anticuerpo de la invención administrado como una monoterapia o en combinación con cisplatino o Avastin, se llevó a cabo un estudio de xenoinjerto de cáncer ovárico.

La línea de células de adenocarcinoma ovárico humano EFO27 se manipuló genéticamente para sobre-expresar HB-EGF. El clon EFO27-CI58 se seleccionó para estudios de xenoinjerto en ratones SCID. $3x10^6$ Células EFO27-CI58 en 100 µl de PBS/Matrigel (1:1) fueron inyectadas subcutáneamente en el flanco izquierdo de ratones SCID C.B-17 hembra de 7 semanas de edad. Los ratones portadores de tumor con volúmenes de tumor medio entre 75 y 175 mm^3 fueron aleatorizados en grupos que contenían 10 animales. Los animales fueron tratados intraperitonealmente con dosis semanales de 25 mg/kg de U2-39, 25 mg/kg de Avastin o 5 mg/kg de cisplatino o vehículo de control, PBS. La combinación de U2-39 con Avastin se dio a 12.5 mg/kg cada una y la combinación de U2-39 con cisplatino se dio a 25 mg/kg de anticuerpo con 5 mg/kg de cisplatino. Los tamaños de tumor

primario se determinaron 3 veces por semana. Después de la medición con calibre, el tamaño del tumor se calculó de acuerdo con la fórmula W2xL/2 con L=longitud y W= el ancho perpendicular del tumor. Se usó el método de clasificación logarítmica de Kaplan-Meier para definir el tiempo a progresión hasta 500 mm^3 (definido como "evento" por razones estadísticas).

La figura 43A demuestra que la combinación de U2-39 con Cisplatino llevó a una reducción de tumor más fuerte durante el periodo de administración que el tratamiento con cisplatino solo. Además, una combinación de U2-39 y cisplatino retrasó el tiempo a progresión del tamaño de tumor medio a 500 mm^3 en comparación con la monoterapia con U2-39.

El resultado en la figura 43B muestra que la combinación de U2-39 con Avastin retrasó significativamente el tiempo a progresión a volúmenes de tumor de 500 mm^3 en comparación con el tratamiento con Avastin con monoterapia aunque sólo la mitad de la dosis de agente individual fue administrada.

Todas las patentes y publicaciones referenciadas o mencionadas en la presente son indicadoras de los niveles de capacidad de aquellos expertos en la técnica a la cual pertenece la invención, y cada una de estas patentes o publicaciones referenciadas se incorpora en la presente a manera de referencia al mismo grado que si se hubieran

incorporado en la presente por referencia en su totalidad individualmente o se mostraran en la presente en su totalidad. Los solicitantes se reservan el derecho de incorporar físicamente en esta descripción cualquiera y todos los materiales e información de cualquiera de estas patentes o publicaciones citadas.

Los métodos y composiciones específicos descritos en la presente son representativos de modalidades preferidas y son ejemplares y no se intenta que sean limitaciones del alcance de la invención. Otros objetivos, aspectos y modalidades ocurrirán para aquellos expertos en la técnica después de la consideración de esta descripción, y son abarcados dentro del espíritu de la invención como el definido por el alcance de las reivindicaciones. Será fácilmente aparente para alguien capacitado en la técnica que sustituciones y modificaciones variables pueden hacerse a la invención descrita en la presente sin alejarse del alcance y espíritu de la invención. La invención descrita en forma ilustrativa en la presente puede llevarse a la práctica adecuadamente en ausencia de cualquier elemento o elementos, o limitación o limitaciones, los cuales no se describan específicamente en la presente como esenciales. Los métodos y procesos descritos de manera ilustrativa en la presente de manera adecuada pueden llevarse a la práctica en diferentes órdenes de etapas, y no necesariamente están restringidos a

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los órdenes de etapas indicados en la presente o en las reivindicaciones. Según se usa en la presente y en las reivindicaciones anexas, las formas singulares "un", "uno" y "el" y "la" incluyen referencias plurales a menos que el contexto claramente indique lo contrario. Así, por ejemplo, una referencia a "un anticuerpo" incluye una pluralidad (por ejemplo, una solución de anticuerpos o una serie de preparaciones de anticuerpos) de estos anticuerpos, y así sucesivamente. Bajo ninguna circunstancia la patente puede ser interpretada como limitada a los ejemplos específicos o modalidades o métodos específicamente descritos aquí. Bajo ninguna circunstancia la patente puede interpretarse como limitada por ninguna declaración hecha por ningún examinador o cualquier otro funcionario o empleado de la Oficina de Patentes y Marcas a menos que esta declaración sea específicamente y sin calificación o reservación adoptada expresamente en una carta escrita por los solicitantes.

Los términos y expresiones que han sido empleados se usan como términos de descripción y no de limitación, y no existe la intención en el uso de estos términos y expresiones de excluir algún equivalente de las características mostradas o descritas o porciones de las mismas, sino que se reconoce que varias modificaciones son posibles dentro del alcance de la invención reclamada. Así, se entenderá que aunque la presente invención ha sido descrita específicamente por

modalidades preferidas y características opcionales, puede recurrirse a la modificación y variación de los conceptos aquí descritos por aquellos en la técnica, y estas modificaciones y variaciones se considera que están dentro del alcance de esta invención como el definido por las reivindicaciones anexas.

La invención ha sido descrita ampliamente y genéricamente en la presente. Cada una de las especies más estrechas y grupos subgenéricos que estén dentro de la descripción genérica también forman parte de la invención. Esto incluye la descripción genérica de la invención con una condición o limitación negativa que elimine cualquier materia del género, no obstante de si el material eliminado se describe o no específicamente en la presente.

REIVINDICACIONES

1. Una proteína de unión a antígeno aislada que se une a HB-EGF, caracterizada porque comprende:

A) una o más regiones de determinación de complementariedad de la cadena ligera (CDRL) seleccionadas del grupo que consiste en:

(i) una CDRL1 seleccionada del grupo que consiste en SEQ ID NOs: 189-217;

(ii) una CDRL2 seleccionada del grupo que consiste en SEQ ID NOs:218-233;

(iii) una CDRL3 seleccionada del grupo que consiste en SEQ ID NOs:234-274; y

(iv) una CDRL de (i), (ii) o (iii) que contiene una o más sustituciones, supresiones o inserciones de aminoácido de no más de cuatro aminoácidos; o

B) una o más regiones de determinación de complementariedad de la cadena pesada (CDRH) seleccionada del grupo que consiste en:

(i) una CDRH1 seleccionada del grupo que consiste en SEQ ID NOs:275-299;

(ii) una CDRH2 seleccionada del grupo que consiste en SEQ ID NOs:300-331;

(iii) una CDRH3 seleccionada del grupo que consiste en SEQ ID NOs:332-372; y

(iv) una CDRH de (i), (ii) o (iii) que contiene una o más sustituciones, supresiones o inserciones de aminoácido de no más de cuatro aminoácidos.

2. La proteína de unión a antígeno aislada de conformidad con la reivindicación 1, caracterizada porque comprende una o más CDRL de la cadena ligera de A), y una o más CDRH de la cadena pesada de B).

3. La proteína de unión a antígeno aislada de conformidad con la reivindicación 1, caracterizada porque comprende al menos dos CDRL de A) y al menos dos CDRH de B).

4. La proteína de unión a antígeno aislada de conformidad con la reivindicación 1, caracterizada porque comprende las CDRH 1, CDRH2, CDRH3, CDRL1, CDRL2 y CDRL3.

5. La proteína de unión a antígeno aislada de conformidad con la reivindicación 1, caracterizada porque

la CDRL de A) se selecciona del grupo que consiste en:

(i) una CDRL1 seleccionada del grupo que consiste en SEQ ID NOs:189-217;

(ii) una CDRL2 seleccionada del grupo que consiste en SEQ ID NOs:218-233;

(iii) una CDRL3 seleccionada del grupo que consiste en SEQ ID NOs:234-274; y

(iv) una CDRL de (i), (ii) o (iii) que contiene una o más sustituciones, supresiones o inserciones

de aminoácido de no más de dos aminoácidos;

la CDRH de B) se selecciona del grupo que consiste en:

(i) una CDRH1 seleccionada del grupo que consiste en SEQ ID NOs:275-299;

(ii) una CDRH2 seleccionada del grupo que consiste en SEQ ID NOs:300-331;

(iii) una CDRH3 seleccionada del grupo que consiste en SEQ ID NOs:332-372; y

(iv) una CDRH de (i), (ii) o (iii) que contiene una o más sustituciones, supresiones o inserciones de aminoácido de no más de dos aminoácidos; o

C) una o más CDRL de la cadena ligera de A) y una o más CDRH de la cadena pesada de B).

6. La proteína de unión a antígeno aislada de conformidad con la reivindicación 1, caracterizada porque comprende

A) una CDRL seleccionada del grupo que consiste en

(i) una CDRL1 seleccionada del grupo que consiste en SEQ ID NOs:189-217;

(ii) una CDRL2 seleccionada del grupo que consiste en SEQ ID NOs:218-233; y

(iii) una CDRL3 seleccionada del grupo que consiste en SEQ ID NOs:234-274;

B) una CDRH seleccionada del grupo que consiste en

(i) una CDRH1 seleccionada del grupo que consiste en SEQ ID NOs:275-299;

(ii) una CDRH2 seleccionada del grupo que consiste en SEQ ID NOs:300-331; y

(iii) una CDRH3 seleccionada del grupo que consiste en SEQ ID NOs:332-372; o

C) una o más CDRL de la cadena ligera de A) y una o más CDRH de la cadena pesada de B).

7. La proteína de unión a antígeno aislada de conformidad con la reivindicación 6, caracterizada porque comprende

A) una CDRL1 de SEQ ID NOs:189-217, una CDRL2 de SEQ ID NOs:218-233, y una CDRL3 de SEQ ID NOs:234-274, y/o

B) una CDRH1 de SEQ ID NOs:275-299, una CDRH2 de SEQ ID NOs:300-331, y una CDRH3 de SEQ ID NOs:332-372.

8. La proteína de unión a antígeno aislada de conformidad con la reivindicación 1, caracterizada porque comprende una región variable de la cadena ligera (V_L) que tiene al menos 80% de identidad de secuencia con una secuencia de aminoácidos seleccionada del grupo que consiste en SEQ ID NOs:94-141, y/o región variable de la cadena pesada (V_H) que tiene al menos 80% de identidad de secuencia con una secuencia de aminoácidos seleccionada del grupo que consiste en SEQ ID NOs:142-186.

9. La proteína de unión a antígeno aislada de

conformidad con la reivindicación 8, caracterizada porque la V_L tiene al menos 90% de identidad de secuencia con una secuencia de aminoácidos seleccionada del grupo que consiste en SEQ ID NOs:94-141, y/o la V_H tiene al menos 90% de identidad de secuencia con una secuencia de aminoácidos seleccionada del grupo que consiste en SEQ ID NOs: 142-186.

10. La proteína de unión a antígeno aislada de conformidad con la reivindicación 8, caracterizada porque la V_L se selecciona del grupo que consiste en SEQ ID NOs:94-141, y/o la V_H se selecciona del grupo que consiste en SEQ ID NOs: 142-186.

11. Una proteína de unión a antígeno aislada, caracterizada porque reconoce específicamente al menos un epítopo que contiene IHGE y/o un dominio tipo EGF de HB-EGF.

12. Una proteína de unión a antígeno aislada, caracterizada porque compite por la unión con la proteína de unión a antígeno de conformidad con la reivindicación 1.

13. Una proteína de unión a antígeno aislada que se une a HB-EGF, caracterizada porque comprende:

A) una o más CDR de la cadena ligera (CDRL) seleccionada del grupo que consiste en:

(i) una CDRL1 con al menos 80% de identidad de secuencia con SEQ ID NOs:189-217;

(ii) una CDRL2 con al menos 80% de identidad de secuencia con SEQ ID NOs:218-233; y

(iii) una CDRL3 con al menos 80% de identidad de secuencia con SEQ ID NOs:234-274;

B) una o más CDR de la cadena pesada (CDRH) seleccionada del grupo que consiste en:

(i) una CDRH1 con al menos 80% de identidad de secuencia con SEQ ID NOs:275-299;

(ii) una CDRH2 con al menos 80% de identidad de secuencia con SEQ ID NOs:300-331; y

(iii) una CDRH3 con al menos 80% de identidad de secuencia con SEQ ID NOs:332-372; o

C) una o más CDRL de la cadena ligera de A) y una o más CDRH de la cadena pesada de B).

14. La proteína de unión a antígeno aislada de conformidad con la reivindicación 13, caracterizada porque comprende:

A) una o más CDRL seleccionada del grupo que consiste en:

(i) una CDRL1 con al menos 90% de identidad de secuencia con SEQ ID NOs: 189-217;

(ii) una CDRL2 con al menos 90% de identidad de secuencia con SEQ ID NOs:218-233; y

(iii) una CDRL3 con al menos 90% de identidad de secuencia con SEQ ID NOs:234-274;

B) una o más CDRH seleccionada del grupo que consiste en:

(i) una CDRH 1 con al menos 90% de identidad de secuencia con SEQ ID NOs:275-299;

(ii) una CDRH2 con al menos 90% de identidad de secuencia con SEQ ID NOs:300-331; y

(iii) una CDRH3 con al menos 90% de identidad de secuencia con SEQ ID NOs:332-372; o

C) una o más CDRL de la cadena ligera de A) y una o más CDRH de la cadena pesada de B).

15. Una proteína de unión a antígeno aislada que se une a HB-EGF, caracterizada porque comprende:

A) una región de determinación de complementariedad de la cadena ligera (CDRL) seleccionada del grupo que consiste en

(i) una CDRL3 seleccionada del grupo que consiste en SEQ ID NOs:234-274,

(ii) una CDRL3 que difiere en secuencia de aminoácidos de la CDRL3 de (i) por una adición, supresión o sustitución de aminoácido de no más de dos aminoácidos; y

(iii) una secuencia de aminoácidos de CDRL3 seleccionada del grupo que consiste en

$X_1QX_2X_3X_4X_5PX_6X_7$ (SEQ ID NO:1046), en donde

X_1 se selecciona del grupo que consiste en I y M,

X_2 se selecciona del grupo que consiste en A, G y S,

X_3 se selecciona del grupo que consiste en I y T,

X_4 se selecciona del grupo que consiste en H y Q,

X_5 se selecciona del grupo que consiste en F, L y W,

$7X_6$ se selecciona del grupo que consiste en C, I, H, L y T,

X_7 se selecciona del grupo que consiste en S y T;

$QQX_1X_2X_3X_4X_5IT$ (SEQ ID NO:1047), en donde

X_1 se selecciona del grupo que consiste en I y S,

X_2 se selecciona del grupo que consiste en F y Y,

X_3 se selecciona del grupo que consiste en F, I, S y Y,

X_4 se selecciona del grupo que consiste en A, S y T,

X_5 se selecciona del grupo que consiste en P y S;

$X_1X_2X_3X_4X_5X_6X_7X_8T$ (SEQ ID NO: 1048), en donde

X_1 se selecciona del grupo que consiste en L y Q,

X_2 se selecciona del grupo que consiste en K,

N y Q,

X_3 se selecciona del grupo que consiste en A, H, S y Y,

X_4 se selecciona del grupo que consiste en H, N y Y,

X_5 se selecciona del grupo que consiste en N, S y T,

X_6 se selecciona del grupo que consiste en A, F, I, T, V y Y,

X_7 se selecciona del grupo que consiste en P y ningún aminoácido,

X_8 se selecciona del grupo que consiste en F, L y P;

$QX_1X_2DX_3LPX_4X_5$ (SEQ ID NO:1049), en donde

X_1 se selecciona del grupo que consiste en H y Q,

X_2 se selecciona del grupo que consiste en C y Y,

X_3 se selecciona del grupo que consiste en D, I, N, S y Y,

X_4 se selecciona del grupo que consiste en F, I y L,

X_5 se selecciona del grupo que consiste en A, S y T;

$QQX_1X_2X_3X_4PX_5X_6X_7$ (SEQ ID NO: 1050), en donde

X_1 se selecciona del grupo que consiste en H y Y,

X_2 se selecciona del grupo que consiste en G y N,

X_3 se selecciona del grupo que consiste en N y S,

X_4 se selecciona del grupo que consiste en S y W,

X_5 se selecciona del grupo que consiste en P y ningún aminoácido,

X_6 se selecciona del grupo que consiste en R y W,

X_7 se selecciona del grupo que consiste en S y T; y

$X_1QYX_2X_3X_4X_5X_6X_7F$ (SEQ ID NO: 1051), en donde

X_1 se selecciona del grupo que consiste en H y Q,

X_2 se selecciona del grupo que consiste en F y Y,

X_3 se selecciona del grupo que consiste en G, I y S,

X_4 se selecciona del grupo que consiste en F, I y T,

X_5 se selecciona del grupo que consiste en M, P, S y T,

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X_6 se selecciona del grupo que consiste en F, L, R y W,

X_7 se selecciona del grupo que consiste en S y T; y/o

B) una región de determinación de complementariedad de la cadena pesada (CDRH) seleccionada del grupo que consiste en

(i) una CDRH3 seleccionada del grupo que consiste en SEQ ID NOs:332-372,

(ii) una CDRH3 que difiere en secuencia de aminoácidos de la CDRH3 de (i) por una adición, supresión o sustitución de aminoácido de no más de dos aminoácidos; y

(iii) una secuencia de aminoácidos de CDRH3 seleccionada del grupo que consiste en

$X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}DX_{12}$ (SEQ ID NO:1065), en donde

X_1 se selecciona del grupo que consiste en E y S,

X_2 se selecciona del grupo que consiste en D, G y ningún aminoácido,

X_3 se selecciona del grupo que consiste en D, N y ningún aminoácido,

X_4 se selecciona del grupo que consiste en G y ningún aminoácido,

X_5 se selecciona del grupo que consiste en G y ningún aminoácido,

X_6 se selecciona del grupo que consiste en W, Y y ningún aminoácido,

X_7 se selecciona del grupo que consiste en I, N y Y,

X_8 se selecciona del grupo que consiste en A y Y,

X_9 se selecciona del grupo que consiste en G, V y Y,

X_{10} se selecciona del grupo que consiste en A, F y G,

X_{11} se selecciona del grupo que consiste en F, L y M,

X_{12} se selecciona del grupo que consiste en V y Y;

$QX_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}YX_{12}X_{13}X_{14}DX_{15}$ (SEQ ID NO:1066), en donde

X_1 se selecciona del grupo que consiste en G y ningún aminoácido,

X_2 se selecciona del grupo que consiste en K, L y Y,

X_3 se selecciona del grupo que consiste en A, G y S,

X_4 se selecciona del grupo que consiste en S, V y Y,

X_5 se selecciona del grupo que consiste en A y

G,

X_6 se selecciona del grupo que consiste en G y ningún aminoácido,

X_7 se selecciona del grupo que consiste en T y ningún aminoácido,

X_8 se selecciona del grupo que consiste en S y ningún aminoácido,

X_9 se selecciona del grupo que consiste en Y y ningún aminoácido,

X_{10} se selecciona del grupo que consiste en W y Y,

X_{11} se selecciona del grupo que consiste en G, S y Y,

X_{12} se selecciona del grupo que consiste en F y Y,

X_{13} se selecciona del grupo que consiste en G y ningún aminoácido,

X_{14} se selecciona del grupo que consiste en M y ningún aminoácido,

X_{15} se selecciona del grupo que consiste en V y Y;

$X_1X_2X_3X_4X_5X_6X_7XeX_9X_{10}X_{11}X_{12}X_{13}X_{14}$ (SEQ ID NO:1067), en donde

X_1 se selecciona del grupo que consiste en D, G, L, S y ningún aminoácido,

X_2 se selecciona del grupo que consiste en G, H, W, Y y ningún aminoácido,

X_3 se selecciona del grupo que consiste en A, F, W, Y y ningún aminoácido,

X_4 se selecciona del grupo que consiste en D, G, Q, T y ningún aminoácido,

X_5 se selecciona del grupo que consiste en G, I, Q, S y ningún aminoácido,

X_6 se selecciona del grupo que consiste en A, D, N, Q, S y ningún aminoácido,

X_7 se selecciona del grupo que consiste en G, Y y ningún aminoácido,

X_8 se selecciona del grupo que consiste en D, Y y ningún aminoácido,

X_9 se selecciona del grupo que consiste en Y y ningún aminoácido,

X_{10} se selecciona del grupo que consiste en A, E, N y Y,

X_{11} se selecciona del grupo que consiste en G, P, T, V y Y,

X_{12} se selecciona del grupo que consiste en F y I,

X_{13} se selecciona del grupo que consiste en D y Q,

X_{14} se selecciona del grupo que consiste en C,

H, V y Y;

$X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}DX_{18}$ (SEQ ID NO: 1068), en donde

X_1 se selecciona del grupo que consiste en E, D y ningún aminoácido,

X_2 se selecciona del grupo que consiste en G, R y ningún aminoácido,

X_3 se selecciona del grupo que consiste en I, V, Y y ningún aminoácido,

X_4 se selecciona del grupo que consiste en A, G, L y N,

X_5 se selecciona del grupo que consiste en A, G, V y W,

X_6 se selecciona del grupo que consiste en A, N, R y T,

X_7 se selecciona del grupo que consiste en G, N, P y ningún aminoácido,

X_8 se selecciona del grupo que consiste en G, T y ningún aminoácido,

X_9 se selecciona del grupo que consiste en A y ningún aminoácido,

X_{10} se selecciona del grupo que consiste en D, E y ningún aminoácido,

X_{11} se selecciona del grupo que consiste en S, Y y ningún aminoácido,

X_{12} se selecciona del grupo que consiste en G, Y y ningún aminoácido,

X_{13} se selecciona del grupo que consiste en N, Y y ningún aminoácido,

X_{14} se selecciona del grupo que consiste en Y y ningún aminoácido,

X_{15} se selecciona del grupo que consiste en D, Y y ningún aminoácido,

X_{16} se selecciona del grupo que consiste en A, G y ningún aminoácido,

X_{17} se selecciona del grupo que consiste en F y M,

X_{18} se selecciona del grupo que consiste en I, V y Y;

$X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}X_{18}X_{19}X_{20}X_{21}X_{22}X_{23}$ (SEQ ID NO: 1069), en donde

X_1 se selecciona del grupo que consiste en A, D, G, S y T,

X_2 se selecciona del grupo que consiste en A, E, G, L, N, R, Y y ningún aminoácido,

X_3 se selecciona del grupo que consiste en A, G, L, N, R, T, Y y ningún aminoácido,

X_4 se selecciona del grupo que consiste en D, G, R, S, V, Y y ningún aminoácido,

X_5 se selecciona del grupo que consiste en A,

G, I, S, V, Y y ningún aminoácido,

X_6 se selecciona del grupo que consiste en F, G, L, R, V y ningún aminoácido,

X_7 se selecciona del grupo que consiste en L, T, Y y ningún aminoácido,

X_8 se selecciona del grupo que consiste en Y y ningún aminoácido,

X_9 se selecciona del grupo que consiste en Y y ningún aminoácido,

X_{10} se selecciona del grupo que consiste en D y ningún aminoácido,

X_{11} se selecciona del grupo que consiste en S y ningún aminoácido,

X_{12} se selecciona del grupo que consiste en S y ningún aminoácido,

X_{13} se selecciona del grupo que consiste en G y ningún aminoácido,

X_{14} se selecciona del grupo que consiste en D, L, M, S, Y y ningún aminoácido,

X_{15} se selecciona del grupo que consiste en H, I, P, V, W y ningún aminoácido,

X_{16} se selecciona del grupo que consiste en F, G, L, R, S, Y y ningún aminoácido,

X_{17} se selecciona del grupo que consiste en D, F, V, W, Y y ningún aminoácido,

X_{18} se selecciona del grupo que consiste en C, F, L, P, S y Y,

X_{19} se selecciona del grupo que consiste en D, F, G y Y,

X_{20} se selecciona del grupo que consiste en A, C, G, P, R, V y Y,

X_{21} se selecciona del grupo que consiste en F, L, M, S y ningún aminoácido,

X_{22} se selecciona del grupo que consiste en A, D y ningún aminoácido,

X_{23} se selecciona del grupo que consiste en I, L, V, Y y ningún aminoácido;

$X_1YSSGWX_2X_3YGX_4X_5DX_6$ (SEQ ID NO: 1070), en donde

X_1 se selecciona del grupo que consiste en M y V,

X_2 se selecciona del grupo que consiste en S y ningún aminoácido,

X_3 se selecciona del grupo que consiste en F y ningún aminoácido,

X_4 se selecciona del grupo que consiste en V y ningún aminoácido,

X_5 se selecciona del grupo que consiste en F y M,

X_6 se selecciona del grupo que consiste en V y Y; y

$RX_1X_2X_3PFX_4Y$ (SEQ ID NO:1071), en donde

X_1 se selecciona del grupo que consiste en G, H, L, N y R,

X_2 se selecciona del grupo que consiste en E, T y W,

X_3 se selecciona del grupo que consiste en L, N, T y V,

X_4 se selecciona del grupo que consiste en D y E.

16. La proteína de unión a antígeno aislada de conformidad con la reivindicación 15, caracterizada porque comprende además:

A) una CDRL seleccionada del grupo que consiste en:

(i) una CDRL1 seleccionada del grupo que consiste en SEQ ID NOs:189-217;

(ii) una CDRL1 que difiere en secuencia de aminoácidos de la CDRL1 de (i) por una adición, supresión o sustitución de aminoácido de no más de dos aminoácidos;

(iii) una secuencia de aminoácidos de CDRL1 seleccionada del grupo que consiste en

$X_1SSQSLX_2X_3SDGX_4TYLX_5$ (SEQ ID NO:1035), en donde

X_1 se selecciona del grupo que consiste en K y R,

X_2 se selecciona del grupo que consiste en L y V,

X_3 se selecciona del grupo que consiste en H y Y,

X_4 se selecciona del grupo que consiste en K y N,

X_5 se selecciona del grupo que consiste en N, S y Y;

$RASQX_1ISX_2YLN$ (SEQ ID NO: 1036), en donde

X_1 se selecciona del grupo que consiste en R, S y T,

X_2 se selecciona del grupo que consiste en R y S;

$RASQX_1IX_2X_3X_4LX_5$ (SEQ ID NO: 1037), en donde

X_1 se selecciona del grupo que consiste en D, G, S y T,

X_2 se selecciona del grupo que consiste en A, R y S,

X_3 se selecciona del grupo que consiste en H, I, N, R, S y T,

X_4 se selecciona del grupo que consiste en D, W y Y,

X_5 se selecciona del grupo que consiste en A, G y N;

$QASQDIX_1X_2X_3LN$ (SEQ ID NO: 1038), en donde

X_1 se selecciona del grupo que consiste en S y T,

X_2 se selecciona del grupo que consiste en D y N,

X_3 se selecciona del grupo que consiste en S y Y;

RASQX_1V$X_2X_3X_4X_5$LA (SEQ ID NO:1039), en donde

X_1 se selecciona del grupo que consiste en S y T,

X_2 se selecciona del grupo que consiste en I y S,

X_3 se selecciona del grupo que consiste en R y S,

X_4 se selecciona del grupo que consiste en S, N y ningún aminoácido,

X_5 se selecciona del grupo que consiste en Y y ningún aminoácido; y

KSSQX_1X_2LX_3X_4SNNKNYLX_5 (SEQ ID NO:1040), en donde X_1 se selecciona del grupo que consiste en N y S,

X_2 se selecciona del grupo que consiste en I y V,

X_3 se selecciona del grupo que consiste en D y Y,

X_4 se selecciona del grupo que consiste en N, R y S,

X_5 se selecciona del grupo que consiste en A y V;

(iv) una CDRL2 seleccionada del grupo que consiste en SEQ ID NOs:218-233;

(v) una CDRL2 que difiere en secuencia de aminoácidos de la CDRL2 de (iv) por una adición, supresión o sustitución de aminoácido de no más de dos aminoácidos; y

(vi) una secuencia de aminoácidos de CDRL2 seleccionada del grupo que consiste en

$X_1X_2SNX_3X_4S$ (SEQ ID NO:1041), en donde

X_1 se selecciona del grupo que consiste en E y K,

X_2 se selecciona del grupo que consiste en I y V,

X_3 se selecciona del grupo que consiste en R y W,

X_4 se selecciona del grupo que consiste en D y F;

$X_1X_2SX_3LQS$ (SEQ ID NO: 1042), en donde

X_1 se selecciona del grupo que consiste en A y T,

X_2 se selecciona del grupo que consiste en A, E y V,

X_3 se selecciona del grupo que consiste en S y T;

X_1ASX_2LQS (SEQ ID NO:1043), en donde

X_1 se selecciona del grupo que consiste en A y

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V,

X_2 se selecciona del grupo que consiste en S y T;

$DASX_1LET$ (SEQ ID NO:1044), en donde

X_1 se selecciona del grupo que consiste en I y N;

GASSRAT (SEQ ID NO:223); y

$WASX_1RES$ (SEQ ID NO: 1045), en donde

X_1 se selecciona del grupo que consiste en A y T; o

B) una CDRH seleccionada del grupo que consiste en:

(i) una CDRH1 seleccionada del grupo que consiste en SEQ ID NOs:275-299;

(ii) una CDRH1 que difiere en secuencia de aminoácidos de la CDRH1 de (i) por una adición, supresión o sustitución de aminoácido de no más de dos aminoácidos;

(iii) una secuencia de aminoácidos de CDRH1 seleccionada del grupo que consiste en

$GYTX_1TX_2X_3X_4X_5X_6$ (SEQ ID NO: 1052), en donde

X_1 se selecciona del grupo que consiste en F y L,

X_2 se selecciona del grupo que consiste en E, G y S,

X_3 se selecciona del grupo que consiste en H, L y Y,

X_4 se selecciona del grupo que consiste en G, S y Y,

X_5 se selecciona del grupo que consiste en I y M,

X_6 se selecciona del grupo que consiste en H y S;

$GYX_1FTSYWIG$ (SEQ ID NO: 1053), en donde

X_1 se selecciona del grupo que consiste en R y S;

$GFTFX_1SX_2X_3MH$ (SEQ ID NO: 1054), en donde

X_1 se selecciona del grupo que consiste en R y S,

X_2 se selecciona del grupo que consiste en H y Y,

X_3 se selecciona del grupo que consiste en D y G;

$GFX_1FSX_2YX_3MX_4$ (SEQ ID NO:1055), en donde

X_1 se selecciona del grupo que consiste en P y T,

X_2 se selecciona del grupo que consiste en A, R y S,

X_3 se selecciona del grupo que consiste en A y S,

X_4 se selecciona del grupo que consiste en N y S;

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$GX_1SX_2SX_3X_4X_5X_6X_7WX_8$ (SEQ ID NO:1056), en donde

X_1 se selecciona del grupo que consiste en D y G,

X_2 se selecciona del grupo que consiste en F, I y V,

X_3 se selecciona del grupo que consiste en R, S y ningún aminoácido,

X_4 se selecciona del grupo que consiste en G, Y y ningún aminoácido,

X_5 se selecciona del grupo que consiste en D, G, S y ningún aminoácido,

X_6 se selecciona del grupo que consiste en A, S y Y,

X_7 se selecciona del grupo que consiste en A y Y,

X_8 se selecciona del grupo que consiste en N y S;

GFSLSNARMGVS (SEQ ID NO:279); y

$GFSLX_1TGGVGVG$ (SEQ ID NO: 1057), en donde

X_1 se selecciona del grupo que consiste en S y N;

(iv) una CDRH2 seleccionada del grupo que consiste en SEQ ID NOs:300-331;

(v) una CDRH2 que difiere en secuencia de aminoácidos de la CDRH2 de (iv) por una adición, supresión o

sustitución de aminoácido de no más de dos aminoácidos; y

(vi) una secuencia de aminoácidos de CDRH2 seleccionada del grupo que consiste en

$X_1X_2X_3X_4X_5X_6GX_7TX_8X_9X_{10}QKX_{11}X_{12}$ (SEQ ID NO:1058), en donde X_1 se selecciona del grupo que consiste en S y W,

X_2 se selecciona del grupo que consiste en F y I,

X_3 se selecciona del grupo que consiste en D, N y S,

X_4 se selecciona del grupo que consiste en A y P,

X_5 se selecciona del grupo que consiste en E, N y S,

X_6 se selecciona del grupo que consiste en D, N y S,

X_7 se selecciona del grupo que consiste en E, G y N,

X_8 se selecciona del grupo que consiste en I y N,

X_9 se selecciona del grupo que consiste en C, H y Y,

X_{10} se selecciona del grupo que consiste en A y T,

X_{11} se selecciona del grupo que consiste en F y

L,

X_{12} se selecciona del grupo que consiste en D y G;

IIYPX_1DSDX_2RYSPSFQG (SEQ ID NO: 1059), en donde

X_1 se selecciona del grupo que consiste en D y G,

X_2 se selecciona del grupo que consiste en A, I y T;

X_1IX_2X_3DGS$X_4X_5X_6$YX_7DSVX_8G (SEQ ID NO:1060), en donde

X_1 se selecciona del grupo que consiste en F y V,

X_2 se selecciona del grupo que consiste en S y W,

X_3 se selecciona del grupo que consiste en D, S y Y,

X_4 se selecciona del grupo que consiste en I, N y T,

X_5 se selecciona del grupo que consiste en K y Q,

X_6 se selecciona del grupo que consiste en N, R y Y,

X_7 se selecciona del grupo que consiste en A, T y V,

X_8 se selecciona del grupo que consiste en K y R;

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$X_1ISX_2SX_3X_4X_5X_6YYADSVKG$ (SEQ ID NO:1061), en donde

X_1 se selecciona del grupo que consiste en A, H y Y,

X_2 se selecciona del grupo que consiste en G, R y S,

X_3 se selecciona del grupo que consiste en G y S,

X_4 se selecciona del grupo que consiste en G, R y S,

X_5 se selecciona del grupo que consiste en S, T y Y,

X_6 se selecciona del grupo que consiste en I y T;

$X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}YX_{12}X_{13}SX_{14}KS$ (SEQ ID NO: 1062), en donde

X_1 se selecciona del grupo que consiste en E, R y Y,

X_2 se selecciona del grupo que consiste en I y T,

X_3 se selecciona del grupo que consiste en H, N y Y,

X_4 se selecciona del grupo que consiste en C, H, S, T y Y,

X_5 se selecciona del grupo que consiste en S y R,

X_6 se selecciona del grupo que consiste en G y S,

X_7 se selecciona del grupo que consiste en G, K, S y T,

X_8 se selecciona del grupo que consiste en T y W,

X_9 se selecciona del grupo que consiste en N y Y,

X_{10} se selecciona del grupo que consiste en N y ningún aminoácido,

X_{11} se selecciona del grupo que consiste en D y ningún aminoácido,

X_{12} se selecciona del grupo que consiste en A y N,

X_{13} se selecciona del grupo que consiste en P y V,

X_{14} se selecciona del grupo que consiste en L y V;

X_1IFSNDEKSYSTSLKS (SEQ ID NO:1063), en donde

X_1 se selecciona del grupo que consiste en H y Ll; y

LIYWNX_1X_2KRYSPSLX_3S (SEQ ID NO: 1064), en donde

X_1 se selecciona del grupo que consiste en D y V,

X_2 se selecciona del grupo que consiste en D y

E,

X_3 se selecciona del grupo que consiste en K y R.

17. La proteína de unión a antígeno aislada de conformidad con la reivindicación 16, caracterizada porque comprende la primera secuencia de aminoácidos y la segunda secuencia de aminoácidos.

18. La proteína de unión a antígeno aislada de conformidad con la reivindicación 17, caracterizada porque la primera secuencia de aminoácidos está unida covalentemente a la segunda secuencia de aminoácidos.

19. La proteína de unión a antígeno aislada de conformidad con la reivindicación 17, caracterizada porque la primera secuencia de aminoácidos comprende la CDRL3 de SEQ ID NOs:234-274, CDRL2 de SEQ ID NOs:218-233, y CDRL1 de SEQ ID NOs: 189-217, y la segunda secuencia de aminoácidos comprende la CDRH3 de SEQ ID NOs:332-372, CDRH2 de SEQ ID NOs:300-331, y CDRH1 de SEQ ID NOs:275-299.

20. La proteína de unión a antígeno aislada de conformidad con cualquier reivindicación 1-19, caracterizada porque es un anticuerpo monoclonal, un anticuerpo policlonal, un anticuerpo recombinante, un anticuerpo humano, un anticuerpo humanizado, un anticuerpo quimérico, un anticuerpo multiespecífico, o un fragmento de anticuerpo de los mismos.

21. La proteína de unión a antígeno aislada de

conformidad con la reivindicación 20, caracterizada porque el fragmento de anticuerpo es un fragmento Fab, un fragmento Fab', un fragmento $F(ab')_2$, un fragmento Fv, un dicuerpo o una molécula de anticuerpo de cadena individual.

22. La proteína de unión a antígeno aislada de conformidad con la reivindicación 20, caracterizada porque es un anticuerpo humano.

23. La proteína de unión a antígeno aislada de conformidad con la reivindicación 20, caracterizada porque la proteína de unión a antígeno es un anticuerpo monoclonal.

24. La proteína de unión a antígeno aislada de conformidad con cualquiera de las reivindicaciones 1-19, caracterizada porque es del tipo IgG1, lgG2, lgG3 o lgG4.

25. La proteína de unión a antígeno aislada de conformidad con la reivindicación 24, caracterizada porque es del tipo lgG2 o lgG4.

26. La proteína de unión a antígeno aislada de conformidad con cualquiera de las reivindicaciones 1-19, caracterizada porque es acoplada a un grupo marcador.

27. La proteína de unión a antígeno aislada de conformidad con la reivindicación 26, caracterizada porque el grupo marcador es un radioisótopo, radionúclido, un grupo fluorescente, un grupo enzimático, un grupo quimioluminiscente, un grupo biotinilo, o un grupo polipéptido predeterminado.

28. La proteína de unión a antígeno aislada de conformidad con cualquiera de las reivindicaciones 1-19, caracterizada porque es acoplada a un grupo efector.

29. La proteína de unión a antígeno aislada de conformidad con la reivindicación 28, caracterizada porque el grupo efector es un radioisótopo, un radionúclido, una toxina, un grupo terapéutico o un grupo quimioterapéutico.

30. La proteína de unión a antígeno aislada de conformidad con la reivindicación 29, caracterizada porque el grupo terapéutico o grupo quimioterapéutico es caliqueamicina, auristatina-PE, geldanamicina, maitansina o derivados de las mismas.

31. Una proteína de unión a antígeno aislada, caracterizada porque compite por la unión a HB-EGF humano con la proteína de unión a antígeno de conformidad con cualquiera de las reivindicaciones 1-19.

32. La proteína de unión a antígeno aislada de conformidad con la reivindicación 31, caracterizada porque es un anticuerpo monoclonal, un anticuerpo policlonal, un anticuerpo recombinante, un anticuerpo humano, un anticuerpo humanizado, un anticuerpo quimérico, un anticuerpo multiespecífico, o un fragmento de anticuerpo de los mismos.

33. La proteína de unión a antígeno aislada de conformidad con la reivindicación 32, caracterizada porque el fragmento de anticuerpo es un fragmento Fab, un fragmento

Fab', un fragmento $F(ab')_2$, un fragmento Fv, un dicuerpo o una molécula de anticuerpo de cadena individual.

34. La proteína de unión a antígeno aislada de conformidad con la reivindicación 32, caracterizada porque es un anticuerpo humano.

35. La proteína de unión a antígeno aislada de conformidad con la reivindicación 32, caracterizada porque la proteína de unión a antígeno es un anticuerpo monoclonal.

36. La proteína de unión a antígeno aislada de conformidad con la reivindicación 31, caracterizada porque es del tipo IgG1, lgG2, lgG3 o lgG4.

37. La proteína de unión a antígeno aislada de conformidad con la reivindicación 36, caracterizada porque es del tipo lgG2 o lgG4.

38. La proteína de unión a antígeno aislada de conformidad con la reivindicación 31, caracterizada porque es acoplada a un grupo marcador.

39. La proteína de unión a antígeno aislada de conformidad con la reivindicación 38, caracterizada porque el grupo marcador es un radioisótopo, radionúclido, un grupo fluorescente, un grupo enzimático, un grupo quimioluminiscente, un grupo biotinilo, o un grupo polipéptido predeterminado.

40. La proteína de unión a antígeno aislada de conformidad con la reivindicación 31, caracterizada porque es

acoplada a un grupo efector.

41. La proteína de unión a antígeno aislada de conformidad con la reivindicación 40, caracterizada porque el grupo efector es un radioisótopo, un radionúclido, una toxina, un grupo terapéutico o un grupo quimioterapéutico.

42. La proteína de unión a antígeno aislada de conformidad con la reivindicación 41, caracterizada porque el grupo terapéutico o grupo quimioterapéutico es caliqueamicina, auristatina-PE, geldanamicina, maitansina o derivados de las mismas.

43. La proteína de unión a antígeno aislada de conformidad con cualquiera de las reivindicaciones 1-19, caracterizada porque reduce al menos parcialmente la transducción de señales mediada por HB-EGF.

44. Una molécula de ácido nucleico caracterizada porque codifica para la proteína de unión a antígeno aislada de conformidad con cualquiera de las reivindicaciones 1-19.

45. La molécula de ácido nucleico de conformidad con la reivindicación 44, caracterizada porque está enlazada operablemente a una secuencia de control.

46. Un vector caracterizado porque comprende la molécula de ácido nucleico de conformidad con la reivindicación 44.

47. Un vector caracterizado porque comprende la molécula de ácido nucleico de conformidad con la

reivindicación 45.

48. Una célula hospedera caracterizada porque comprende la molécula de ácido nucleico de conformidad con la reivindicación 45.

49. Una célula hospedera caracterizada porque comprende el vector de conformidad con cualquiera de la reivindicación 46 ó 47.

50. Un método para elaborar la proteína de unión a antígeno de conformidad con cualquiera de las reivindicaciones 1-19, caracterizado porque comprende la etapa de preparar la proteína de unión a antígeno a partir de una célula hospedera que secrete la proteína de unión a antígeno.

51. Una composición farmacéutica caracterizada porque comprende al menos una proteína de unión a antígeno de conformidad con cualquiera de las reivindicaciones 1-19, y portadores, diluyentes y/o adyuvantes farmacéuticamente aceptables.

52. La composición farmacéutica de conformidad con la reivindicación 51, caracterizada porque comprende además un agente activo adicional.

53. La composición farmacéutica de conformidad con la reivindicación 52, caracterizada porque el por lo menos un agente activo adicional es un agente antineoplásico.

54. La composición farmacéutica de conformidad con

la reivindicación 53, caracterizada porque el agente antineoplásico es un anticuerpo anti-tumor.

55. La composición farmacéutica de conformidad con la reivindicación 54, caracterizada porque el anticuerpo anti-tumor es un anticuerpo dirigido contra una tirosina cinasa receptora.

56. La composición farmacéutica de conformidad con la reivindicación 53, caracterizada porque el anticuerpo anti-tumor es dirigido contra EGFR.

57. La composición farmacéutica de conformidad con la reivindicación 51, caracterizada porque es para el diagnóstico, prevención o tratamiento de una enfermedad hiperproliferativa.

58. La composición farmacéutica de conformidad con la reivindicación 57, caracterizada porque la enfermedad hiperproliferativa está asociada con expresión de HB-EGF.

59. La composición farmacéutica de conformidad con la reivindicación 57, caracterizada porque la enfermedad hiperproliferativa está asociada con o acompañada por, por ejemplo, una activación alterada patológicamente incrementada, del receptor de factor de crecimiento.

60. La composición farmacéutica de conformidad con la reivindicación 59, caracterizada porque la activación patológicamente incrementada del receptor de factor de crecimiento está asociada con o es causada por un incremento

patológico en la actividad de una proteína G y/o un receptor acoplado a proteína G.

61. La composición farmacéutica de conformidad con la reivindicación 51, caracterizada porque es para el diagnóstico, prevención o tratamiento de cáncer.

62. La composición farmacéutica de conformidad con la reivindicación 61, caracterizada porque el cáncer se selecciona del grupo que consiste en cáncer de seno, cáncer gastrointestinal, cáncer de páncreas, cáncer de próstata, cáncer ovárico, cáncer de estómago, cáncer endometrial, cáncer de glándulas salivales, cáncer pulmonar, cáncer de riñón, cáncer de colon, cáncer colorrectal, cáncer de tiroides, cáncer de vejiga, glioma, melanoma, carcinoma, en particular carcinoma epitelial o escamoso, otros cánceres que expresen o sobre-expresen HB-EGF y formación de metástasis tumorales.

63. Uso de al menos una la proteína de unión a antígeno de conformidad con las reivindicaciones 1-19, en la elaboración de una composición farmacéutica para el diagnóstico, prevención o tratamiento de una enfermedad hiperproliferativa.

64. El uso de conformidad con la reivindicación 63, en donde la enfermedad hiperproliferativa es una enfermedad hiperproliferativa como la definida en la reivindicación 58.

65. Un método para diagnosticar una afección

asociada con la expresión de HB-EGF, caracterizado porque comprende poner en contacto una muestra con la proteína de unión a antígeno de conformidad con las reivindicaciones 1-19, y determinar la presencia de HB-EGF en la muestra.

66. El método de conformidad con la reivindicación 65, caracterizado porque la afección es una enfermedad hiperproliferativa como la definida en la reivindicación 58.

67. Un método para prevenir o tratar una afección asociada con la expresión de HB-EGF en un paciente, caracterizado porque comprende administrar a un paciente que lo requiera una cantidad efectiva de al menos una proteína de unión a antígeno de conformidad con las reivindicaciones 57 a 60.

68. El método de conformidad con la reivindicación 62, caracterizado porque la afección es una enfermedad hiperproliferativa como la definida en cualquiera de las reivindicaciones 57-60.

69. El método de conformidad con la reivindicación 57, caracterizado porque el paciente es un paciente mamífero.

70. Un kit caracterizado porque comprende la proteína de unión a antígeno de conformidad con las reivindicaciones 1-19, la molécula de ácido nucleico de conformidad con la reivindicación 44 ó 45 o el vector de conformidad con la reivindicación 46 ó 47.

71. El kit de conformidad con la reivindicación 70,

caracterizado porque comprende al menos un agente activo adicional.

72. El kit de conformidad con la reivindicación 71, caracterizado porque el agente activo adicional es un agente antineoplásico.

73. La composición farmacéutica de conformidad con la reivindicación 53, caracterizada porque el agente antineoplásico es cisplatino o Avastin.

74. La composición farmacéutica de conformidad con cualquiera de las reivindicaciones 51 a 62, caracterizada porque es para ser administrada como monoterapia o en combinación con una composición farmacéutica adicional que comprenda preferiblemente un agente antineoplásico tal como cisplatino o Avastin.

RESUMEN DE LA INVENCIÓN

Se proporcionan en la presente proteínas de unión a antígeno, por ejemplo, anticuerpos humanos y/o monoclonales que tienen afinidad para factor de crecimiento tipo factor de crecimiento epidérmico de unión a heparina (HB-EGF) y neutralizan las funciones biológicas de este factor de crecimiento.

U-V_L-1 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:94)**

DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWFQQRPGQSPRRLIYKVSNWDSGVPDRFNGSGSGTDFTLKISRVEAEDVG

CDR1 CDR2

VYYCMQSTHWPITFGQGTRLEIK

CDR3

U-V_L-2 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:95)**

DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWFQQRPGQSPRRLIYKVSNWDSGVPDRFSGSGSGTDFTLKISRVEAEDVG

CDR1 CDR2

VYYCIQGTHWPTTFGQGTRLEIK

CDR3

U-V_L-3 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:96)**

DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWLQQRPGQSPRRLIYKVSNWDSGVPDRFSGSGSGTDFTLKISRVEAEDVG

CDR1 CDR2

VYYCMQGTHWPITFGQGTRLEIK

CDR3

U-V_L-4 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:96)**

DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWLQQRPGQSPRRLIYKVSNWDSGVPDRFSGSGSGTDFTLKISRVEAEDVG

CDR1 CDR2

VYYCMQGTHWPITFGQGTRLEIK

CDR3

FIGURA 1A

U-V_L-5 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:97)**

DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWYLQKPGQPPQLLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVG
CDR1 CDR2

VYYCMQGIQLPCSFGQGTKLEIK
CDR3

U-V_L-6 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:98)**

DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWYLQKPGQPPQLLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVG
CDR1 CDR2

VYYCMQSIQLPLTFGGGTKVEIK
CDR3

U-V_L-7 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:98)**

DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWYLQKPGQPPQLLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVG
CDR1 CDR2

VYYCMQSIQLPLTFGGGTKVEIK
CDR3

U-V_L-8 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:99)**

DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWFLQKPGQPPQPLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVG
CDR1 CDR2

VYYCMQSIQLPITFGHGTRLEIK
CDR3

FIGURA 1B

U-V_L-9 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:99)**

DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWFLQKPGQPPQPLIYEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVG
CDR1 CDR2

VYYCMQSIQLPITFGHGTRLEIK
CDR3

U-V_L-11 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:100)**

DIQMTQSPSSLSASVGDRVTITCRASQGIANYLAWYQQKPGKVPKLLIYVASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQ
CDR1 CDR2

NYNSAPFTFGPGTKVDIK
CDR3

U-V_L-12 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:101)**

DIQMTQSPSSLSASVGDRVTIICRASQGISNDLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQ
CDR1 CDR2

KYNSVPLTFGGGTKVEIK
CDR3

U-V_L-13 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:102)**

NIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYKISNRFSGVPDRFSGSGAGTDFTLKISRVEAEDVG
CDR1 CDR2

VYYCMQATQFPHTFGPGTKVDIK
CDR3

FIGURA 1C

U-V_L-14 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:102)**

NIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYKISNRFSGVPDRFSGSGAGTDFTLKISRVEAEDVG
CDR1 CDR2

VYYCMQATQFPHTFGPGTKVDIK
CDR3

U-V_L-15 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:103)**

EIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYKISNRFSGVPDRFSGTGAGTDFTLKISRVEAEDVG
CDR1 CDR2

VYYCMQATQFPHTFGGGTKVEIK
CDR3

U-V_L-16 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:104)**

EIVLTQSPGTLSLSPGERATLSCRASQTVISSYLAWYQQKPGQAPRLLISGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC
CDR1 CDR2

QQYGSSPRTFGQGTKVEIK
CDR3

U-V_L-17 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:105)**

EIVLTQSPGTLSLSPGERATLSCRASQSVSRLAWYQQKPGQAPRLLIYGASRRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQ
CDR1 CDR2

YGSSPRSFGQGTKLEIK
CDR3

FIGURA 1D

U-V_L-18 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:106)**

DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCL
CDR1 CDR2

QHNSYPPTFGQGTKVEIK
CDR3

U-V_L-19 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:107)**

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLVWYQQKPGQPPKLFIYWASTRESGVPDRFTGSGSGTDFTLTISSLQAEDV
CDR1 CDR2

AVYYCQQYYSFPWTFGQGTKVEIK
CDR3

U-V_L-20 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:107)**

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLVWYQQKPGQPPKLFIYWASTRESGVPDRFTGSGSGTDFTLTISSLQAEDV
CDR1 CDR2

AVYYCQQYYSFPWTFGQGTKVEIK
CDR3

U-V_L-21 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:108)**

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDV
CDR1 CDR2

AVYYCQQYYSTTWTFGQGTKVEIK
CDR3

FIGURA 1E

U-V_L-22 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:109)**

DIVMTQSPDSLAVSLGERATINCKSSQNVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDV
CDR1 CDR2

AVYFCQQYYGTPRTFGQGTKVEIK
CDR3

U-V_L-23 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:110)**

DIVMTQSPDSLAVSLGERATINCKSSQNVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDV
CDR1 CDR2

AVYFCQQYYGTPRTFGQGTKVEIK
CDR3

U-V_L-24 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:111)**

DIVMTQSPDSLTVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFGGSGSGTDFTLTISSLQAEDV
CDR1 CDR2

AVYYCQQYYSISRTFGQGTKVEIK
CDR3

U-V_L-25 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:111)**

DIVMTQSPDSLTVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFGGSGSGTDFTLTISSLQAEDV
CDR1 CDR2

AVYYCQQYYSISRTFGQGTKVEIK
CDR3

FIGURA 1F

U-V_L-26 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:112)**

DIVMTQSPDSLAVSLGERATINCKSSQSVLYNSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQADDV
CDR1 CDR2

AVYYCQQYYSTTWTFGPGTKVEIK
CDR3

U-V_L-27 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:113)**

DIVMTQSPDSLAVSLGERATINCKSSQSVLYNSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQADDV
CDR1 CDR2

AVYYCQQYYSTTWTFGPGTKVEIK
CDR3

U-V_L-28 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:114)**

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKVLIYWASTRKSGVPDRFSGSGSGTDFTLTISGLQAEDV
CDR1 CDR2

ALYYCQQYYSTMFSFGQGTKLEIK
CDR3

U-V_L-29 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:114)**

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKVLIYWASTRKSGVPDRFSGSGSGTDFTLTISGLQAEDV
CDR1 CDR2

ALYYCQQYYSTMFSFGQGTKLEIK
CDR3

FIGURA 1G

U-V_L-30 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:115)**

DIVMTQSPDSLAVSLGERATINCKSSQSVLDSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDV
CDR1 CDR2

AVFYCHQYYSTPLTFGGGTKVAIK
CDR3

U-V_L-31 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:115)**

DIVMTQSPDSLAVSLGERATINCKSSQSVLDSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDV
CDR1 CDR2

AVFYCHQYYSTPLTFGGGTKVAIK
CDR3

U-V_L-32 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:116)**

DIVMTQSPDSLAVSLGERATINCKSSQSILYRSNNKNYLAWYQQKPGQPPKLLIYWASARESGVPDRFSGSGSGTDFTLTISSLQAEDV
CDR1 CDR2

AVYFCQQYFITPLTFGGGTKVEIK
CDR3

U-V_L-33 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:116)**

DIVMTQSPDSLAVSLGERATINCKSSQSILYRSNNKNYLAWYQQKPGQPPKLLIYWASARESGVPDRFSGSGSGTDFTLTISSLQAEDV
CDR1 CDR2

AVYFCQQYFITPLTFGGGTKVEIK
CDR3

FIGURA 1H

U-V_L-34 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:117)**

DIQMTQSPSSLSASVGDRVTITCRASQDISHYLAWFQQKPGKAPKSLIYAASSLQSGVPSKFSGSGSGTDFTLTISSLQPEDFATYYCQ
CDR1 CDR2

QYNNYPFTFGPGTKVDIK
CDR3

U-V_L-35 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:118)**

DIQMTQSPSSLSASVGDRVAITCRASQDISNYLAWLQQKPGKAPKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ
CDR1 CDR2

QYNTYPFTFGPGTKMDIK
CDR3

U-V_L-36 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:119)**

EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQDPGQAPRLLIYGASRRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQ
CDR1 CDR2

QHNNWPPWTFGQGTKVEIK
CDR3

U-V_L-37 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:119)**

EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQDPGQAPRLLIYGASRRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQ
CDR1 CDR2

QHNNWPPWTFGQGTKVEIK
CDR3

FIGURA 1I

U-V_L-38 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:120)**

DIQMTQSPSSVSASVGDRVTITCRASQDISRWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ
CDR1 CDR2

QANSFPPTFGQGTKVEFK
CDR3

U-V_L-39 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:121)**

DIQMTQSPSSLSASVGDRVTITCRASQSISTYLNWYQQKPGKAPKFLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFAAYYCQ
CDR1 CDR2

QSHSAPFTFGPGTKVDIK
CDR3

U-V_L-40 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:122)**

DIQMTQSPSSLSASLGDRVTITCRASQTISIYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ
CDR1 CDR2

QSYSTLTFGGGTKVEIK
CDR3

U-V_L-41 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:123)**

DIQMTQSPSSLSASVGDRVTITCRASQSIRSYLNWYQQRPGNAPKLLIYAASSLQSGVPSRVSGSGSGTDFTLTIRSLQPEDFATYYCQ
CDR1 CDR2

QSYSIPLTFGGGTKVEIK
CDR3

FIGURA 1J

1691

U-V_L-42 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:124)**

DIQMTQSPSSRSASVGDRVTITCRASQTISRYLNWYQQKPGKAPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTLSSLQPEDFATYYCQ
CDR1 CDR2

QIYSTSITFGQGTRLEIK
CDR3

U-V_L-43 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:125)**

DIQMTQSPSSLSASVGDRVTITCRASQRISSYLNWYQQKPGKAPKVLIYAESSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ
CDR1 CDR2

QSYITPITFGQGTRLEII
CDR3

U-V_L-44 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:126)**

DIQMTQSPSSLSASVGDRVTITCRASQSISRYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTISSLQPENFATYYCQ
CDR1 CDR2

QSYFTPITFGQGTRLEIK
CDR3

U-V_L-45 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:127)**

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTFSSLQPEDFATYYCQ
CDR1 CDR2

QSYFSPITFGQGTRLEIK
CDR3

FIGURA 1K

U-V_L-46 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:128)**

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTLSSLQPEDFASYYCQ
CDR1 CDR2

QSFYTPITFGQGTRLEIK
CDR3

U-V_L-47 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:128)**

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTLSSLQPEDFASYYCQ
CDR1 CDR2

QSFYTPITFGQGTRLEIK
CDR3

U-V_L-48 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:129)**

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTVSSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ
CDR1 CDR2

QSYFTPITFGQGTRLEIK
CDR3

U-V_L-49 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:129)**

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTVSSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ
CDR1 CDR2

QSYFTPITFGQGTRLEIK
CDR3

FIGURA 1L

U-V_L-50 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:129)**

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTVSSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ
CDR1 CDR2

QSYFTPITFGQGTRLEIK
CDR3

U-V_L-51 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:130)**

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFASYYCQ
CDR1 CDR2

QSFYAPITFGQGTRLEIK
CDR3

U-V_L-52 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:130)**

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFASYYCQ
CDR1 CDR2

QSFYAPITFGQGTRLEIK
CDR3

U-V_L-53 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:131)**

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQ
CDR1 CDR2

QSYFTPITFGQGTRLEIK
CDR3

FIGURA 1M

U-V_L-54 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:132)**

DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQ
CDR1 CDR2

QYDYLPFTFGPGTKVDIK
CDR3

U-V_L-55 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:132)**

DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQ
CDR1 CDR2

QYDYLPFTFGPGTKVDIK
CDR3

U-V_L-56 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:133)**

DIQMTQSPSSLSASVGDRVTITCQASQDISNSLNWYQQKPGKAPELLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQ
CDR1 CDR2

QCDDLPLTFGGGTKVEIK
CDR3

U-V_L-57 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:134)**

DIQMTQSPSSLSASVGDRVTITCQASQDISDYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQ
CDR1 CDR2

HYDNLPLTFGGGTKVEIK
CDR3

FIGURA 1N

U-V_L-58 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:135)**

DIQMTQSPSSLSASVGDRVAITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQ
CDR1 CDR2

QYDNLPLTFGGGTKVEIK
CDR3

U-V_L-59 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:135)**

DIQMTQSPSSLSASVGDRVAITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQ
CDR1 CDR2

QYDNLPLTFGGGTKVEIK
CDR3

U-V_L-60 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:136)**

DIQMTQSPSSLSASVGDRVTITCQASQDISNSLNWYQQKPGKAPKLLIYDASILETGVPSRFSGSGSETDFTFTISSLQPEDIATYYCQ
CDR1 CDR2

QCDILPLSFGGGTKVEIK
CDR3

U-V_L-61 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:137)**

DIQMTQSPSSLSASVGDRVTITCQASQDISNSLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQ
CDR1 CDR2

QYDNLPLAFGGGTKVEIR
CDR3

FIGURA 10

U-V_L-62 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:138)**

DIQMTQSPSSLSASVGDGVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQ
CDR1 CDR2

QYDSLPITFGQGTRLEIK
CDR3

U-V_L-63 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:139)**

DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKLGKAPKLLIHDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQ
CDR1 CDR2

QYDNLPITFGQGTRLEIK
CDR3

U-V_L-64 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:140)**

DIQMTQSPSSLSASVGDRVTITCQASQDISDYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQ
CDR1 CDR2

HYDNLPITFGQGTRLEIK
CDR3

U-V_L-65 : Secuencia de aminoácidos de la región variable de la cadena ligera **(SEQ ID NO:141)**

DIQMTQSPSSLSASVGDRVTITCQASQDISNSLNWYQQKPGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQ
CDR1 CDR2

HYDNLPITFGQGTRLEIK
CDR3

FIGURA 1P

U-V_H-1 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:142)**

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISASNGNTNYAQKLQDRVTMTTDTSTSTAYMELRSLRSD
CDR1 CDR2

DTAVYYCAREDNWNYGFFDYWGQGTLVTVSS
CDR3

U-V_H-2 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:142)**

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISASNGNTNYAQKLQDRVTMTTDTSTSTAYMELRSLRSD
CDR1 CDR2

DTAVYYCAREDNWNYGFFDYWGQGTLVTVSS
CDR3

U-V_H-3 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:143)**

QVHLVQSGAEVKKPGASVKVSCKVSGYTFTGHYMHWVRQAPGQGLEWMGWINPNSGGTNCAQKFQGRVTMTRDTSISTAYMELSRLRSD
CDR1 CDR2

DTAVYYCARSIAVALDYWGQGTLVTVSS
CDR3

U-V_H-4 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:144)**

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNHTQKFQGRVTMTRDTSISTAYMELSRLRSD
CDR1 CDR2

DTAVYYCARSIAVALDYWGQGTLVTVSS
CDR3

FIGURA 2A

1658

U-V_H-5 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:145)**

QVQLVQSGAEVRKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGSFDPEDGETIYAQKFQGRVTMLEDTSTDTAYMELSSLRSE
CDR1 CDR2

DTAVYYCATEGDGGYYYYGMDVWGQGTTVTVSS
CDR3

U-V_H-6 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:145)**

QVQLVQSGAEVRKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGSFDPEDGETIYAQKFQGRVTMLEDTSTDTAYMELSSLRSE
CDR1 CDR2

DTAVYYCATEGDGGYYYYGMDVWGQGTTVTVSS
CDR3

U-V_H-7 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:146)**

QVTLKESGPVLVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTSLKSRLTISKDTSKSQVVLTMTNMDP
CDR1 CDR2

VDTATYYCARMYSSGWYGVFDYWGQGTLVTVSS
CDR3

U-V_H-8 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:147)**

QVTLKESGPVLVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKALEWLVLIFSNDEKSYSTSLKSRLTISKDTSKSQVVLTMTNMDP
CDR1 CDR2

VDTATYYCARVYSSGWSFYGMDVWGQGTTVTVSS
CDR3

FIGURA 2B

U-V_H-9 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:148)**

QITLKESGPTLVKPTQTLTLTCTFSGFSLSTGGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSRLTITKDTSKNQVVLTMTNMDP
CDR1 CDR2

VDTATYYCAHRRELPFDYWGQGTLVTVSS
CDR3

U-V_H-10 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:149)**

QITLKESGPTLVKPTQTLTLTCTFSGFSLSTGGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSRLTITKDTSKTQVVLTVTDMDP
CDR1 CDR2

VDTATYYCAHRNWTPFDYWGQGTLVTVSS
CDR3

U-V_H-11 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:150)**

QITLKESGPTLVKPTQTLTLTCTFSGFSLNTGGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSRLTITKDTSKNQVVLTMTNMDP
CDR1 CDR2

VDTATYYCAHRLELPFDYWGQGTLVTVSS
CDR3

U-V_H-12 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:151)**

QITLKESGPTLVKPTQTLTLTCTFSGFSLSTGGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSRLTITKDTSKNQVVLTMTNLDP
CDR1 CDR2

VDTATYYCAHRREVPFDYWGQGTLVTVSS
CDR3

FIGURA 2C

1661

U-V_H-13 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:152)**

QITLKESGPTLVKPTQTLTLTCTFSGFSLSTGGVGVGWIRQPPGKALEWLALIYWNVEKRYSPSLRSRLTITKATSKNQVVLTMTNMDP
CDR1 CDR2

VDTATYYCAHRHTNPFEYWGQGTLVTVSS
CDR3

U-V_H-14 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:153)**

QITLKESGPTLVKPTQTLTLTCTFSGFSLSTGGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSRLTITKDTSKNQVVLTMTNMDP
CDR1 CDR2

VDTATYYCAHRGELPFDYWGQGTLVTVSS
CDR3

U-V_H-15 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:153)**

QITLKESGPTLVKPTQTLTLTCTFSGFSLSTGGVGVGWIRQPPGKALEWLALIYWNDDKRYSPSLKSRLTITKDTSKNQVVLTMTNMDP
CDR1 CDR2

VDTATYYCAHRGELPFDYWGQGTLVTVSS
CDR3

U-V_H-16 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:154)**

EVQLVESGGGLVKPGGSLRLSCAASGFPFSRYSMNWVRQAPGKGLEWVSAISSSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRAE
CDR1 CDR2

DTAVYYCARDRVGATPDAFDIWGQGTMVTVSS
CDR3

FIGURA 2D

U-V_H-17 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:155)**

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAE
CDR1 CDR2

DTAVYYCAKEGIAVAGTAEYYYYYAMDVWGQGTTVTVSS
CDR3

U-V_H-18 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:156)**

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAE
CDR1 CDR2

DTAVYYCAKEGIAARDSYYYYAMDVWGQGTTVTVSS
CDR3

U-V_H-19 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:157)**

EVQLLESGGGLVQPGGSLRLSCTASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAE
CDR1 CDR2

DTAEYYCAKEGIAGRDSYYYYGMDVWGQGTTVTVSS
CDR3

U-V_H-20 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:157)**

EVQLLESGGGLVQPGGSLRLSCTASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAE
CDR1 CDR2

DTAEYYCAKEGIAGRDSYYYYGMDVWGQGTTVTVSS
CDR3

FIGURA 2E

1957

U-V_H-21 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:158)**

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFISDDGSTKYYADSVKGRFTISRDNSMNTLYLQMNSLRAE
CDR1 CDR2

DTAVYYCARSYYDSSGYYYGFDYWGQGTLVTVSS
CDR3

U-V_H-22 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:158)**

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFISDDGSTKYYADSVKGRFTISRDNSMNTLYLQMNSLRAE
CDR1 CDR2

DTAVYYCARSYYDSSGYYYGFDYWGQGTLVTVSS
CDR3

U-V_H-23 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:159)**

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAE
CDR1 CDR2

DTAVYYCARNVIDYWGQGTLVTVSS
CDR3

U-V_H-24 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:160)**

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVIWYDGSIKYYADSVKGRFTISRDNSKNTLYLQMNSLRAE
CDR1 CDR2

DTAVYYCARGGATGAEYFQHWGQGTLVTVSS
CDR3

FIGURA 2F

U-V_H-25 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:160)**

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVIWYDGSIKYYADSVKGRFTISRDNSKNTLYLQMNSLRAE
CDR1 CDR2

DTAVYYCARGGATGAEYFQHWGQGTLVTVSS
CDR3

U-V_H-26 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:161)**

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAE
CDR1 CDR2

DTAVYYCVLLWFGETFDYWGQGSLVTVSP
CDR3

U-V_H-27 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:162)**

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWSDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAE
CDR1 CDR2

DTAVYYCARNLPFDYWGQGTLVTVSS
CDR3

U-V_H-28 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:163)**

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWDDGSNQYYTDSVKGRFTVSRDNSKNTLFLQMNSLRAE
CDR1 CDR2

DTAVYYCARSHYGGDYDYYGMDVWGQGTTVTVSS
CDR3

FIGURA 2G

U-V_H-29 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:164)**

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKRYVDSVKGRFTISRDNSKNTLYLQMNSLRAE
CDR1 CDR2

DTAVYYCARDGWQQQAPFDYWGQGTLVTVSS
CDR3

U-V_H-30 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:165)**

QVQLVESGGGVVQPGRSLRLSCAASGFTFRSHGMHWVRQAPGKGLEWVAVIWYDGSNKNYADSVRGRFTISRDNSKNTLDLQMNSLRAE
CDR1 CDR2

DTAVYYCARWGISAPFDCWGQGTLVTVSS
CDR3

U-V_H-31 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:166)**

EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYSMNWVRQAPGKGLEWVSYISSSGRTIYYADSVKGRFTISRDNAKNSLFLQMNSLRDE
CDR1 CDR2

DTAVYYCALWAPFDYWGQGTLVTVSS
CDR3

U-V_H-32 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:167)**

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSHISSSSRTIYYADSVKGRFTISRDNAKNSVYLQMNSLRDE
CDR1 CDR2

DTAVYYCARDGYNWNGGGNYYGMDVWGQGTTVTVSS
CDR3

FIGURA 2H

U-V_H-33 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:168)**

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSHISRSSRTIYYADSVKGRFTISRDNAKNSLYLQMNSLRDE
CDR1 CDR2

DTAVYYCARDGYNWNNGGYYYGMDVWGQGTTVTVSS
CDR3

U-V_H-34 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:168)**

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSHISRSSRTIYYADSVKGRFTISRDNAKNSLYLQMNSLRDE
CDR1 CDR2

DTAVYYCARDGYNWNNGGYYYGMDVWGQGTTVTVSS
CDR3

U-V_H-35 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:169)**

QVQLQESGPGLVKPSQTLSLTCTVSGGSVSSGGYYWSWIRQHPGKGLEWIGYIHSSGSTYYNPSLKSRVTISVDTSKNQFSLNLSSVTA
CDR1 CDR2

ADTAVYYCARGPYYGMDVWGQGTTVTVSS
CDR3

U-V_H-36 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:170)**

QVQLQESGPGLVKPSQTLSLTCTVSGGSISRGGYYWSWIRQHPGKGLEWIGYIYHSGSTYYNPSLKSRVNMSVDTSKNQFSLKLSSVTA
CDR1 CDR2

ADTAVYYCARALRGIVLMVYVLGALDIWGQGTKVTVSS
CDR3

FIGURA 2I

U-V_H-37 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:170)**

QVQLQESGPGLVKPSQTLSLTCTVSGGSISRGGYYWSWIRQHPGKGLEWIGYIYHSGSTYYNPSLKSRVNMSVDTSKNQFSLKLSSVTA
CDR1 CDR2

ADTAVYYCARALRGIVLMVYVLGALDIWGQGTKVTVSS
CDR3

U-V_H-38 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:171)**

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTA
CDR1 CDR2

ADTAVYYCARDETVVRGLIRYCYGMDVWGQGTTVTVSS
CDR3

U-V_H-39 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:172)**

QVQLQESGPGLVKPSQTLSLNCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIHYSGSTYYNPSLKSRITISADTSKNQFSLKLNSVTA
CDR1 CDR2

ADTAVYYCARDRGGGDYGRMDVWGQGTTVTVSS
CDR3

U-V_H-40 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:173)**

QVQLQESGPGLVKPSQTLSLNCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIHYSGSTYYNPSLKSRITISADTSKNQFSLKLNSVTA
CDR1 CDR2

ADTAVYYCARDRGGGDYGRMDVWGQGTTVTVSS
CDR3

FIGURA 2J

U-V_H-41 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:174)**

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIHSSGSTYYNPSLKSRITKSVDTSKNQFSLKLSSVTA
CDR1 CDR2

ADTAVYYCARSNNYGCFALWGRGTLVTVSS
CDR3

U-V_H-42 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:175)**

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIHSSGSTYYNPSLKSRITKSVDTSKNQFSLKLSSVTA
CDR1 CDR2

ADTAVYYCARSNNYGCFALWGRGTLVTVSS
CDR3

U-V_H-43 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:176)**

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIHYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTA
CDR1 CDR2

ADTAVYYCASGYNYGLYYYDSSGYPSYYYGMDVWGQGTTVTVSS
CDR3

U-V_H-44 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:177)**

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGDYYWNWVRQHPGKGLEWIGYIYYSGGTYYNPSLKSRVTISVDTSKNQFSLKLFSVTA
CDR1 CDR2

ADTAVYFCARTYYDILTGYPFYFDYWGQGTLVTVSS
CDR3

FIGURA 2K

U-V_H-45 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:178)**

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGDYYWNWVRQHPGKGLEWIGYIYYSGGTYYNPSLKSRVTISVDTSKNQFSLKLFSVTA
CDR1 CDR2

ADTAVYFCARTYYDILTGYPFYFDYWGQGTLVTVSS
CDR3

U-V_H-46 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:179)**

QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAAD
CDR1 CDR2

TAVYYCARGGYSSSWYWFDPWGQGTLVTVSS
CDR3

U-V_H-47 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:180)**

QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAAD
CDR1 CDR2

TAVYYCARGGYSSSWFWFDPWGQGTLVTVSS
CDR3

U-V_H-48 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:180)**

QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAAD
CDR1 CDR2

TAVYYCARGGYSSSWFWFDPWGQGTLVTVSS
CDR3

FIGURA 2L

U-V_H-49 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:180)**

QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAAD
CDR1 CDR2

TAVYYCARGGYSSSWFWFDPWGQGTLVTVSS
CDR3

U-V_H-50 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:180)**

QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAAD
CDR1 CDR2

TAVYYCARGGYSSSWFWFDPWGQGTLVTVSS
CDR3

U-V_H-51 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:181)**

QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPAGKGLEWIGRIYTSGTTNYNPSLKSRVTMSVDTSKNQFSLKLSSVTAAD
CDR1 CDR2

TAVYYCARDGYSYGHYYYYGMDVWGQGTTVTVSS
CDR3

U-V_H-52 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:182)**

QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGGSYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISIVTSRNQFSLKLSSVTA
CDR1 CDR2

ADTAVYYCARSALRYFDWLFSDVSDIWGQGTMVTVSS
CDR3

FIGURA 2M

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U-V_H-53 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:182)**

QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGGSYWSWIRQPPGKGLEWIGYIYYSGSTNYNPSLKSRVTISIVTSRNQFSLKLSSVTA
CDR1 CDR2

ADTAVYYCARSALRYFDWLFSDVSDIWGQGTMVTVSS
CDR3

U-V_H-54 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:183)**

EVQLVQSGAELKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIIYPDDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKAS
CDR1 CDR2

DTAMYYCARQKSYGYSYFDYWGQGTLVTVSS
CDR3

U-V_H-55 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:184)**

EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPDDSDARYSPSFQGQVTISADKSINTAYLQWSSLKAS
CDR1 CDR2

DTAMYYCARQGYGSGWGYFDYWGQGTLVTVSS
CDR3

U-V_H-56 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:185)**

EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDIRYSPSFQGQVTISADKSISTAYLQWSSLKAS
CDR1 CDR2

DTAMYYCARQGLAVAGTSYYYYYGMDVWGQGTTVTVSS
CDR3

FIGURA 2N

U-V_H-57 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:186)**

QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSYSAAWNWIRQSPSRGLEWLGRTYCRSKWYNDYAVSVKSRITINPDTSKNQFSLQLNSV
CDR1 CDR2

TPEDTAVYYCARDRAVAGYYYGMDVWGQGTTVTVSS
CDR3

U-V_H-58 : Secuencia de aminoácidos de la región variable de la cadena pesada **(SEQ ID NO:166)**

EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYSMNWVRQAPGKGLEWVSYISSSGRTIYYADSVKGRFTISRDNAKNSLFLQMNSLRDE
CDR1 CDR2

DTAVYYCALWAPFDYWGQGTLVTVSS
CDR3

FIGURA 2O

1672

U_L-1: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:1)
DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWFQQRPGQSPRRLIYKVSNWDSGVP
DRFNGSGSGTDFTLKISRVEAEDVGVYYCMQSTHWPITFGQGTRLEIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-2: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:2)
DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWFQQRPGQSPRRLIYKVSNWDSGVP
DRFSGSGSGTDFTLKISRVEAEDVGVYYCIQGTHWPTTFGQGTRLEIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-3: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:3)
DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWLQQRPGQSPRRLIYKVSNWDSGVP
DRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWPITFGQGTRLEIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-4: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:3)
DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWLQQRPGQSPRRLIYKVSNWDSGVP
DRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWPITFGQGTRLEIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-5: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:4)
DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWYLQKPGQPPQLLIYEVSNRFSGVP
DRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGIQLPCSFGQGTKLEIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-6: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:5)
DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWYLQKPGQPPQLLIYEVSNRFSGVP
DRFSGSGSGTDFTLKISRVEAEDVGVYYCMQSIQLPLTFGGGTKVEIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURA 3A

U_L-7 : Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:5)
DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWYLQKPGQPPQLLIYEVSNRFSGVP
DRFSGSGSGTDFTLKISRVEAEDVGVYYCMQSIQLPLTFGGGTKVEIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-8 : Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:6)
DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWFLQKPGQPPQPLIYEVSNRFSGVP
DRFSGSGSGTDFTLKISRVEAEDVGVYYCMQSIQLPITFGHGTRLEIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-9 : Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:6)
DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWFLQKPGQPPQPLIYEVSNRFSGVP
DRFSGSGSGTDFTLKISRVEAEDVGVYYCMQSIQLPITFGHGTRLEIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-11 : Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:7)
DIQMTQSPSSLSASVGDRVTITCRASQGIANYLAWYQQKPGKVPKLLIYVASTLQSGVPSRFSG
SGSGTDFTLTISSLQPEDVATYYCQNYNSAPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-12 : Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:8)
DIQMTQSPSSLSASVGDRVTIICRASQGISNDLAWYQQKPGKVPKLLIYAASTLQSGVPSRFSG
SGSGTDFTLTISSLQPEDVATYYCQKYNSVPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-13 : Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:9)
NIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYKISNRFSGVP
DRFSGSGAGTDFTLKISRVEAEDVGVYYCMQATQFPHTFGPGTKVDIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURA 3B

U_L-14: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:9)
NIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYKISNRFSGVP
DRFSGSGAGTDFTLKISRVEAEDVGVYYCMQATQFPHTFGPGTKVDIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-15: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:10)
EIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLIYKISNRFSGVP
DRFSGTGAGTDFTLKISRVEAEDVGVYYCMQATQFPHTFGGGTKVEIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYE
KHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-16: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:11)
EIVLTQSPGTLSLSPGERATLSCRASQTVISSYLAWYQQKPGQAPRLLISGASSRATGIPDRFS
GSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPRTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKS
GTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKV
YACEVTHQGLSSPVTKSFNRGEC

U_L-17: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:12)
EIVLTQSPGTLSLSPGERATLSCRASQSVSRLAWYQQKPGQAPRLLIYGASRRATGIPDRFSGS
GSGTDFTLTISRLEPEDFAVYYCQQYGSSPRSFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGT
ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYA
CEVTHQGLSSPVTKSFNRGEC

U_L-18: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:13)
DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASSLQSGVPSRFSG
SGSGTEFTLTISSLQPEDFATYYCLQHNSYPPTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-19: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:14)
DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLVWYQQKPGQPPKLFIYWASTRESGV
PDRFTGSGSGTDFTLTISSLQAEDVAVYYCQQYYSFPWTFGQGTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURA 3C

U_L-20: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:14)
DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLVWYQQKPGQPPKLFIYWASTRESGV
PDRFTGSGSGTDFTLTISSLQAEDVAVYYCQQYYSFPWTFGQGTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-21: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:15)
DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGV
PDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTTWTFGQGTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-22: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:16)
DIVMTQSPDSLAVSLGERATINCKSSQNVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGV
PDRFSGSGSGTDFTLTISSLQAEDVAVYFCQQYYGTPRTFGQGTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-23: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:17)
DIVMTQSPDSLAVSLGERATINCKSSQNVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGV
PDRFSGSGSGTDFTLTISSLQAEDVAVYFCQQYYGTPRTFGQGTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-24: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:18)
DIVMTQSPDSLTVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGV
PDRFGGSGSGTDFTLTISSLQAEDVAVYYCQQYYSISRTFGQGTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-25: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:18)
DIVMTQSPDSLTVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGV
PDRFGGSGSGTDFTLTISSLQAEDVAVYYCQQYYSISRTFGQGTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURA 3D

U_L-26: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:19)

DIVMTQSPDSLAVSLGERATINCKSSQSVLYNSNNKNYLAWYQQKPGQPPKLLIYWASTRESGV
PDRFSGSGSGTDFTLTISSLQADDVAVYYCQQYYSTTWTFGPGTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-27: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:20)

DIVMTQSPDSLAVSLGERATINCKSSQSVLYNSNNKNYLAWYQQKPGQPPKLLIYWASTRESGV
PDRFSGSGSGTDFTLTISSLQADDVAVYYCQQYYSTTWTFGPGTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-28: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:21)

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKVLIYWASTRKSGV
PDRFSGSGSGTDFTLTISGLQAEDVALYYCQQYYSTMFSFGQGTKLEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-29: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:21)

DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKVLIYWASTRKSGV
PDRFSGSGSGTDFTLTISGLQAEDVALYYCQQYYSTMFSFGQGTKLEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-30: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:22)

DIVMTQSPDSLAVSLGERATINCKSSQSVLDSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGV
PDRFSGSGSGTDFTLTISSLQAEDVAVFYCHQYYSTPLTFGGGTKVAIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-31: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:22)

DIVMTQSPDSLAVSLGERATINCKSSQSVLDSSNNKNYLAWYQQKPGQPPKLLIYWASTRESGV
PDRFSGSGSGTDFTLTISSLQAEDVAVFYCHQYYSTPLTFGGGTKVAIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

FIGURA 3E

U_L-32 : Secuencia de aminoácidos de la cadena ligera **(SEQ ID NO:23)**

DIVMTQSPDSLAVSLGERATINCKSSQSILYRSNNKNYLAWYQQKPGQPPKLLIYWASARESGV
PDRFSGSGSGTDFTLTISSLQAEDVAVYFCQQYFITPLTFGGGTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-33 : Secuencia de aminoácidos de la cadena ligera **(SEQ ID NO:23)**

DIVMTQSPDSLAVSLGERATINCKSSQSILYRSNNKNYLAWYQQKPGQPPKLLIYWASARESGV
PDRFSGSGSGTDFTLTISSLQAEDVAVYFCQQYFITPLTFGGGTKVEIKRTVAAPSVFIFPPSD
EQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
EKHKVYACEVTHQGLSSPVTKSFNRGEC

U_L-34 : Secuencia de aminoácidos de la cadena ligera **(SEQ ID NO:24)**

DIQMTQSPSSLSASVGDRVTITCRASQDISHYLAWFQQKPGKAPKSLIYAASSLQSGVPSKFSG
SGSGTDFTLTISSLQPEDFATYYCQQYNNYPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-35 : Secuencia de aminoácidos de la cadena ligera **(SEQ ID NO:25)**

DIQMTQSPSSLSASVGDRVAITCRASQDISNYLAWLQQKPGKAPKSLIYAASSLQSGVPSRFSG
SGSGTDFTLTISSLQPEDFATYYCQQYNTYPFTFGPGTKMDIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-36 : Secuencia de aminoácidos de la cadena ligera **(SEQ ID NO:26)**

EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQDPGQAPRLLIYGASRRATGIPARFSG
SGSGTEFTLTISSLQSEDFAVYYCQQHNNWPPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKS
GTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKV
YACEVTHQGLSSPVTKSFNRGEC

U_L-37 : Secuencia de aminoácidos de la cadena ligera **(SEQ ID NO:26)**

EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQDPGQAPRLLIYGASRRATGIPARFSG
SGSGTEFTLTISSLQSEDFAVYYCQQHNNWPPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKS
GTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKV
YACEVTHQGLSSPVTKSFNRGEC

FIGURA 3F

U_L-38: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:27)
DIQMTQSPSSVSASVGDRVTITCRASQDISRWLAWYQQKPGKAPKLLIYAASSLQSGVPSRFSG
SGSGTDFTLTISSLQPEDFATYYCQQANSFPPTFGQGTKVEFKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-39: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:28)
DIQMTQSPSSLSASVGDRVTITCRASQSISTYLNWYQQKPGKAPKFLIYAASSLQSGVPSRFSG
SGSGTDFTLTISSLQPEDFAAYYCQQSHSAPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-40: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:29)
DIQMTQSPSSLSASLGDRVTITCRASQTISIYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSG
SGSGTDFTLTISSLQPEDFATYYCQQSYSTLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGT
ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYA
CEVTHQGLSSPVTKSFNRGEC

U_L-41: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:30)
DIQMTQSPSSLSASVGDRVTITCRASQSIRSYLNWYQQRPGNAPKLLIYAASSLQSGVPSRVSG
SGSGTDFTLTIRSLQPEDFATYYCQQSYSIPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-42: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:31)
DIQMTQSPSSRSASVGDRVTITCRASQTISRYLNWYQQKPGKAPKLLIYAASTLQSGVPSRFSG
SGSGTDFTLTLSSLQPEDFATYYCQQIYSTSITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-43: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:32)
DIQMTQSPSSLSASVGDRVTITCRASQRISSYLNWYQQKPGKAPKVLIYAESSLQSGVPSRFSG
SGSGTDFTLTISSLQPEDFATYYCQQSYITPITFGQGTRLEIIRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

FIGURA 3G

U_L-44: Secuencia de aminoácidos de la cadena ligera **(SEQ ID NO:33)**
DIQMTQSPSSLSASVGDRVTITCRASQSISRYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSG
SGSGTDFTLTISSLQPENFATYYCQQSYFTPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-45: Secuencia de aminoácidos de la cadena ligera **(SEQ ID NO:34)**
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSG
SGSGTDFTLTFSSLQPEDFATYYCQQSYFSPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-46: Secuencia de aminoácidos de la cadena ligera **(SEQ ID NO:35)**
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSG
SGSGTDFTLTLSSLQPEDFASYYCQQSFYTPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-47: Secuencia de aminoácidos de la cadena ligera **(SEQ ID NO:35)**
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSG
SGSGTDFTLTLSSLQPEDFASYYCQQSFYTPITFGQGTRLEIKASTKGPSVFPLAPCSRSTSES
TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNV
DHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
PEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEK
TISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPML
DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_L-48: Secuencia de aminoácidos de la cadena ligera **(SEQ ID NO:36)**
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTVSSLQSGVPSRFSG
SGSGTDFTLTISSLQPEDFATYYCQQSYFTPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-49: Secuencia de aminoácidos de la cadena ligera **(SEQ ID NO:36)**
DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTVSSLQSGVPSRFSG
SGSGTDFTLTISSLQPEDFATYYCQQSYFTPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

FIGURA 3H

U_L-50 : Secuencia de aminoácidos de la cadena ligera **(SEQ ID NO:36)**

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTVSSLQSGVPSRFSG
SGSGTDFTLTISSLQPEDFATYYCQQSYFTPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-51 : Secuencia de aminoácidos de la cadena ligera **(SEQ ID NO:37)**

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSG
SGSGTDFTLTISSLQPEDFASYYCQQSFYAPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-52 : Secuencia de aminoácidos de la cadena ligera **(SEQ ID NO:37)**

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSG
SGSGTDFTLTISSLQPEDFASYYCQQSFYAPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-53 : Secuencia de aminoácidos de la cadena ligera **(SEQ ID NO:38)**

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYTASSLQSGVPSRFSG
SGSGTDFTLTISSLQPEDFATYYCQQSYFTPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-54 : Secuencia de aminoácidos de la cadena ligera **(SEQ ID NO:39)**

DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSG
SGSGTDFTFTISSLQPEDIATYYCQQYDYLPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-55 : Secuencia de aminoácidos de la cadena ligera **(SEQ ID NO:39)**

DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSG
SGSGTDFTFTISSLQPEDIATYYCQQYDYLPFTFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

FIGURA 3I

U_L-56: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:40)
DIQMTQSPSSLSASVGDRVTITCQASQDISNSLNWYQQKPGKAPELLIYDASNLETGVPSRFSG
SGSGTDFTFTISSLQPEDIATYYCQQCDDLPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-57: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:41)
DIQMTQSPSSLSASVGDRVTITCQASQDISDYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSG
SGSGTDFTFTISSLQPEDIATYYCQHYDNLPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-58: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:42)
DIQMTQSPSSLSASVGDRVAITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSG
SGSGTDFTFTISSLQPEDIATYYCQQYDNLPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-59: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:42)
DIQMTQSPSSLSASVGDRVAITCQASQDISNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSG
SGSGTDFTFTISSLQPEDIATYYCQQYDNLPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-60: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:43)
DIQMTQSPSSLSASVGDRVTITCQASQDISNSLNWYQQKPGKAPKLLIYDASILETGVPSRFSG
SGSETDFTFTISSLQPEDIATYYCQQCDILPLSFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-61: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:44)
DIQMTQSPSSLSASVGDRVTITCQASQDISNSLNWYQQKPGKAPKLLIYDASNLETGVPSRFSG
SGSGTDFTFTISSLQPEDIATYYCQQYDNLPLAFGGGTKVEIRRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

FIGURA 3J

U_L-62: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:45)
DIQMTQSPSSLSASVGDGVTITCQASQDITNYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSG
SGSGTDFTFTISSLQPEDIATYYCQQYDSLPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-63: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:46)
DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKLGKAPKLLIHDASNLETGVPSRFSG
SGSGTDFTFTISSLQPEDIATYYCQQYDNLPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-64: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:47)
DIQMTQSPSSLSASVGDRVTITCQASQDISDYLNWYQQKPGKAPKLLIYDASNLETGVPSRFSG
SGSGTDFTFTISSLQPEDIATYYCQHYDNLPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

U_L-65: Secuencia de aminoácidos de la cadena ligera (SEQ ID NO:48)
DIQMTQSPSSLSASVGDRVTITCQASQDISNSLNWYQQKPGKAPKLLIYDASNLETGVPSRFSG
SGSGTDFTFTISSLQPEDIATYYCQHYDNLPITFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSG
TASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVY
ACEVTHQGLSSPVTKSFNRGEC

FIGURA 3K

U_H-1 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:49)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISASNGNTNYAQKL
QDRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAREDNWNYGFFDYWGQGTLVTVSSASTKGPSV
FPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTP
EVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC
KVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_H-2 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:49)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISASNGNTNYAQKL
QDRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAREDNWNYGFFDYWGQGTLVTVSSASTKGPSV
FPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTP
EVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC
KVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_H-3 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:50)

QVHLVQSGAEVKKPGASVKVSCKVSGYTFTGHYMHWVRQAPGQGLEWMGWINPNSGGTNCAQKF
QGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARSIAVALDYWGQGTLVTVSSASTKGPSVFPL
APCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSN
FGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVT
CVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVS
NKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
NNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_H-4: Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:51)

QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNHTQKF
QGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARSIAVALDYWGQGTLVTVSSASTKGPSVFPL
APCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSN
FGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVT
CVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVS
NKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
NNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

FIGURA 4A

U_H-5 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:52)

QVQLVQSGAEVRKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGSFDPEDGETIYAQKF
QGRVTMLEDTSTDTAYMELSSLRSEDTAVYYCATEGDGGYYYYGMDVWGQGTTVTVSSASTKGP
SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT
VPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISR
TPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEY
KCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_H-6 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:52)

QVQLVQSGAEVRKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGSFDPEDGETIYAQKF
QGRVTMLEDTSTDTAYMELSSLRSEDTAVYYCATEGDGGYYYYGMDVWGQGTTVTVSSASTKGP
SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT
VPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISR
TPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEY
KCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_H-7 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:53)

QVTLKESGPVLVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKALEWLAHIFSNDEKSYSTS
LKSRLTISKDTSKSQVVLTMTNMDPVDTATYYCARMYSSGWYGVFDYWGQGTLVTVSSASTKGP
SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT
VPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISR
TPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEY
KCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_H-8 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:54)

QVTLKESGPVLVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKALEWLVLIFSNDEKSYSTS
LKSRLTISKDTSKSQVVLTMTNMDPVDTATYYCARVYSSGWSFYGMDVWGQGTTVTVSSASTKG
PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV
TVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMIS
RTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKE
YKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

FIGURA 4B

U_B-9 : Secuencia de aminoácidos de la cadena pesada **(SEQ ID NO:55)**

QITLKESGPTLVKPTQTLTLTCTFSGFSLSTGGVGVGWIRQPPGKALEWLALIYWNDDKRYSPS
LKSRLTITKDTSKNQVVLTMTNMDPVDTATYYCAHRRELPFDYWGQGTLVTVSSASTKGPSVFP
LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
NFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV
SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-10: Secuencia de aminoácidos de la cadena pesada **(SEQ ID NO:56)**

QITLKESGPTLVKPTQTLTLTCTFSGFSLSTGGVGVGWIRQPPGKALEWLALIYWNDDKRYSPS
LKSRLTITKDTSKTQVVLTVTDMDPVDTATYYCAHRNWTPFDYWGQGTLVTVSSASTKGPSVFP
LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
NFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV
SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-11 : Secuencia de aminoácidos de la cadena pesada **(SEQ ID NO:57)**

QITLKESGPTLVKPTQTLTLTCTFSGFSLNTGGVGVGWIRQPPGKALEWLALIYWNDDKRYSPS
LKSRLTITKDTSKNQVVLTMTNMDPVDTATYYCAHRLELPFDYWGQGTLVTVSSASTKGPSVFP
LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
NFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV
SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-12 : Secuencia de aminoácidos de la cadena pesada **(SEQ ID NO:58)**

QITLKESGPTLVKPTQTLTLTCTFSGFSLSTGGVGVGWIRQPPGKALEWLALIYWNDDKRYSPS
LKSRLTITKDTSKNQVVLTMTNLDPVDTATYYCAHRREVPFDYWGQGTLVTVSSASTKGPSVFP
LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
NFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV
SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

FIGURA 4C

U_B-13 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:59)

QITLKESGPTLVKPTQTLTLTCTFSGFSLSTGGVGVGWIRQPPGKALEWLALIYWNVEKRYSPS
LRSRLTITKATSKNQVVLTMTNMDPVDTATYYCAHRHTNPFEYWGQGTLVTVSSASTKGPSVFP
LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
NFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV
SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-14 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:60)

QITLKESGPTLVKPTQTLTLTCTFSGFSLSTGGVGVGWIRQPPGKALEWLALIYWNDDKRYSPS
LKSRLTITKDTSKNQVVLTMTNMDPVDTATYYCAHRGELPFDYWGQGTLVTVSSASTKGPSVFP
LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
NFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV
SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-15 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:60)

QITLKESGPTLVKPTQTLTLTCTFSGFSLSTGGVGVGWIRQPPGKALEWLALIYWNDDKRYSPS
LKSRLTITKDTSKNQVVLTMTNMDPVDTATYYCAHRGELPFDYWGQGTLVTVSSASTKGPSVFP
LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
NFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV
SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-16 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:61)

EVQLVESGGGLVKPGGSLRLSCAASGFPFSRYSMNWVRQAPGKGLEWVSAISSSSSYIYYADSV
KGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDRVGATPDAFDIWGQGTMVTVSSASTKGPS
VFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTV
PSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRT
PEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYK
CKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN
GQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

FIGURA 4D

U_B-17: Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:62)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMNWVRQAPGKGLEWVSAISGSGGSTYYADSV
KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKEGIAVAGTAEYYYYYAMDVWGQGTTVTVSS
ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS
LSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKD
TLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDW
LNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI
AVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL
SLSPGK

U_B-18: Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:63)

EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSV
KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKEGIAARDSYYYYAMDVWGQGTTVTVSSASTK
GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV
VTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGK
EYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

U_B-19: Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:64)

EVQLLESGGGLVQPGGSLRLSCTASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSV
KGRFTISRDNSKNTLYLQMNSLRAEDTAEYYCAKEGIAGRDSYYYYGMDVWGQGTTVTVSSASTK
GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV
VTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGK
EYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

U_B-20: Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:64)

EVQLLESGGGLVQPGGSLRLSCTASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSV
KGRFTISRDNSKNTLYLQMNSLRAEDTAEYYCAKEGIAGRDSYYYYGMDVWGQGTTVTVSSASTK
GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV
VTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGK
EYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

FIGURA 4E

U_H-21 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:65)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFISDDGSTKYYADSV
KGRFTISRDNSMNTLYLQMNSLRAEDTAVYYCARSYYDSSGYYYGFDYWGQGTLVTVSSASTKG
PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV
TVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMIS
RTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKE
YKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_H-22 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:65)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFISDDGSTKYYADSV
KGRFTISRDNSMNTLYLQMNSLRAEDTAVYYCARSYYDSSGYYYGFDYWGQGTLVTVSSASTKG
PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV
TVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMIS
RTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKE
YKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_H-23 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:66)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYYADSV
KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARNVIDYWGQGTLVTVSSASTKGPSVFPLAPC
SRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGT
QTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVV
VDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKG
LPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
KTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_H-24 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:67)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVIWYDGSIKYYADSV
KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGGATGAEYFQHWGQGTLVTVSSASTKGPSV
FPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTP
EVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC
KVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

FIGURA 4F

U_H-25 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:67)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYDMHWVRQAPGKGLEWVAVIWYDGSIKYYADSV
KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARGGATGAEYFQHWGQGTLVTVSSASTKGPSV
FPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTP
EVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC
KVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_H-26 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:68)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYYADSV
KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCVLLWFGETFDYWGQGSLVTVSPASTKGPSVFP
LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
NFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV
SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_H-27 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:69)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWSDGSNKYYADSV
KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARNLPFDYWGQGTLVTVSSASTKGPSVFPLAP
CSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFG
TQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNK
GLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN
YKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_H-28 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:70)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWDDGSNQYYTDSV
KGRFTVSRDNSKNTLFLQMNSLRAEDTAVYYCARSHYGGDYDYYGMDVWGQGTTVTVSSASTKG
PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV
TVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMIS
RTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKE
YKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

FIGURA 4G

U_H-29 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:71)

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKRYVDSV
KGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGWQQQAPFDYWGQGTLVTVSSASTKGPSV
FPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTP
EVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC
KVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_H-30: Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:72)

QVQLVESGGGVVQPGRSLRLSCAASGFTFRSHGMHWVRQAPGKGLEWVAVIWYDGSNKNYADSV
RGRFTISRDNSKNTLDLQMNSLRAEDTAVYYCARWGISAPFDCWGQGTLVTVSSASTKGPSVFP
LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
NFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV
SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_H-31 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:73)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYSMNWVRQAPGKGLEWVSYISSSGRTIYYADSV
KGRFTISRDNAKNSLFLQMNSLRDEDTAVYYCALWAPFDYWGQGTLVTVSSASTKGPSVFPLAP
CSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFG
TQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNK
GLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN
YKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_H-32 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:74)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSHISSSSRTIYYADSV
KGRFTISRDNAKNSVYLQMNSLRDEDTAVYYCARDGYNWNGGGNYYGMDVWGQGTTVTVSSASTK
GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV
VTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGK
EYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

FIGURA 4H

U_H-33 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:75)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSHISRSSRTIYYADSV
KGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCARDGYNWNNGGYYYGMDVWGQGTTVTVSSASTK
GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV
VTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGK
EYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

U_H-34 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:75)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSHISRSSRTIYYADSV
KGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCARDGYNWNNGGYYYGMDVWGQGTTVTVSSASTK
GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV
VTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGK
EYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

U_H-35 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:76)

QVQLQESGPGLVKPSQTLSLTCTVSGGSVSSGGYYWSWIRQHPGKGLEWIGYIHSSGSTYYNPS
LKSRVTISVDTSKNQFSLNLSSVTAADTAVYYCARGPYYGMDVWGQGTTVTVSSASTKGPSVFP
LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSS
NFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEV
TCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKV
SNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_H-36 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:77)

QVQLQESGPGLVKPSQTLSLTCTVSGGSISRGGYYWSWIRQHPGKGLEWIGYIYHSGSTYYNPS
LKSRVNMSVDTSKNQFSLKLSSVTAADTAVYYCARALRGIVLMVYVLGALDIWGQGTKVTVSSA
STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL
SSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDT
LMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWL
NGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
LSPGK

FIGURA 4I

U_B-37: Secuencia de aminoácidos de la cadena pesada **(SEQ ID NO:77)**

QVQLQESGPGLVKPSQTLSLTCTVSGGSISRGGYYWSWIRQHPGKGLEWIGYIYHSGSTYYNPS
LKSRVNMSVDTSKNQFSLKLSSVTAADTAVYYCARALRGIVLMVYVLGALDIWGQGTKVTVSSA
STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL
SSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDT
LMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWL
NGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
LSPGK

U_B-38: Secuencia de aminoácidos de la cadena pesada **(SEQ ID NO:78)**

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIYYSGSTYYNPS
LKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDETVVRGLIRYCYGMDVWGQGTTVTVSSA
STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL
SSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDT
LMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWL
NGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
LSPGK

U_B-39: Secuencia de aminoácidos de la cadena pesada **(SEQ ID NO:79)**

QVQLQESGPGLVKPSQTLSLNCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIHYSGSTYYNPS
LKSRITISADTSKNQFSLKLNSVTAADTAVYYCARDRGGGDYGRMDVWGQGTTVTVSSASTKGP
SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT
VPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISR
TPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEY
KCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-40: Secuencia de aminoácidos de la cadena pesada **(SEQ ID NO:80)**

QVQLQESGPGLVKPSQTLSLNCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIHYSGSTYYNPS
LKSRITISADTSKNQFSLKLNSVTAADTAVYYCARDRGGGDYGRMDVWGQGTTVTVSSASTKGP
SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVT
VPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISR
TPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEY
KCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWES
NGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

FIGURA 4J

U_H-41 : Secuencia de aminoácidos de la cadena pesada **(SEQ ID NO:81)**

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWI81RQHPGKGLEWIGYIHSSGSTYYN
PSLKSRITKSVDTSKNQFSLKLSSVTAADTAVYYCARSNNYGCFALWGRGTLVTVSSASTKGPS
VFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTV
PSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRT
PEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYK
CKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN
GQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_H-42 : Secuencia de aminoácidos de la cadena pesada **(SEQ ID NO:82)**

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIHSSGSTYYNPS
LKSRITKSVDTSKNQFSLKLSSVTAADTAVYYCARSNNYGCFALWGRGTLVTVSSASTKGPSVF
PLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPS
SNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPE
VTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCK
VSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ
PENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_H-43 : Secuencia de aminoácidos de la cadena pesada **(SEQ ID NO:83)**

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIGYIHYSGSTYYNPS
LKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCASGYNYGLYYYDSSGYPSYYYGMDVWGQGTT
VTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
SGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFP
PKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTV
VHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
YPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHY
TQKSLSLSPGK

U_H-44 : Secuencia de aminoácidos de la cadena pesada **(SEQ ID NO:84)**

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGDYYWNWVRQHPGKGLEWIGYIYYSGGTYYNPS
LKSRVTISVDTSKNQFSLKLFSVTAADTAVYFCARTYYDILTGYPFYFDYWGQGTLVTVSSASTK
GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV
VTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGK
EYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

FIGURA 4K

U_B-45: Secuencia de aminoácidos de la cadena pesada **(SEQ ID NO:85)**

QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGDYYWNWVRQHPGKGLEWIGYIYYSGGTYYNPS
LKSRVTISVDTSKNQFSLKLFSVTAADTAVYFCARTYYDILTGYPFYFDYWGQGTLVTVSSASTK
GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV
VTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGK
EYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

U_B-46: Secuencia de aminoácidos de la cadena pesada **(SEQ ID NO:86)**

QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLK
SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGYSSSWYWFDPWGQGTLVTVSSASTKGPSV
FPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTP
EVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC
KVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-47: Secuencia de aminoácidos de la cadena pesada **(SEQ ID NO:87)**

QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLK
SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGYSSSWFWFDPWGQGTLVTVSSASTKGPSV
FPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTP
EVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC
KVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-48: Secuencia de aminoácidos de la cadena pesada **(SEQ ID NO:87)**

QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLK
SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGYSSSWFWFDPWGQGTLVTVSSASTKGPSV
FPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTP
EVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC
KVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

FIGURA 4L

U_B-49 : Secuencia de aminoácidos de la cadena pesada **(SEQ ID NO:87)**

QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLK
SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGYSSSWFWFDPWGQGTLVTVSSASTKGPSV
FPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTP
EVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC
KVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-50 : Secuencia de aminoácidos de la cadena pesada **(SEQ ID NO:87)**

QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLK
SRVTISVDTSKNQFSLKLSSVTAADTAVYYCARGGYSSSWFWFDPWGQGTLVTVSSASTKGPSV
FPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTP
EVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC
KVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-51 : Secuencia de aminoácidos de la cadena pesada **(SEQ ID NO:88)**

QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPAGKGLEWIGRIYTSGTTNYNPSLK
SRVTMSVDTSKNQFSLKLSSVTAADTAVYYCARDGYSYGHYYYYGMDVWGQGTTVTVSSASTKG
PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVV
TVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMIS
RTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKE
YKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE
SNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-52 : Secuencia de aminoácidos de la cadena pesada **(SEQ ID NO:89)**

QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGGSYWSWIRQPPGKGLEWIGYIYYSGSTNYNPS
LKSRVTISIVTSRNQFSLKLSSVTAADTAVYYCARSALRYFDWLFSDVSDIWGQGTMVTVSSAS
TKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLS
SVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTL
MISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLN
GKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV
EWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
SPGK

FIGURA 4M

U_B-53 : Secuencia de aminoácidos de la cadena pesada **(SEQ ID NO:89)**

QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGGSYWSWIRQPPGKGLEWIGYIYYSGSTNYNPS
LKSRVTISIVTSRNQFSLKLSSVTAADTAVYYCARSALRYFDWLFSDVSDIWGQGTMVTVSSAS
TKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLS
SVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTL
MISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLN
GKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAV
EWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
SPGK

U_B-54 : Secuencia de aminoácidos de la cadena pesada **(SEQ ID NO:90)**

EVQLVQSGAELKKPGESLKISCKGSGYRFTSYWIGWVRQMPGKGLEWMGIIYPDDSDTRYSPSF
QGQVTISADKSISTAYLQWSSLKASDTAMYYCARQKSYGYSYFDYWGQGTLVTVSSASTKGPSV
FPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP
SSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTP
EVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKC
KVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-55 : Secuencia de aminoácidos de la cadena pesada **(SEQ ID NO:91)**

EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPDDSDARYSPSF
QGQVTISADKSINTAYLQWSSLKASDTAMYYCARQGYGSGWGYFDYWGQGTLVTVSSASTKGPS
VFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTV
PSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRT
PEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYK
CKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESN
GQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

U_B-56 : Secuencia de aminoácidos de la cadena pesada **(SEQ ID NO:92)**

EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIIYPGDSDIRYSPSF
QGQVTISADKSISTAYLQWSSLKASDTAMYYCARQGLAVAGTSYYYYYGMDVWGQGTTVTVSSA
STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL
SSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDT
LMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWL
NGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIA
VEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
LSPGK

FIGURA 4N

U_R-57 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:93)

QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSYSAAWNWIRQSPSRGLEWLGRTYCRSKWYNDYA
VSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCARDRAVAGYYYGMDVWGQGTTVTVSSASTK
GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSV
VTVPSSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGK
EYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW
ESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
GK

U_R-58 : Secuencia de aminoácidos de la cadena pesada (SEQ ID NO:73)

EVQLVESGGGLVQPGGSLRLSCAASGFTFSAYSMNWVRQAPGKGLEWVSYISSSGRTIYYADSV
KGRFTISRDNAKNSLFLQMNSLRDEDTAVYYCALWAPFDYWGQGTLVTVSSASTKGPSVFPLAP
CSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFG
TQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCV
VVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNK
GLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN
YKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

FIGURA 4O

REGIÓN CONSTANTE: SECUENCIA DE AMINOÁCIDOS DE LA CADENA LIGERA

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKA
DYEKHKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:187)

FIGURA 5A

REGIÓN CONSTANTE: SECUENCIA DE AMINOÁCIDOS DE LA CADENA PESADA

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFG
TQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF
NWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLP
PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMH
EALHNHYTQKSLSLSPGK (SEQ ID NO:188)

FIGURA 5B

CDRS DE LA CADENA LIGERA

NOMBRE	SECUENCIA	SEQ ID NO:
CDRL1-1	RSSQSLVYSDGNTYLN	189
CDRL1-2	RSSQSLVYSDGNTYLN	189
CDRL1-3	RSSQSLVYSDGNTYLN	189
CDRL1-4	RSSQSLVYSDGNTYLN	189
CDRL1-5	KSSQSLLHSDGKTYLY	190
CDRL1-6	KSSQSLLHSDGKTYLY	190
CDRL1-7	KSSQSLLHSDGKTYLY	190
CDRL1-8	KSSQSLLHSDGKTYLY	190
CDRL1-9	KSSQSLLHSDGKTYLY	190
CDRL1-11	RASQGIANYLA	191
CDRL1-12	RASQGISNDLA	192
CDRL1-13	RSSQSLVHSDGNTYLS	193
CDRL1-14	RSSQSLVHSDGNTYLS	193
CDRL1-15	RSSQSLVHSDGNTYLS	193
CDRL1-16	RASQTVISSYLA	194
CDRL1-17	RASQSVSRLA	195
CDRL1-18	RASQGIRNDLG	196
CDRL1-19	KSSQSVLYSSNNKNYLV	197
CDRL1-20	KSSQSVLYSSNNKNYLV	197
CDRL1-21	KSSQSVLYSSNNKNYLA	198
CDRL1-22	KSSQNVLYSSNNKNYLA	199
CDRL1-23	KSSQNVLYSSNNKNYLA	199
CDRL1-24	KSSQSVLYSSNNKNYLA	198
CDRL1-25	KSSQSVLYSSNNKNYLA	198
CDRL1-26	KSSQSVLYNSNNKNYLA	200
CDRL1-27	KSSQSVLYNSNNKNYLA	200
CDRL1-28	KSSQSVLYSSNNKNYLA	198
CDRL1-29	KSSQSVLYSSNNKNYLA	198
CDRL1-30	KSSQSVLDSSNNKNYLA	201
CDRL1-31	KSSQSVLDSSNNKNYLA	201
CDRL1-32	KSSQSILYRSNNKNYLA	202
CDRL1-33	KSSQSILYRSNNKNYLA	202
CDRL1-34	RASQDISHYLA	203
CDRL1-35	RASQDISNYLA	204

FIGURA 6A

NOMBRE	SECUENCIA	SEQ ID NO:
CDRL1-36	RASQSVSSNLA	205
CDRL1-37	RASQSVSSNLA	205
CDRL1-38	RASQDISRWLA	206
CDRL1-39	RASQSISTYLN	207
CDRL1-40	RASQTISIYLN	208
CDRL1-41	RASQSIRSYLN	209
CDRL1-42	RASQTISRYLN	210
CDRL1-43	RASQRISSYLN	211
CDRL1-44	RASQSISRYLN	212
CDRL1-45	RASQSISSYLN	213
CDRL1-46	RASQSISSYLN	213
CDRL1-47	RASQSISSYLN	213
CDRL1-48	RASQSISSYLN	213
CDRL1-49	RASQSISSYLN	213
CDRL1-50	RASQSISSYLN	213
CDRL1-51	RASQSISSYLN	213
CDRL1-52	RASQSISSYLN	213
CDRL1-53	RASQSISSYLN	213
CDRL1-54	QASQDISNYLN	214
CDRL1-55	QASQDISNYLN	214
CDRL1-56	QASQDISNSLN	215
CDRL1-57	QASQDISDYLN	216
CDRL1-58	QASQDISNYLN	214
CDRL1-59	QASQDISNYLN	214
CDRL1-60	QASQDISNSLN	215
CDRL1-61	QASQDISNSLN	215
CDRL1-62	QASQDITNYLN	217
CDRL1-63	QASQDISNYLN	214
CDRL1-64	QASQDISDYLN	216
CDRL1-65	QASQDISNSLN	215
CDRL2-1	KVSNWDS	218
CDRL2-2	KVSNWDS	218
CDRL2-3	KVSNWDS	218
CDRL2-4	KVSNWDS	218
CDRL2-5	EVSNRFS	219
CDRL2-6	EVSNRFS	219

FIGURA 6B

NOMBRE	SECUENCIA	SEQ ID NO:
CDRL2-7	EVSNRFS	219
CDRL2-8	EVSNRFS	219
CDRL2-9	EVSNRFS	219
CDRL2-11	VASTLQS	220
CDRL2-12	AASTLQS	221
CDRL2-13	KISNRFS	222
CDRL2-14	KISNRFS	222
CDRL2-15	KISNRFS	222
CDRL2-16	GASSRAT	223
CDRL2-17	GASRRAT	224
CDRL2-18	AASSLQS	225
CDRL2-19	WASTRES	226
CDRL2-20	WASTRES	226
CDRL2-21	WASTRES	226
CDRL2-22	WASTRES	226
CDRL2-23	WASTRES	226
CDRL2-24	WASTRES	226
CDRL2-25	WASTRES	226
CDRL2-26	WASTRES	226
CDRL2-27	WASTRES	226
CDRL2-28	WASTRKS	227
CDRL2-29	WASTRKS	227
CDRL2-30	WASTRES	226
CDRL2-31	WASTRES	226
CDRL2-32	WASARES	228
CDRL2-33	WASARES	228
CDRL2-34	AASSLQS	225
CDRL2-35	AASSLQS	225
CDRL2-36	GASRRAT	224
CDRL2-37	GASRRAT	224
CDRL2-38	AASSLQS	225
CDRL2-39	AASSLQS	225
CDRL2-40	AASSLQS	225
CDRL2-41	AASSLQS	225
CDRL2-42	AASTLQS	221
CDRL2-43	AESSLQS	229

FIGURA 6C

NOMBRE	SECUENCIA	SEQ ID NO:
CDRL2-44	TASSLQS	230
CDRL2-45	TASSLQS	230
CDRL2-46	TASSLQS	230
CDRL2-47	TASSLQS	230
CDRL2-48	TVSSLQS	231
CDRL2-49	TVSSLQS	231
CDRL2-50	TVSSLQS	231
CDRL2-51	TASSLQS	230
CDRL2-52	TASSLQS	230
CDRL2-53	TASSLQS	230
CDRL2-54	DASNLET	232
CDRL2-55	DASNLET	232
CDRL2-56	DASNLET	232
CDRL2-57	DASNLET	232
CDRL2-58	DASNLET	232
CDRL2-59	DASNLET	232
CDRL2-60	DASILET	233
CDRL2-61	DASNLET	232
CDRL2-62	DASNLET	232
CDRL2-63	DASNLET	232
CDRL2-64	DASNLET	232
CDRL2-65	DASNLET	232
CDRL3-1	MQSTHWPIT	234
CDRL3-2	IQGTHWPTT	235
CDRL3-3	MQGTHWPIT	236
CDRL3-4	MQGTHWPIT	236
CDRL3-5	MQGIQLPCS	237
CDRL3-6	MQSIQLPLT	238
CDRL3-7	MQSIQLPLT	238
CDRL3-8	MQSIQLPIT	239
CDRL3-9	MQSIQLPIT	239
CDRL3-11	QNYNSAPFT	240
CDRL3-12	QKYNSVPLT	241
CDRL3-13	MQATQFPHT	242
CDRL3-14	MQATQFPHT	242
CDRL3-15	MQATQFPHT	242

FIGURA 6D

NOMBRE	SECUENCIA	SEQ ID NO:
CDRL3-16	QQYGSSPRT	243
CDRL3-17	QQYGSSPRS	244
CDRL3-18	LQHNSYPPT	245
CDRL3-19	QQYYSFPWT	246
CDRL3-20	QQYYSFPWT	246
CDRL3-21	QQYYSTTWT	247
CDRL3-22	QQYYGTPRT	248
CDRL3-23	QQYYGTPRT	248
CDRL3-24	QQYYSISRT	249
CDRL3-25	QQYYSISRT	249
CDRL3-26	QQYYSTTWT	247
CDRL3-27	QQYYSTTWT	247
CDRL3-28	QQYYSTMFS	250
CDRL3-29	QQYYSTMFS	250
CDRL3-30	HQYYSTPLT	251
CDRL3-31	HQYYSTPLT	251
CDRL3-32	QQYFITPLT	252
CDRL3-33	QQYFITPLT	252
CDRL3-34	QQYNNYPFT	253
CDRL3-35	QQYNTYPFT	254
CDRL3-36	QQHNNWPPWT	255
CDRL3-37	QQHNNWPPWT	255
CDRL3-38	QQANSFPPT	256
CDRL3-39	QQSHSAPFT	257
CDRL3-40	QQSYSTLT	258
CDRL3-41	QQSYSIPLT	259
CDRL3-42	QQIYSTSIT	260
CDRL3-43	QQSYITPIT	261
CDRL3-44	QQSYFTPIT	262
CDRL3-45	QQSYFSPIT	263
CDRL3-46	QQSFYTPIT	264
CDRL3-47	QQSFYTPIT	264
CDRL3-48	QQSYFTPIT	262
CDRL3-49	QQSYFTPIT	262
CDRL3-50	QQSYFTPIT	262
CDRL3-51	QQSFYAPIT	265

FIGURA 6E

NOMBRE	SECUENCIA	SEQ ID NO:
CDRL3-52	QQSFYAPIT	265
CDRL3-53	QQSYFTPIT	262
CDRL3-54	QQYDYLPFT	266
CDRL3-55	QQYDYLPFT	266
CDRL3-56	QQCDDLPLT	267
CDRL3-57	QHYDNLPLT	268
CDRL3-58	QQYDNLPLT	269
CDRL3-59	QQYDNLPLT	269
CDRL3-60	QQCDILPLS	270
CDRL3-61	QQYDNLPLA	271
CDRL3-62	QQYDSLPIT	272
CDRL3-63	QQYDNLPIT	273
CDRL3-64	QHYDNLPIT	274
CDRL3-65	QHYDNLPIT	274

FIGURA 6F

CDRS DE LA CADENA PESADA

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
CDRH1-1	CDRH1-10.1	GYTFTSYGIS	275
CDRH1-2	CDRH1-10	GYTFTSYGIS	275
CDRH1-3	CDRH1-42	GYTFTGHYMH	276
CDRH1-4	CDRH1-40	GYTFTGYYMH	277
CDRH1-5	CDRH1-30	GYTLTELSMH	278
CDRH1-6	CDRH1-31	GYTLTELSMH	278
CDRH1-7	CDRH1-29	GFSLSNARMGVS	279
CDRH1-8	CDRH1-20	GFSLSNARMGVS	279
CDRH1-9	CDRH1-65	GFSLSTGGVGVG	280
CDRH1-10	CDRH1-56	GFSLSTGGVGVG	280
CDRH1-11	CDRH1-62	GFSLNTGGVGVG	281
CDRH1-12	CDRH1-2	GFSLSTGGVGVG	280
CDRH1-13	CDRH1-59	GFSLSTGGVGVG	280
CDRH1-14	CDRH1-57	GFSLSTGGVGVG	280
CDRH1-15	CDRH1-64	GFSLSTGGVGVG	280
CDRH1-16	CDRH1-41	GFPFSRYSMN	282
CDRH1-17	CDRH1-45	GFTFSSYAMN	283
CDRH1-18	CDRH1-47	GFTFSSYAMS	284
CDRH1-19	CDRH1-51	GFTFSSYAMS	284
CDRH1-20	CDRH1-52	GFTFSSYAMS	284
CDRH1-21	CDRH1-13	GFTFSSYGMH	285
CDRH1-22	CDRH1-14	GFTFSSYGMH	285
CDRH1-23	CDRH1-1	GFTFSSYGMH	285
CDRH1-24	CDRH1-22	GFTFSSYDMH	286
CDRH1-25	CDRH1-23	GFTFSSYDMH	286
CDRH1-26	CDRH1-12	GFTFSSYGMH	285
CDRH1-27	CDRH1-5	GFTFSSYGMH	285
CDRH1-28	CDRH1-15	GFTFSSYGMH	285
CDRH1-29	CDRH1-7	GFTFSSYGMH	285
CDRH1-30	CDRH1-61	GFTFRSHGMH	287
CDRH1-31	CDRH1-39	GFTFSAYSMN	288
CDRH1-32	CDRH1-34	GFTFSSYSMN	289
CDRH1-33	CDRH1-6	GFTFSSYSMN	289
CDRH1-34	CDRH1-35	GFTFSSYSMN	289
CDRH1-35	CDRH1-21	GGSVSSGGYYWS	290
CDRH1-36	CDRH1-8	GGSISRGGYYWS	291
CDRH1-37	CDRH1-9	GGSISRGGYYWS	291
CDRH1-38	CDRH1-18	GGSISSGGYYWS	292

FIGURA 7A

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
CDRH1-39	CDRH1-24	GGSISSGGYYWS	292
CDRH1-40	CDRH1-25	GGSISSGGYYWS	292
CDRH1-41	CDRH1-26	GGSISSGGYYWS	292
CDRH1-42	CDRH1-27	GGSISSGGYYWS	292
CDRH1-43	CDRH1-38	GGSISSGGYYWS	292
CDRH1-44	CDRH1-54	GGSISSGDYYWN	293
CDRH1-45	CDRH1-55	GGSISSGDYYWN	293
CDRH1-46	CDRH1-43	GGSFSGYYWS	294
CDRH1-47	CDRH1-44	GGSFSGYYWS	294
CDRH1-48	CDRH1-49	GGSFSGYYWS	294
CDRH1-49	CDRH1-50	GGSFSGYYWS	294
CDRH1-50	CDRH1-53	GGSFSGYYWS	294
CDRH1-51	CDRH1-33	GGSISSYYWS	295
CDRH1-52	CDRH1-3	GGSVSSGGSYWS	296
CDRH1-53	CDRH1-4	GGSVSSGGSYWS	296
CDRH1-54	CDRH1-16	GYRFTSYWIG	297
CDRH1-55	CDRH1-17	GYSFTSYWIG	298
CDRH1-56	CDRH1-11	GYSFTSYWIG	298
CDRH1-57	CDRH1-37	GDSVSSYSAAWN	299
CDRH1-58	CDRH1-39.1	GFTFSAYSMN	288
CDRH2-1	CDRH2-10.1	WISASNGNTNYAQKLQD	300
CDRH2-2	CDRH2-10	WISASNGNTNYAQKLQD	300
CDRH2-3	CDRH2-42	WINPNSGGTNCAQKFQG	301
CDRH2-4	CDRH2-40	WINPNSGGTNHTQKFQG	302
CDRH2-5	CDRH2-30	SFDPEDGETIYAQKFQG	303
CDRH2-6	CDRH2-31	SFDPEDGETIYAQKFQG	303
CDRH2-7	CDRH2-29	HIFSNDEKSYSTSLKS	304
CDRH2-8	CDRH2-20	LIFSNDEKSYSTSLKS	305
CDRH2-9	CDRH2-65	LIYWNDDKRYSPSLKS	306
CDRH2-10	CDRH2-56	LIYWNDDKRYSPSLKS	306
CDRH2-11	CDRH2-62	LIYWNDDKRYSPSLKS	306
CDRH2-12	CDRH2-2	LIYWNDDKRYSPSLKS	306
CDRH2-13	CDRH2-59	LIYWNVEKRYSPSLRS	307
CDRH2-14	CDRH2-57	LIYWNDDKRYSPSLKS	306
CDRH2-15	CDRH2-64	LIYWNDDKRYSPSLKS	306
CDRH2-16	CDRH2-41	AISSSSSYIYYADSVKG	308
CDRH2-17	CDRH2-45	AISGSGGSTYYADSVKG	309
CDRH2-18	CDRH2-47	AISGSGGSTYYADSVKG	309
CDRH2-19	CDRH2-51	AISGSGGSTYYADSVKG	309
CDRH2-20	CDRH2-52	AISGSGGSTYYADSVKG	309

FIGURA 7B

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
CDRH2-21	CDRH2-13	FISDDGSTKYYADSVKG	310
CDRH2-22	CDRH2-14	FISDDGSTKYYADSVKG	310
CDRH2-23	CDRH2-1	VIWYDGSNKYYADSVKG	311
CDRH2-24	CDRH2-22	VIWYDGSIKYYADSVKG	312
CDRH2-25	CDRH2-23	VIWYDGSIKYYADSVKG	312
CDRH2-26	CDRH2-12	VIWYDGSNKYYADSVKG	311
CDRH2-27	CDRH2-5	VIWSDGSNKYYADSVKG	313
CDRH2-28	CDRH2-15	VIWDDGSNQYYTDSVKG	314
CDRH2-29	CDRH2-7	VIWYDGSNKRYVDSVKG	315
CDRH2-30	CDRH2-61	VIWYDGSNKNYADSVRG	316
CDRH2-31	CDRH2-39	YISSSGRTIYYADSVKG	317
CDRH2-32	CDRH2-34	HISSSSRTIYYADSVKG	318
CDRH2-33	CDRH2-6	HISRSSRTIYYADSVKG	319
CDRH2-34	CDRH2-35	HISRSSRTIYYADSVKG	319
CDRH2-35	CDRH2-21	YIHSSGSTYYNPSLKS	320
CDRH2-36	CDRH2-8	YIYHSGSTYYNPSLKS	321
CDRH2-37	CDRH2-9	YIYHSGSTYYNPSLKS	321
CDRH2-38	CDRH2-18	YIYYSGSTYYNPSLKS	322
CDRH2-39	CDRH2-24	YIHYSGSTYYNPSLKS	323
CDRH2-40	CDRH2-25	YIHYSGSTYYNPSLKS	323
CDRH2-41	CDRH2-26	YIHSSGSTYYNPSLKS	320
CDRH2-42	CDRH2-27	YIHSSGSTYYNPSLKS	320
CDRH2-43	CDRH2-38	YIHYSGSTYYNPSLKS	323
CDRH2-44	CDRH2-54	YIYYSGGTYYNPSLKS	324
CDRH2-45	CDRH2-55	YIYYSGGTYYNPSLKS	324
CDRH2-46	CDRH2-43	EINHSGSTNYNPSLKS	325
CDRH2-47	CDRH2-44	EINHSGSTNYNPSLKS	325
CDRH2-48	CDRH2-49	EINHSGSTNYNPSLKS	325
CDRH2-49	CDRH2-50	EINHSGSTNYNPSLKS	325
CDRH2-50	CDRH2-53	EINHSGSTNYNPSLKS	325
CDRH2-51	CDRH2-33	RIYTSGTTNYNPSLKS	326
CDRH2-52	CDRH2-3	YIYYSGSTNYNPSLKS	327
CDRH2-53	CDRH2-4	YIYYSGSTNYNPSLKS	327
CDRH2-54	CDRH2-16	IIYPDDSDTRYSPSFQG	328
CDRH2-55	CDRH2-17	IIYPDDSDARYSPSFQG	329
CDRH2-56	CDRH2-11	IIYPGDSDIRYSPSFQG	330
CDRH2-57	CDRH2-37	RTYCRSKWYNDYAVSVKS	331
CDRH2-58	CDRH2-39.1	YISSSGRTIYYADSVKG	317
CDRH3-1	CDRH3-10.1	EDNWNYGFFDY	332
CDRH3-2	CDRH3-10	EDNWNYGFFDY	332

FIGURA 7C

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
CDRH3-3	CDRH3-42	SIAVALDY	333
CDRH3-4	CDRH3-40	SIAVALDY	333
CDRH3-5	CDRH3-30	EGDGGYYYYGMDV	334
CDRH3-6	CDRH3-31	EGDGGYYYYGMDV	334
CDRH3-7	CDRH3-29	MYSSGWYGVFDY	335
CDRH3-8	CDRH3-20	VYSSGWSFYGMDV	336
CDRH3-9	CDRH3-65	RRELPFDY	337
CDRH3-10	CDRH3-56	RNWTPFDY	338
CDRH3-11	CDRH3-62	RLELPFDY	339
CDRH3-12	CDRH3-2	RREVPFDY	340
CDRH3-13	CDRH3-59	RHTNPFEY	341
CDRH3-14	CDRH3-57	RGELPFDY	342
CDRH3-15	CDRH3-64	RGELPFDY	342
CDRH3-16	CDRH3-41	DRVGATPDAFDI	343
CDRH3-17	CDRH3-45	EGIAVAGTAEYYYYYAMDV	344
CDRH3-18	CDRH3-47	EGIAARDSYYYYAMDV	345
CDRH3-19	CDRH3-51	EGIAGRDSYYYYGMDV	346
CDRH3-20	CDRH3-52	EGIAGRDSYYYYGMDV	346
CDRH3-21	CDRH3-13	SYYDSSGYYYGFDY	347
CDRH3-22	CDRH3-14	SYYDSSGYYYGFDY	347
CDRH3-23	CDRH3-1	NVIDY	348
CDRH3-24	CDRH3-22	GGATGAEYFQH	349
CDRH3-25	CDRH3-23	GGATGAEYFQH	349
CDRH3-26	CDRH3-12	LWFGETFDY	350
CDRH3-27	CDRH3-5	NLPFDY	351
CDRH3-28	CDRH3-15	SHYGGDYDYYGMDV	352
CDRH3-29	CDRH3-7	DGWQQQAPFDY	353
CDRH3-30	CDRH3-61	WGISAPFDC	354
CDRH3-31	CDRH3-39	WAPFDY	355
CDRH3-32	CDRH3-34	DGYNWNGGGNYYGMDV	356
CDRH3-33	CDRH3-6	DGYNWNNGGYYYGMDV	357
CDRH3-34	CDRH3-35	DGYNWNNGGYYYGMDV	357
CDRH3-35	CDRH3-21	GPYYGMDV	358
CDRH3-36	CDRH3-8	ALRGIVLMVYVLGALDI	359
CDRH3-37	CDRH3-9	ALRGIVLMVYVLGALDI	359
CDRH3-38	CDRH3-18	DETVVRGLIRYCYGMDV	360
CDRH3-39	CDRH3-24	DRGGGDYGRMDV	361
CDRH3-40	CDRH3-25	DRGGGDYGRMDV	361
CDRH3-41	CDRH3-26	SNNYGCFAL	362
CDRH3-42	CDRH3-27	SNNYGCFAL	362

FIGURA 7D

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
CDRH3-43	CDRH3-38	GYNYGLYYYDSSGYPSYYYGMDV	363
CDRH3-44	CDRH3-54	TYYDILTGYPFYFDY	364
CDRH3-45	CDRH3-55	TYYDILTGYPFYFDY	364
CDRH3-46	CDRH3-43	GGYSSSWYWFDP	365
CDRH3-47	CDRH3-44	GGYSSSWFWFDP	366
CDRH3-48	CDRH3-49	GGYSSSWFWFDP	366
CDRH3-49	CDRH3-50	GGYSSSWFWFDP	366
CDRH3-50	CDRH3-53	GGYSSSWFWFDP	366
CDRH3-51	CDRH3-33	DGYSYGHYYYYGMDV	367
CDRH3-52	CDRH3-3	SALRYFDWLFSDVSDI	368
CDRH3-53	CDRH3-4	SALRYFDWLFSDVSDI	368
CDRH3-54	CDRH3-16	QKSYGYSYFDY	369
CDRH3-55	CDRH3-17	QGYGSGWGYFDY	370
CDRH3-56	CDRH3-11	QGLAVAGTSYYYYYGMDV	371
CDRH3-57	CDRH3-37	DRAVAGYYYGMDV	372
CDRH3-58	CDRH3-39.1	WAPFDY	355

FIGURA 7E

FRS DE LA CADENA LIGERA

NOMBRE	SECUENCIA	SEQ ID NO:
FRL1-1	DVVMTQSPLSLPVTLGQPASISC	388
FRL1-2	DVVMTQSPLSLPVTLGQPASISC	388
FRL1-3	DVVMTQSPLSLPVTLGQPASISC	389
FRL1-4	DVVMTQSPLSLPVTLGQPASISC	389
FRL1-5	DIVMTQTPLSLSVTPGQPASISC	390
FRL1-6	DIVMTQTPLSLSVTPGQPASISC	390
FRL1-7	DIVMTQTPLSLSVTPGQPASISC	390
FRL1-8	DIVMTQTPLSLSVTPGQPASISC	391
FRL1-9	DIVMTQTPLSLSVTPGQPASISC	391
FRL1-11	DIQMTQSPSSLSASVGDRVTITC	392
FRL1-12	DIQMTQSPSSLSASVGDRVTIIC	392
FRL1-13	NIVMTQTPLSSPVTLGQPASISC	393
FRL1-14	NIVMTQTPLSSPVTLGQPASISC	393
FRL1-15	EIVMTQTPLSSPVTLGQPASISC	393
FRL1-16	EIVLTQSPGTLSLSPGERATLSC	394
FRL1-17	EIVLTQSPGTLSLSPGERATLSC	395
FRL1-18	DIQMTQSPSSLSASVGDRVTITC	396
FRL1-19	DIVMTQSPDSLAVSLGERATINC	397
FRL1-20	DIVMTQSPDSLAVSLGERATINC	397
FRL1-21	DIVMTQSPDSLAVSLGERATINC	398
FRL1-22	DIVMTQSPDSLAVSLGERATINC	398
FRL1-23	DIVMTQSPDSLAVSLGERATINC	398
FRL1-24	DIVMTQSPDSLTVSLGERATINC	398
FRL1-25	DIVMTQSPDSLTVSLGERATINC	398
FRL1-26	DIVMTQSPDSLAVSLGERATINC	398
FRL1-27	DIVMTQSPDSLAVSLGERATINC	398
FRL1-28	DIVMTQSPDSLAVSLGERATINC	399
FRL1-29	DIVMTQSPDSLAVSLGERATINC	399
FRL1-30	DIVMTQSPDSLAVSLGERATINC	398
FRL1-31	DIVMTQSPDSLAVSLGERATINC	398
FRL1-32	DIVMTQSPDSLAVSLGERATINC	398
FRL1-33	DIVMTQSPDSLAVSLGERATINC	398
FRL1-34	DIQMTQSPSSLSASVGDRVTITC	400
FRL1-35	DIQMTQSPSSLSASVGDRVAITC	401

FIGURA 8A

NOMBRE	SECUENCIA	SEQ ID NO:
FRL1-36	EIVMTQSPATLSVSPGERATLSC	402
FRL1-37	EIVMTQSPATLSVSPGERATLSC	402
FRL1-38	DIQMTQSPSSVSASVGDRVTITC	403
FRL1-39	DIQMTQSPSSLSASVGDRVTITC	404
FRL1-40	DIQMTQSPSSLSASLGDRVTITC	403
FRL1-41	DIQMTQSPSSLSASVGDRVTITC	405
FRL1-42	DIQMTQSPSSRSASVGDRVTITC	403
FRL1-43	DIQMTQSPSSLSASVGDRVTITC	406
FRL1-44	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-45	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-46	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-47	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-48	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-49	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-50	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-51	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-52	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-53	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-54	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-55	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-56	DIQMTQSPSSLSASVGDRVTITC	407
FRL1-57	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-58	DIQMTQSPSSLSASVGDRVAITC	403
FRL1-59	DIQMTQSPSSLSASVGDRVAITC	403
FRL1-60	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-61	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-62	DIQMTQSPSSLSASVGDGVTITC	403
FRL1-63	DIQMTQSPSSLSASVGDRVTITC	408
FRL1-64	DIQMTQSPSSLSASVGDRVTITC	403
FRL1-65	DIQMTQSPSSLSASVGDRVTITC	403
FRL2-1	WFQQRPGQSPRRLIY	408
FRL2-2	WFQQRPGQSPRRLIY	408
FRL2-3	WLQQRPGQSPRRLIY	409
FRL2-4	WLQQRPGQSPRRLIY	409
FRL2-5	WYLQKPGQPPQLLIY	410
FRL2-6	WYLQKPGQPPQLLIY	410

FIGURA 8B

NOMBRE	SECUENCIA	SEQ ID NO:
FRL2-7	WYLQKPGQPPQLLIY	410
FRL2-8	WFLQKPGQPPQPLIY	411
FRL2-9	WFLQKPGQPPQPLIY	411
FRL2-11	WYQQKPGKVPKLLIY	412
FRL2-12	WYQQKPGKVPKLLIY	412
FRL2-13	WLQQRPGQPPRLLIY	413
FRL2-14	WLQQRPGQPPRLLIY	413
FRL2-15	WLQQRPGQPPRLLIY	413
FRL2-16	WYQQKPGQAPRLLIS	414
FRL2-17	WYQQKPGQAPRLLIY	415
FRL2-18	WYQQKPGKAPKRLIY	416
FRL2-19	WYQQKPGQPPKLFIY	417
FRL2-20	WYQQKPGQPPKLFIY	417
FRL2-21	WYQQKPGQPPKLLIY	418
FRL2-22	WYQQKPGQPPKLLIY	418
FRL2-23	WYQQKPGQPPKLLIY	418
FRL2-24	WYQQKPGQPPKLLIY	418
FRL2-25	WYQQKPGQPPKLLIY	418
FRL2-26	WYQQKPGQPPKLLIY	418
FRL2-27	WYQQKPGQPPKLLIY	418
FRL2-28	WYQQKPGQPPKVLIY	419
FRL2-29	WYQQKPGQPPKVLIY	419
FRL2-30	WYQQKPGQPPKLLIY	418
FRL2-31	WYQQKPGQPPKLLIY	418
FRL2-32	WYQQKPGQPPKLLIY	418
FRL2-33	WYQQKPGQPPKLLIY	418
FRL2-34	WFQQKPGKAPKSLIY	420
FRL2-35	WLQQKPGKAPKSLIY	421
FRL2-36	WYQQDPGQAPRLLIY	422
FRL2-37	WYQQDPGQAPRLLIY	422
FRL2-38	WYQQKPGKAPKLLIY	423
FRL2-39	WYQQKPGKAPKFLIY	424
FRL2-40	WYQQKPGKAPKLLIY	423
FRL2-41	WYQQRPGNAPKLLIY	425
FRL2-42	WYQQKPGKAPKLLIY	423
FRL2-43	WYQQKPGKAPKVLIY	426

FIGURA 8C

NOMBRE	SECUENCIA	SEQ ID NO:
FRL2-44	WYQQKPGKAPKLLIY	423
FRL2-45	WYQQKPGKAPKLLIY	423
FRL2-46	WYQQKPGKAPKLLIY	423
FRL2-47	WYQQKPGKAPKLLIY	423
FRL2-48	WYQQKPGKAPKLLIY	423
FRL2-49	WYQQKPGKAPKLLIY	423
FRL2-50	WYQQKPGKAPKLLIY	423
FRL2-51	WYQQKPGKAPKLLIY	423
FRL2-52	WYQQKPGKAPKLLIY	423
FRL2-53	WYQQKPGKAPKLLIY	423
FRL2-54	WYQQKPGKAPKLLIY	423
FRL2-55	WYQQKPGKAPKLLIY	423
FRL2-56	WYQQKPGKAPELLIY	427
FRL2-57	WYQQKPGKAPKLLIY	423
FRL2-58	WYQQKPGKAPKLLIY	423
FRL2-59	WYQQKPGKAPKLLIY	423
FRL2-60	WYQQKPGKAPKLLIY	423
FRL2-61	WYQQKPGKAPKLLIY	423
FRL2-62	WYQQKPGKAPKLLIY	423
FRL2-63	WYQQKLGKAPKLLIH	428
FRL2-64	WYQQKPGKAPKLLIY	423
FRL2-65	WYQQKPGKAPKLLIY	423
FRL3-1	GVPDRFNGSGSGTDFTLKISRVEAEDVGVYYC	429
FRL3-2	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	430
FRL3-3	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	430
FRL3-4	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	430
FRL3-5	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	430
FRL3-6	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	430
FRL3-7	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	430
FRL3-8	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	430
FRL3-9	GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC	430
FRL3-11	GVPSRFSGSGSGTDFTLTISSLQPEDVATYYC	431
FRL3-12	GVPSRFSGSGSGTDFTLTISSLQPEDVATYYC	431
FRL3-13	GVPDRFSGSGAGTDFTLKISRVEAEDVGVYYC	432
FRL3-14	GVPDRFSGSGAGTDFTLKISRVEAEDVGVYYC	432

FIGURA 8D

NOMBRE	SECUENCIA	SEQ ID NO:
FRL3-15	GVPDRFSGTGAGTDFTLKISRVEAEDVGVYYC	433
FRL3-16	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	434
FRL3-17	GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYC	434
FRL3-18	GVPSRFSGSGSGTEFTLTISSLQPEDFATYYC	435
FRL3-19	GVPDRFTGSGSGTDFTLTISSLQAEDVAVYYC	436
FRL3-20	GVPDRFTGSGSGTDFTLTISSLQAEDVAVYYC	436
FRL3-21	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC	437
FRL3-22	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYFC	438
FRL3-23	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYFC	438
FRL3-24	GVPDRFGGSGSGTDFTLTISSLQAEDVAVYYC	439
FRL3-25	GVPDRFGGSGSGTDFTLTISSLQAEDVAVYYC	439
FRL3-26	GVPDRFSGSGSGTDFTLTISSLQADDVAVYYC	440
FRL3-27	GVPDRFSGSGSGTDFTLTISSLQADDVAVYYC	440
FRL3-28	GVPDRFSGSGSGTDFTLTISGLQAEDVALYYC	441
FRL3-29	GVPDRFSGSGSGTDFTLTISGLQAEDVALYYC	441
FRL3-30	GVPDRFSGSGSGTDFTLTISSLQAEDVAVFYC	442
FRL3-31	GVPDRFSGSGSGTDFTLTISSLQAEDVAVFYC	442
FRL3-32	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYFC	438
FRL3-33	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYFC	438
FRL3-34	GVPSKFSGSGSGTDFTLTISSLQPEDFATYYC	443
FRL3-35	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	444
FRL3-36	GIPARFSGSGSGTEFTLTISSLQSEDFAVYYC	445
FRL3-37	GIPARFSGSGSGTEFTLTISSLQSEDFAVYYC	445
FRL3-38	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	444
FRL3-39	GVPSRFSGSGSGTDFTLTISSLQPEDFAAYYC	446
FRL3-40	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	444
FRL3-41	GVPSRVSGSGSGTDFTLTIRSLQPEDFATYYC	447
FRL3-42	GVPSRFSGSGSGTDFTLTLSSLQPEDFATYYC	448
FRL3-43	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	444
FRL3-44	GVPSRFSGSGSGTDFTLTISSLQPENFATYYC	449
FRL3-45	GVPSRFSGSGSGTDFTLTFSSLQPEDFATYYC	450
FRL3-46	GVPSRFSGSGSGTDFTLTLSSLQPEDFASYYC	451
FRL3-47	GVPSRFSGSGSGTDFTLTLSSLQPEDFASYYC	451
FRL3-48	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	444
FRL3-49	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	444
FRL3-50	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	444

FIGURA 8E

NOMBRE	SECUENCIA	SEQ ID NO:
FRL3-51	GVPSRFSGSGSGTDFTLTISSLQPEDFASYYC	452
FRL3-52	GVPSRFSGSGSGTDFTLTISSLQPEDFASYYC	452
FRL3-53	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC	444
FRL3-54	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	453
FRL3-55	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	453
FRL3-56	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	453
FRL3-57	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	453
FRL3-58	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	453
FRL3-59	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	453
FRL3-60	GVPSRFSGSGSETDFTFTISSLQPEDIATYYC	454
FRL3-61	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	453
FRL3-62	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	453
FRL3-63	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	453
FRL3-64	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	453
FRL3-65	GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC	453
FRL4-1	FGQGTRLEIK	455
FRL4-2	FGQGTRLEIK	455
FRL4-3	FGQGTRLEIK	455
FRL4-4	FGQGTRLEIK	455
FRL4-5	FGQGTKLEIK	457
FRL4-6	FGGGTKVEIK	458
FRL4-7	FGGGTKVEIK	458
FRL4-8	FGHGTRLEIK	459
FRL4-9	FGHGTRLEIK	459
FRL4-11	FGPGTKVDIK	460
FRL4-12	FGGGTKVEIK	458
FRL4-13	FGPGTKVDIK	460
FRL4-14	FGPGTKVDIK	460
FRL4-15	FGGGTKVEIK	458
FRL4-16	FGQGTKVEIK	461
FRL4-17	FGQGTKLEIK	457
FRL4-18	FGQGTKVEIK	461
FRL4-19	FGQGTKVEIK	461
FRL4-20	FGQGTKVEIK	461
FRL4-21	FGQGTKVEIK	461
FRL4-22	FGQGTKVEIK	461

FIGURA 8F

NOMBRE	SECUENCIA	SEQ ID NO:
FRL4-23	FGQGTKVEIK	461
FRL4-24	FGQGTKVEIK	461
FRL4-25	FGQGTKVEIK	461
FRL4-26	FGPGTKVEIK	462
FRL4-27	FGPGTKVEIK	462
FRL4-28	FGQGTKLEIK	457
FRL4-29	FGQGTKLEIK	457
FRL4-30	FGGGTKVAIK	463
FRL4-31	FGGGTKVAIK	463
FRL4-32	FGGGTKVEIK	458
FRL4-33	FGGGTKVEIK	458
FRL4-34	FGPGTKVDIK	460
FRL4-35	FGPGTKMDIK	464
FRL4-36	FGQGTKVEIK	461
FRL4-37	FGQGTKVEIK	461
FRL4-38	FGQGTKVEFK	465
FRL4-39	FGPGTKVDIK	460
FRL4-40	FGGGTKVEIK	458
FRL4-41	FGGGTKVEIK	458
FRL4-42	FGQGTRLEIK	455
FRL4-43	FGQGTRLEII	456
FRL4-44	FGQGTRLEIK	455
FRL4-45	FGQGTRLEIK	455
FRL4-46	FGQGTRLEIK	455
FRL4-47	FGQGTRLEIK	455
FRL4-48	FGQGTRLEIK	455
FRL4-49	FGQGTRLEIK	455
FRL4-50	FGQGTRLEIK	455
FRL4-51	FGQGTRLEIK	455
FRL4-52	FGQGTRLEIK	455
FRL4-53	FGQGTRLEIK	455
FRL4-54	FGPGTKVDIK	460
FRL4-55	FGPGTKVDIK	460
FRL4-56	FGGGTKVEIK	458
FRL4-57	FGGGTKVEIK	458
FRL4-58	FGGGTKVEIK	458

FIGURA 8G

NOMBRE	SECUENCIA	SEQ ID NO:
FRL4-59	FGGGTKVEIK	458
FRL4-60	FGGGTKVEIK	458
FRL4-61	FGGGTKVEIR	466
FRL4-62	FGQGTRLEIK	455
FRL4-63	FGQGTRLEIK	455
FRL4-64	FGQGTRLEIK	455
FRL4-65	FGQGTRLEIK	455

FIGURA 8H

FRS DE LA CADENA PESADA

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
FRH1-1	FRH1-10.1	QVQLVQSGAEVKKPGASVKVSCKAS	467
FRH1-2	FRH1-10	QVQLVQSGAEVKKPGASVKVSCKAS	467
FRH1-3	FRH1-42	QVHLVQSGAEVKKPGASVKVSCKVS	468
FRH1-4	FRH1-40	QVQLVQSGAEVKKPGASVKVSCKAS	467
FRH1-5	FRH1-30	QVQLVQSGAEVRKPGASVKVSCKVS	469
FRH1-6	FRH1-31	QVQLVQSGAEVRKPGASVKVSCKVS	469
FRH1-7	FRH1-29	QVTLKESGPVLVKPTETLTLTCTVS	470
FRH1-8	FRH1-20	QVTLKESGPVLVKPTETLTLTCTVS	470
FRH1-9	FRH1-65	QITLKESGPTLVKPTQTLTLTCTFS	471
FRH1-10	FRH1-56	QITLKESGPTLVKPTQTLTLTCTFS	471
FRH1-11	FRH1-62	QITLKESGPTLVKPTQTLTLTCTFS	471
FRH1-12	FRH1-2	QITLKESGPTLVKPTQTLTLTCTFS	471
FRH1-13	FRH1-59	QITLKESGPTLVKPTQTLTLTCTFS	471
FRH1-14	FRH1-57	QITLKESGPTLVKPTQTLTLTCTFS	471
FRH1-15	FRH1-64	QITLKESGPTLVKPTQTLTLTCTFS	471
FRH1-16	FRH1-41	EVQLVESGGGLVKPGGSLRLSCAAS	472
FRH1-17	FRH1-45	EVQLLESGGGLVQPGGSLRLSCAAS	473
FRH1-18	FRH1-47	EVQLLESGGGLVQPGGSLRLSCAAS	473
FRH1-19	FRH1-51	EVQLLESGGGLVQPGGSLRLSCTAS	474
FRH1-20	FRH1-52	EVQLLESGGGLVQPGGSLRLSCTAS	474
FRH1-21	FRH1-13	QVQLVESGGGVVQPGRSLRLSCAAS	475
FRH1-22	FRH1-14	QVQLVESGGGVVQPGRSLRLSCAAS	475
FRH1-23	FRH1-1	QVQLVESGGGVVQPGRSLRLSCAAS	475
FRH1-24	FRH1-22	QVQLVESGGGVVQPGRSLRLSCAAS	475
FRH1-25	FRH1-23	QVQLVESGGGVVQPGRSLRLSCAAS	475
FRH1-26	FRH1-12	QVQLVESGGGVVQPGRSLRLSCAAS	475
FRH1-27	FRH1-5	QVQLVESGGGVVQPGRSLRLSCAAS	475
FRH1-28	FRH1-15	QVQLVESGGGVVQPGRSLRLSCAAS	475
FRH1-29	FRH1-7	QVQLVESGGGVVQPGRSLRLSCAAS	475
FRH1-30	FRH1-61	QVQLVESGGGVVQPGRSLRLSCAAS	475
FRH1-31	FRH1-39	EVQLVESGGGLVQPGGSLRLSCAAS	476
FRH1-32	FRH1-34	EVQLVESGGGLVQPGGSLRLSCAAS	476
FRH1-33	FRH1-6	EVQLVESGGGLVQPGGSLRLSCAAS	476
FRH1-34	FRH1-35	EVQLVESGGGLVQPGGSLRLSCAAS	476
FRH1-35	FRH1-21	QVQLQESGPGLVKPSQTLSLTCTVS	477
FRH1-36	FRH1-8	QVQLQESGPGLVKPSQTLSLTCTVS	477
FRH1-37	FRH1-9	QVQLQESGPGLVKPSQTLSLTCTVS	477

FIGURA 9A

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
FRH1-38	FRH1-18	QVQLQESGPGLVKPSQTLSLTCTVS	477
FRH1-39	FRH1-24	QVQLQESGPGLVKPSQTLSLNCTVS	478
FRH1-40	FRH1-25	QVQLQESGPGLVKPSQTLSLNCTVS	478
FRH1-41	FRH1-26	QVQLQESGPGLVKPSQTLSLTCTVS	477
FRH1-42	FRH1-27	QVQLQESGPGLVKPSQTLSLTCTVS	477
FRH1-43	FRH1-38	QVQLQESGPGLVKPSQTLSLTCTVS	477
FRH1-44	FRH1-54	QVQLQESGPGLVKPSQTLSLTCTVS	477
FRH1-45	FRH1-55	QVQLQESGPGLVKPSQTLSLTCTVS	477
FRH1-46	FRH1-43	QVQLQQWGAGLLKPSETLSLTCAVY	479
FRH1-47	FRH1-44	QVQLQQWGAGLLKPSETLSLTCAVY	479
FRH1-48	FRH1-49	QVQLQQWGAGLLKPSETLSLTCAVY	479
FRH1-49	FRH1-50	QVQLQQWGAGLLKPSETLSLTCAVY	479
FRH1-50	FRH1-53	QVQLQQWGAGLLKPSETLSLTCAVY	479
FRH1-51	FRH1-33	QVQLQESGPGLVKPSETLSLTCTVS	480
FRH1-52	FRH1-3	QVQLQESGPGLVKPSETLSLTCTVS	480
FRH1-53	FRH1-4	QVQLQESGPGLVKPSETLSLTCTVS	480
FRH1-54	FRH1-16	EVQLVQSGAELKKPGESLKISCKGS	481
FRH1-55	FRH1-17	EVQLVQSGAEVKKPGESLKISCKGS	482
FRH1-56	FRH1-11	EVQLVQSGAEVKKPGESLKISCKGS	482
FRH1-57	FRH1-37	QVQLQQSGPGLVKPSQTLSLTCAIS	483
FRH1-58	FRH1-39.1	EVQLVESGGGLVQPGGSLRLSCAAS	476
FRH2-1	FRH2-10.1	WVRQAPGQGLEWMG	484
FRH2-2	FRH2-10	WVRQAPGQGLEWMG	484
FRH2-3	FRH2-42	WVRQAPGQGLEWMG	484
FRH2-4	FRH2-40	WVRQAPGQGLEWMG	484
FRH2-5	FRH2-30	WVRQAPGKGLEWMG	485
FRH2-6	FRH2-31	WVRQAPGKGLEWMG	485
FRH2-7	FRH2-29	WIRQPPGKALEWLA	486
FRH2-8	FRH2-20	WIRQPPGKALEWLV	487
FRH2-9	FRH2-65	WIRQPPGKALEWLA	486
FRH2-10	FRH2-56	WIRQPPGKALEWLA	486
FRH2-11	FRH2-62	WIRQPPGKALEWLA	486
FRH2-12	FRH2-2	WIRQPPGKALEWLA	486
FRH2-13	FRH2-59	WIRQPPGKALEWLA	486
FRH2-14	FRH2-57	WIRQPPGKALEWLA	486
FRH2-15	FRH2-64	WIRQPPGKALEWLA	486
FRH2-16	FRH2-41	WVRQAPGKGLEWVS	488
FRH2-17	FRH2-45	WVRQAPGKGLEWVS	488
FRH2-18	FRH2-47	WVRQAPGKGLEWVS	488
FRH2-19	FRH2-51	WVRQAPGKGLEWVS	488

FIGURA 9B

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
FRH2-20	FRH2-52	WVRQAPGKGLEWVS	488
FRH2-21	FRH2-13	WVRQAPGKGLEWVA	489
FRH2-22	FRH2-14	WVRQAPGKGLEWVA	489
FRH2-23	FRH2-1	WVRQAPGKGLEWVA	489
FRH2-24	FRH2-22	WVRQAPGKGLEWVA	489
FRH2-25	FRH2-23	WVRQAPGKGLEWVA	489
FRH2-26	FRH2-12	WVRQAPGKGLEWVA	489
FRH2-27	FRH2-5	WVRQAPGKGLEWVA	489
FRH2-28	FRH2-15	WVRQAPGKGLEWVA	489
FRH2-29	FRH2-7	WVRQAPGKGLEWVA	489
FRH2-30	FRH2-61	WVRQAPGKGLEWVA	489
FRH2-31	FRH2-39	WVRQAPGKGLEWVS	488
FRH2-32	FRH2-34	WVRQAPGKGLEWVS	488
FRH2-33	FRH2-6	WVRQAPGKGLEWVS	488
FRH2-34	FRH2-35	WVRQAPGKGLEWVS	488
FRH2-35	FRH2-21	WIRQHPGKGLEWIG	490
FRH2-36	FRH2-8	WIRQHPGKGLEWIG	490
FRH2-37	FRH2-9	WIRQHPGKGLEWIG	490
FRH2-38	FRH2-18	WIRQHPGKGLEWIG	490
FRH2-39	FRH2-24	WIRQHPGKGLEWIG	490
FRH2-40	FRH2-25	WIRQHPGKGLEWIG	490
FRH2-41	FRH2-26	WIRQHPGKGLEWIG	490
FRH2-42	FRH2-27	WIRQHPGKGLEWIG	490
FRH2-43	FRH2-38	WIRQHPGKGLEWIG	490
FRH2-44	FRH2-54	WVRQHPGKGLEWIG	491
FRH2-45	FRH2-55	WVRQHPGKGLEWIG	491
FRH2-46	FRH2-43	WIRQPPGKGLEWIG	492
FRH2-47	FRH2-44	WIRQPPGKGLEWIG	492
FRH2-48	FRH2-49	WIRQPPGKGLEWIG	492
FRH2-49	FRH2-50	WIRQPPGKGLEWIG	492
FRH2-50	FRH2-53	WIRQPPGKGLEWIG	492
FRH2-51	FRH2-33	WIRQPAGKGLEWIG	493
FRH2-52	FRH2-3	WIRQPPGKGLEWIG	492
FRH2-53	FRH2-4	WIRQPPGKGLEWIG	492
FRH2-54	FRH2-16	WVRQMPGKGLEWMG	494
FRH2-55	FRH2-17	WVRQMPGKGLEWMG	494
FRH2-56	FRH2-11	WVRQMPGKGLEWMG	494
FRH2-57	FRH2-37	WIRQSPSRGLEWLG	495
FRH2-58	FRH2-39.1	WVRQAPGKGLEWVS	488
FRH3-1	FRH3-10.1	RVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR	496

FIGURA 9C

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
FRH3-2	FRH3-10	RVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR	496
FRH3-3	FRH3-42	RVTMTRDTSISTAYMELSRLRSDDTAVYYCAR	497
FRH3-4	FRH3-40	RVTMTRDTSISTAYMELSRLRSDDTAVYYCAR	497
FRH3-5	FRH3-30	RVTMLEDTSTDTAYMELSSLRSEDTAVYYCAT	498
FRH3-6	FRH3-31	RVTMLEDTSTDTAYMELSSLRSEDTAVYYCAT	498
FRH3-7	FRH3-29	RLTISKDTSKSQVVLTMTNMDPVDTATYYCAR	499
FRH3-8	FRH3-20	RLTISKDTSKSQVVLTMTNMDPVDTATYYCAR	499
FRH3-9	FRH3-65	RLTITKDTSKNQVVLTMTNMDPVDTATYYCAH	500
FRH3-10	FRH3-56	RLTITKDTSKTQVVLTVTDMDPVDTATYYCAH	501
FRH3-11	FRH3-62	RLTITKDTSKNQVVLTMTNMDPVDTATYYCAH	500
FRH3-12	FRH3-2	RLTITKDTSKNQVVLTMTNLDPVDTATYYCAH	502
FRH3-13	FRH3-59	RLTITKATSKNQVVLTMTNMDPVDTATYYCAH	503
FRH3-14	FRH3-57	RLTITKDTSKNQVVLTMTNMDPVDTATYYCAH	500
FRH3-15	FRH3-64	RLTITKDTSKNQVVLTMTNMDPVDTATYYCAH	500
FRH3-16	FRH3-41	RFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR	504
FRH3-17	FRH3-45	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK	505
FRH3-18	FRH3-47	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK	505
FRH3-19	FRH3-51	RFTISRDNSKNTLYLQMNSLRAEDTAEYYCAK	506
FRH3-20	FRH3-52	RFTISRDNSKNTLYLQMNSLRAEDTAEYYCAK	506
FRH3-21	FRH3-13	RFTISRDNSMNTLYLQMNSLRAEDTAVYYCAR	507
FRH3-22	FRH3-14	RFTISRDNSMNTLYLQMNSLRAEDTAVYYCAR	507
FRH3-23	FRH3-1	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	508
FRH3-24	FRH3-22	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	508
FRH3-25	FRH3-23	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	508
FRH3-26	FRH3-12	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCVL	509
FRH3-27	FRH3-5	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	508
FRH3-28	FRH3-15	RFTVSRDNSKNTLFLQMNSLRAEDTAVYYCAR	510
FRH3-29	FRH3-7	RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR	508
FRH3-30	FRH3-61	RFTISRDNSKNTLDLQMNSLRAEDTAVYYCAR	510
FRH3-31	FRH3-39	RFTISRDNAKNSLFLQMNSLRDEDTAVYYCAL	511
FRH3-32	FRH3-34	RFTISRDNAKNSVYLQMNSLRDEDTAVYYCAR	512
FRH3-33	FRH3-6	RFTISRDNAKNSLYLQMNSLRDEDTAVYYCAR	513
FRH3-34	FRH3-35	RFTISRDNAKNSLYLQMNSLRDEDTAVYYCAR	513
FRH3-35	FRH3-21	RVTISVDTSKNQFSLNLSSVTAADTAVYYCAR	514
FRH3-36	FRH3-8	RVNMSVDTSKNQFSLKLSSVTAADTAVYYCAR	515
FRH3-37	FRH3-9	RVNMSVDTSKNQFSLKLSSVTAADTAVYYCAR	515
FRH3-38	FRH3-18	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	516
FRH3-39	FRH3-24	RITISADTSKNQFSLKLNSVTAADTAVYYCAR	517
FRH3-40	FRH3-25	RITISADTSKNQFSLKLNSVTAADTAVYYCAR	517
FRH3-41	FRH3-26	RITKSVDTSKNQFSLKLSSVTAADTAVYYCAR	518

FIGURA 9D

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
FRH3-42	FRH3-27	RITKSVDTSKNQFSLKLSSVTAADTAVYYCAR	518
FRH3-43	FRH3-38	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAS	519
FRH3-44	FRH3-54	RVTISVDTSKNQFSLKLFSVTAADTAVYFCAR	520
FRH3-45	FRH3-55	RVTISVDTSKNQFSLKLFSVTAADTAVYFCAR	520
FRH3-46	FRH3-43	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	516
FRH3-47	FRH3-44	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	516
FRH3-48	FRH3-49	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	516
FRH3-49	FRH3-50	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	516
FRH3-50	FRH3-53	RVTISVDTSKNQFSLKLSSVTAADTAVYYCAR	516
FRH3-51	FRH3-33	RVTMSVDTSKNQFSLKLSSVTAADTAVYYCAR	521
FRH3-52	FRH3-3	RVTISIVTSRNQFSLKLSSVTAADTAVYYCAR	522
FRH3-53	FRH3-4	RVTISIVTSRNQFSLKLSSVTAADTAVYYCAR	522
FRH3-54	FRH3-16	QVTISADKSISTAYLQWSSLKASDTAMYYCAR	523
FRH3-55	FRH3-17	QVTISADKSINTAYLQWSSLKASDTAMYYCAR	524
FRH3-56	FRH3-11	QVTISADKSISTAYLQWSSLKASDTAMYYCAR	523
FRH3-57	FRH3-37	RITINPDTSKNQFSLQLNSVTPEDTAVYYCAR	525
FRH3-58	FRH3-39.1	RFTISRDNAKNSLFLQMNSLRDEDTAVYYCAL	511
FRH4-1	FRH4-10.1	WGQGTLVTVSS	526
FRH4-2	FRH4-10	WGQGTLVTVSS	526
FRH4-3	FRH4-42	WGQGTLVTVSS	526
FRH4-4	FRH4-40	WGQGTLVTVSS	526
FRH4-5	FRH4-30	WGQGTTVTVSS	527
FRH4-6	FRH4-31	WGQGTTVTVSS	527
FRH4-7	FRH4-29	WGQGTLVTVSS	526
FRH4-8	FRH4-20	WGQGTTVTVSS	527
FRH4-9	FRH4-65	WGQGTLVTVSS	526
FRH4-10	FRH4-56	WGQGTLVTVSS	526
FRH4-11	FRH4-62	WGQGTLVTVSS	526
FRH4-12	FRH4-2	WGQGTLVTVSS	526
FRH4-13	FRH4-59	WGQGTLVTVSS	526
FRH4-14	FRH4-57	WGQGTLVTVSS	526
FRH4-15	FRH4-64	WGQGTLVTVSS	526
FRH4-16	FRH4-41	WGQGTMVTVSS	528
FRH4-17	FRH4-45	WGQGTTVTVSS	527
FRH4-18	FRH4-47	WGQGTTVTVSS	527
FRH4-19	FRH4-51	WGQGTTVTVSS	527
FRH4-20	FRH4-52	WGQGTTVTVSS	527
FRH4-21	FRH4-13	WGQGTLVTVSS	526
FRH4-22	FRH4-14	WGQGTLVTVSS	526
FRH4-23	FRH4-1	WGQGTLVTVSS	526

FIGURA 9E

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
FRH4-24	FRH4-22	WGQGTLVTVSS	526
FRH4-25	FRH4-23	WGQGTLVTVSS	526
FRH4-26	FRH4-12	WGQGSLVTVSP	529
FRH4-27	FRH4-5	WGQGTLVTVSS	526
FRH4-28	FRH4-15	WGQGTTVTVSS	527
FRH4-29	FRH4-7	WGQGTLVTVSS	526
FRH4-30	FRH4-61	WGQGTLVTVSS	526
FRH4-31	FRH4-39	WGQGTLVTVSS	526
FRH4-32	FRH4-34	WGQGTTVTVSS	527
FRH4-33	FRH4-6	WGQGTTVTVSS	527
FRH4-34	FRH4-35	WGQGTTVTVSS	527
FRH4-35	FRH4-21	WGQGTTVTVSS	527
FRH4-36	FRH4-8	WGQGTKVTVSS	530
FRH4-37	FRH4-9	WGQGTKVTVSS	530
FRH4-38	FRH4-18	WGQGTTVTVSS	527
FRH4-39	FRH4-24	WGQGTTVTVSS	527
FRH4-40	FRH4-25	WGQGTTVTVSS	527
FRH4-41	FRH4-26	WGRGTLVTVSS	531
FRH4-42	FRH4-27	WGRGTLVTVSS	531
FRH4-43	FRH4-38	WGQGTTVTVSS	527
FRH4-44	FRH4-54	WGQGTLVTVSS	526
FRH4-45	FRH4-55	WGQGTLVTVSS	526
FRH4-46	FRH4-43	WGQGTLVTVSS	526
FRH4-47	FRH4-44	WGQGTLVTVSS	526
FRH4-48	FRH4-49	WGQGTLVTVSS	526
FRH4-49	FRH4-50	WGQGTLVTVSS	526
FRH4-50	FRH4-53	WGQGTLVTVSS	526
FRH4-51	FRH4-33	WGQGTTVTVSS	527
FRH4-52	FRH4-3	WGQGTMVTVSS	528
FRH4-53	FRH4-4	WGQGTMVTVSS	528
FRH4-54	FRH4-16	WGQGTLVTVSS	526
FRH4-55	FRH4-17	WGQGTLVTVSS	526
FRH4-56	FRH4-11	WGQGTTVTVSS	527
FRH4-57	FRH4-37	WGQGTTVTVSS	527
FRH4-58	FRH4-39.1	WGQGTLVTVSS	526

FIGURA 9F

FIGURA 10A: Regiones Variables de la Cadena Ligera

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          1                   20                  40                  60                  80
U2-1    DVVMTQSPLS LPVTLGQPAS ISCRSSQSLV YSDGN.TYLN WFQQRPGQSP RRLIYKVSNW DSGVPDRFNG SGSGTDFTLK
U2-2    DVVMTQSPLS LPVTLGQPAS ISCRSSQSLV YSDGN.TYLN WFQQRPGQSP RRLIYKVSNW DSGVPDRFSG SGSGTDFTLK
U2-3    DVVMTQSPLS LPVTLGQPAS ISCRSSQSLV YSDGN.TYLN WLQQRPGQSP RRLIYKVSNW DSGVPDRFSG SGSGTDFTLK
U2-4    DVVMTQSPLS LPVTLGQPAS ISCRSSQSLV YSDGN.TYLN WLQQRPGQSP RRLIYKVSNW DSGVPDRFSG SGSGTDFTLK
U2-5    DIVMTQTPLS LSVTPGQPAS ISCKSSQSLL HSDGK.TYLY WYLQKPGQPP QLLIYEVSNR FSGVPDRFSG SGSGTDFTLK
U2-6    DIVMTQTPLS LSVTPGQPAS ISCKSSQSLL HSDGK.TYLY WYLQKPGQPP QLLIYEVSNR FSGVPDRFSG SGSGTDFTLK
U2-7    DIVMTQTPLS LSVTPGQPAS ISCKSSQSLL HSDGK.TYLY WYLQKPGQPP QLLIYEVSNR FSGVPDRFSG SGSGTDFTLK
U2-8    DIVMTQTPLS LSVTPGQPAS ISCKSSQSLL HSDGK.TYLY WFLQKPGQPP QPLIYEVSNR FSGVPDRFSG SGSGTDFTLK
U2-9    DIVMTQTPLS LSVTPGQPAS ISCKSSQSLL HSDGK.TYLY WFLQKPGQPP QPLIYEVSNR FSGVPDRFSG SGSGTDFTLK
U2-11   DIQMTQSPSS LSASVGDRVT ITCRASQGIA ....N..YLA WYQQKPGKVP KLLIYVASTL QSGVPSRFSG SGSGTDFTLT
U2-12   DIQMTQSPSS LSASVGDRVT IICRASQGIS .ND.....LA WYQQKPGKVP KLLIYAASTL QSGVPSRFSG SGSGTDFTLT
U2-13   NIVMTQTPLS SPVTLGQPAS ISCRSSQSLV HSDGN.TYLS WLQQRPGQPP RLLIYKISNR FSGVPDRFSG SGAGTDFTLK
U2-14   NIVMTQTPLS SPVTLGQPAS ISCRSSQSLV HSDGN.TYLS WLQQRPGQPP RLLIYKISNR FSGVPDRFSG SGAGTDFTLK
U2-15   EIVMTQTPLS SPVTLGQPAS ISCRSSQSLV HSDGN.TYLS WLQQRPGQPP RLLIYKISNR FSGVPDRFSG TGAGTDFTLK
U2-16   EIVLTQSPGT LSLSPGERAT LSCRASQTVI SS.....YLA WYQQKPGQAP RLLISGASSR ATGIPDRFSG SGSGTDFTLT
U2-17   EIVLTQSPGT LSLSPGERAT LSCRASQSVS R.......LA WYQQKPGQAP RLLIYGASRR ATGIPDRFSG SGSGTDFTLT
U2-18   DIQMTQSPSS LSASVGDRVT ITCRASQGIR .ND.....LG WYQQKPGKAP KRLIYAASSL QSGVPSRFSG SGSGTEFTLT
U2-19   DIVMTQSPDS LAVSLGERAT INCKSSQSVL YSSNNKNYLV WYQQKPGQPP KLFIYWASTR ESGVPDRFTG SGSGTDFTLT
U2-20   DIVMTQSPDS LAVSLGERAT INCKSSQSVL YSSNNKNYLV WYQQKPGQPP KLFIYWASTR ESGVPDRFTG SGSGTDFTLT
U2-21   DIVMTQSPDS LAVSLGERAT INCKSSQSVL YSSNNKNYLA WYQQKPGQPP KLLIYWASTR ESGVPDRFSG SGSGTDFTLT
U2-22   DIVMTQSPDS LAVSLGERAT INCKSSQNVL YSSNNKNYLA WYQQKPGQPP KLLIYWASTR ESGVPDRFSG SGSGTDFTLT
U2-23   DIVMTQSPDS LAVSLGERAT INCKSSQNVL YSSNNKNYLA WYQQKPGQPP KLLIYWASTR ESGVPDRFSG SGSGTDFTLT
U2-24   DIVMTQSPDS LTVSLGERAT INCKSSQSVL YSSNNKNYLA WYQQKPGQPP KLLIYWASTR ESGVPDRFGG SGSGTDFTLT
U2-25   DIVMTQSPDS LTVSLGERAT INCKSSQSVL YSSNNKNYLA WYQQKPGQPP KLLIYWASTR ESGVPDRFGG SGSGTDFTLT
U2-26   DIVMTQSPDS LAVSLGERAT INCKSSQSVL YNSNNKNYLA WYQQKPGQPP KLLIYWASTR ESGVPDRFSG SGSGTDFTLT
U2-27   DIVMTQSPDS LAVSLGERAT INCKSSQSVL YNSNNKNYLA WYQQKPGQPP KLLIYWASTR ESGVPDRFSG SGSGTDFTLT
U2-28   DIVMTQSPDS LAVSLGERAT INCKSSQSVL YSSNNKNYLA WYQQKPGQPP KVLIYWASTR KSGVPDRFSG SGSGTDFTLT
U2-29   DIVMTQSPDS LAVSLGERAT INCKSSQSVL YSSNNKNYLA WYQQKPGQPP KVLIYWASTR KSGVPDRFSG SGSGTDFTLT
U2-30   DIVMTQSPDS LAVSLGERAT INCKSSQSVL DSSNNKNYLA WYQQKPGQPP KLLIYWASTR ESGVPDRFSG SGSGTDFTLT
U2-31   DIVMTQSPDS LAVSLGERAT INCKSSQSVL DSSNNKNYLA WYQQKPGQPP KLLIYWASTR ESGVPDRFSG SGSGTDFTLT
U2-32   DIVMTQSPDS LAVSLGERAT INCKSSQSIL YRSNNKNYLA WYQQKPGQPP KLLIYWASAR ESGVPDRFSG SGSGTDFTLT
U2-33   DIVMTQSPDS LAVSLGERAT INCKSSQSIL YRSNNKNYLA WYQQKPGQPP KLLIYWASAR ESGVPDRFSG SGSGTDFTLT
U2-34   DIQMTQSPSS LSASVGDRVT ITCRASQDIS H......YLA WFQQKPGKAP KSLIYAASSL QSGVPSKFSG SGSGTDFTLT
U2-35   DIQMTQSPSS LSASVGDRVA ITCRASQDIS ......NYLA WLQQKPGKAP KSLIYAASSL QSGVPSRFSG SGSGTDFTLT
U2-36   EIVMTQSPAT LSVSPGERAT LSCRASQSVS ..SN....LA WYQQDPGQAP RLLIYGASRR ATGIPARFSG SGSGTEFTLT
U2-37   EIVMTQSPAT LSVSPGERAT LSCRASQSVS ..SN....LA WYQQDPGQAP RLLIYGASRR ATGIPARFSG SGSGTEFTLT
U2-38   DIQMTQSPSS VSASVGDRVT ITCRASQDIS ..RW....LA WYQQKPGKAP KLLIYAASSL QSGVPSRFSG SGSGTDFTLT
U2-39   DIQMTQSPSS LSASVGDRVT ITCRASQSIS ......TYLN WYQQKPGKAP KFLIYAASSL QSGVPSRFSG SGSGTDFTLT
U2-40   DIQMTQSPSS LSASLGDRVT ITCRASQTIS ......IYLN WYQQKPGKAP KLLIYAASSL QSGVPSRFSG SGSGTDFTLT
U2-41   DIQMTQSPSS LSASVGDRVT ITCRASQSIR ..S....YLN WYQQRPGNAP KLLIYAASSL QSGVPSRVSG SGSGTDFTLT
U2-42   DIQMTQSPSS RSASVGDRVT ITCRASQTIS ......RYLN WYQQKPGKAP KLLIYAASTL QSGVPSRFSG SGSGTDFTLT
U2-43   DIQMTQSPSS LSASVGDRVT ITCRASQRIS ..S....YLN WYQQKPGKAP KVLIYAESSL QSGVPSRFSG SGSGTDFTLT
U2-44   DIQMTQSPSS LSASVGDRVT ITCRASQSIS ......RYLN WYQQKPGKAP KLLIYTASSL QSGVPSRFSG SGSGTDFTLT
U2-45   DIQMTQSPSS LSASVGDRVT ITCRASQSIS ..S....YLN WYQQKPGKAP KLLIYTASSL QSGVPSRFSG SGSGTDFTLT
U2-46   DIQMTQSPSS LSASVGDRVT ITCRASQSIS ..S....YLN WYQQKPGKAP KLLIYTASSL QSGVPSRFSG SGSGTDFTLT
U2-47   DIQMTQSPSS LSASVGDRVT ITCRASQSIS ..S....YLN WYQQKPGKAP KLLIYTASSL QSGVPSRFSG SGSGTDFTLT
U2-48   DIQMTQSPSS LSASVGDRVT ITCRASQSIS ..S....YLN WYQQKPGKAP KLLIYTVSSL QSGVPSRFSG SGSGTDFTLT
U2-49   DIQMTQSPSS LSASVGDRVT ITCRASQSIS ..S....YLN WYQQKPGKAP KLLIYTVSSL QSGVPSRFSG SGSGTDFTLT
U2-50   DIQMTQSPSS LSASVGDRVT ITCRASQSIS ..S....YLN WYQQKPGKAP KLLIYTVSSL QSGVPSRFSG SGSGTDFTLT
U2-51   DIQMTQSPSS LSASVGDRVT ITCRASQSIS ..S....YLN WYQQKPGKAP KLLIYTASSL QSGVPSRFSG SGSGTDFTLT
U2-52   DIQMTQSPSS LSASVGDRVT ITCRASQSIS ..S....YLN WYQQKPGKAP KLLIYTASSL QSGVPSRFSG SGSGTDFTLT
U2-53   DIQMTQSPSS LSASVGDRVT ITCRASQSIS ..S....YLN WYQQKPGKAP KLLIYTASSL QSGVPSRFSG SGSGTDFTLT
U2-54   DIQMTQSPSS LSASVGDRVT ITCQASQDIS ......NYLN WYQQKPGKAP KLLIYDASNL ETGVPSRFSG SGSGTDFTFT
U2-55   DIQMTQSPSS LSASVGDRVT ITCQASQDIS ......NYLN WYQQKPGKAP KLLIYDASNL ETGVPSRFSG SGSGTDFTFT
U2-56   DIQMTQSPSS LSASVGDRVT ITCQASQDIS ......NSLN WYQQKPGKAP ELLIYDASNL ETGVPSRFSG SGSGTDFTFT
U2-57   DIQMTQSPSS LSASVGDRVT ITCQASQDIS ..D....YLN WYQQKPGKAP KLLIYDASNL ETGVPSRFSG SGSGTDFTFT
U2-58   DIQMTQSPSS LSASVGDRVA ITCQASQDIS ......NYLN WYQQKPGKAP KLLIYDASNL ETGVPSRFSG SGSGTDFTFT
U2-59   DIQMTQSPSS LSASVGDRVA ITCQASQDIS ......NYLN WYQQKPGKAP KLLIYDASNL ETGVPSRFSG SGSGTDFTFT
U2-60   DIQMTQSPSS LSASVGDRVT ITCQASQDIS ......NSLN WYQQKPGKAP KLLIYDASIL ETGVPSRFSG SGSETDFTFT
U2-61   DIQMTQSPSS LSASVGDRVT ITCQASQDIS ......NSLN WYQQKPGKAP KLLIYDASNL ETGVPSRFSG SGSGTDFTFT
U2-62   DIQMTQSPSS LSASVGDGVT ITCQASQDIT ......NYLN WYQQKPGKAP KLLIYDASNL ETGVPSRFSG SGSGTDFTFT
U2-63   DIQMTQSPSS LSASVGDRVT ITCQASQDIS ......NYLN WYQQKLGKAP KLLIHDASNL ETGVPSRFSG SGSGTDFTFT
U2-64   DIQMTQSPSS LSASVGDRVT ITCQASQDIS ..D....YLN WYQQKPGKAP KLLIYDASNL ETGVPSRFSG SGSGTDFTFT
U2-65   DIQMTQSPSS LSASVGDRVT ITCQASQDIS ......NSLN WYQQKPGKAP KLLIYDASNL ETGVPSRFSG SGSGTDFTFT
                                 CDR1                                   CDR2
```

FIGURA 10B

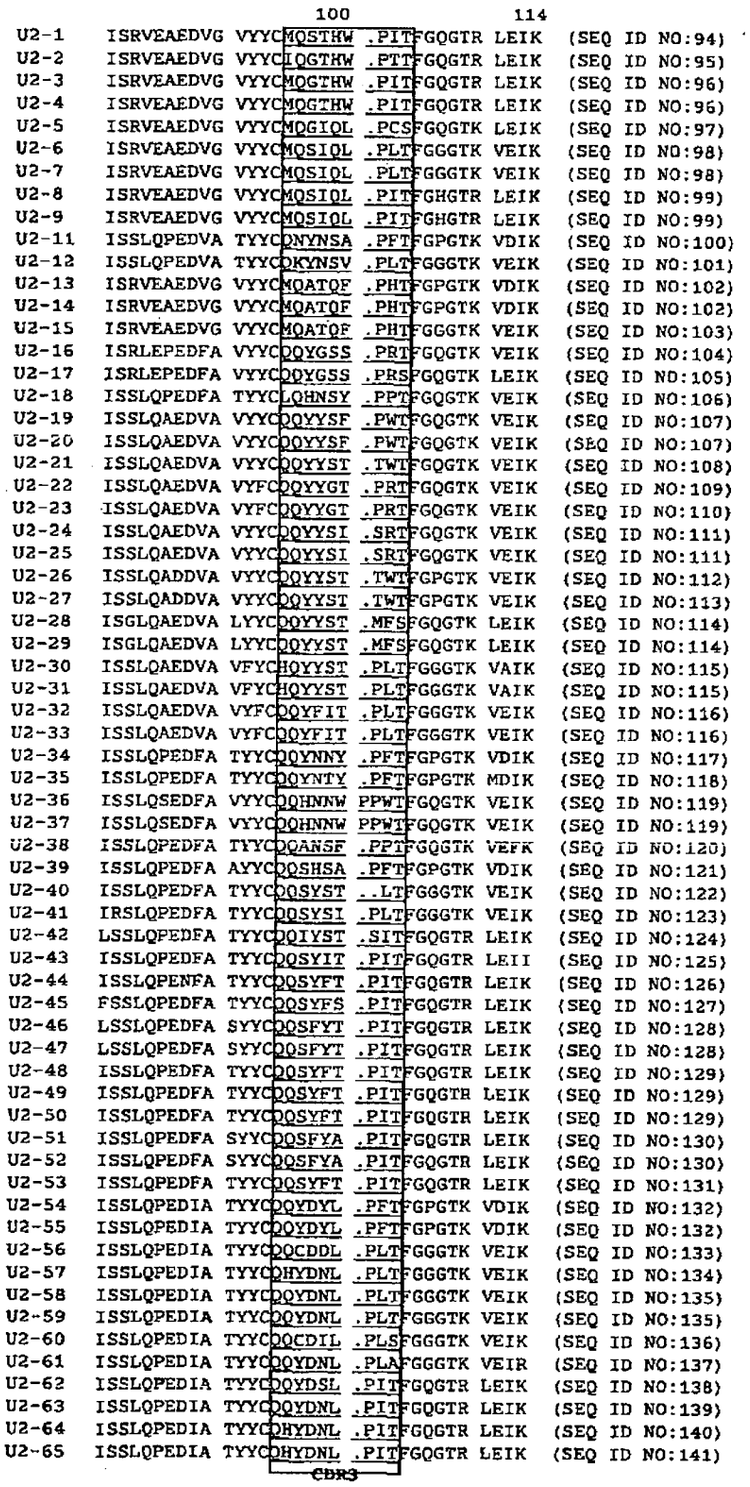

100
114
U2-1 ISRVEAEDVG VYYCMQSTHW .PITFGQGTR LEIK (SEQ ID NO:94)
U2-2 ISRVEAEDVG VYYCIQGTHW .PTTFGQGTR LEIK (SEQ ID NO:95)
U2-3 ISRVEAEDVG VYYCMQGTHW .PITFGQGTR LEIK (SEQ ID NO:96)
U2-4 ISRVEAEDVG VYYCMQGTHW .PITFGQGTR LEIK (SEQ ID NO:96)
U2-5 ISRVEAEDVG VYYCMQGIQL .PCSFGQGTK LEIK (SEQ ID NO:97)
U2-6 ISRVEAEDVG VYYCMQSIQL .PLTFGGGTK VEIK (SEQ ID NO:98)
U2-7 ISRVEAEDVG VYYCMQSIQL .PLTFGGGTK VEIK (SEQ ID NO:98)
U2-8 ISRVEAEDVG VYYCMQSIQL .PITFGHGTR LEIK (SEQ ID NO:99)
U2-9 ISRVEAEDVG VYYCMQSIQL .PITFGHGTR LEIK (SEQ ID NO:99)
U2-11 ISSLQPEDVA TYYCQNYNSA .PFTFGPGTK VDIK (SEQ ID NO:100)
U2-12 ISSLQPEDVA TYYCQKYNSV .PLTFGGGTK VEIK (SEQ ID NO:101)
U2-13 ISRVEAEDVG VYYCMQATQF .PHTFGPGTK VDIK (SEQ ID NO:102)
U2-14 ISRVEAEDVG VYYCMQATQF .PHTFGPGTK VDIK (SEQ ID NO:102)
U2-15 ISRVEAEDVG VYYCMQATQF .PHTFGGGTK VEIK (SEQ ID NO:103)
U2-16 ISRLEPEDFA VYYCQQYGSS .PRTFGQGTK VEIK (SEQ ID NO:104)
U2-17 ISRLEPEDFA VYYCQQYGSS .PRSFGQGTK LEIK (SEQ ID NO:105)
U2-18 ISSLQPEDFA TYYCLQHNSY .PPTFGQGTK VEIK (SEQ ID NO:106)
U2-19 ISSLQAEDVA VYYCQQYYSF .PWTFGQGTK VEIK (SEQ ID NO:107)
U2-20 ISSLQAEDVA VYYCQQYYSF .PWTFGQGTK VEIK (SEQ ID NO:107)
U2-21 ISSLQAEDVA VYYCQQYYST .TWTFGQGTK VEIK (SEQ ID NO:108)
U2-22 ISSLQAEDVA VYFCQQYYGT .PRTFGQGTK VEIK (SEQ ID NO:109)
U2-23 ISSLQAEDVA VYFCQQYYGT .PRTFGQGTK VEIK (SEQ ID NO:110)
U2-24 ISSLQAEDVA VYYCQQYYSI .SRTFGQGTK VEIK (SEQ ID NO:111)
U2-25 ISSLQAEDVA VYYCQQYYSI .SRTFGQGTK VEIK (SEQ ID NO:111)
U2-26 ISSLQADDVA VYYCQQYYST .TWTFGPGTK VEIK (SEQ ID NO:112)
U2-27 ISSLQADDVA VYYCQQYYST .TWTFGPGTK VEIK (SEQ ID NO:113)
U2-28 ISGLQAEDVA LYYCQQYYST .MFSFGQGTK LEIK (SEQ ID NO:114)
U2-29 ISGLQAEDVA LYYCQQYYST .MFSFGQGTK LEIK (SEQ ID NO:114)
U2-30 ISSLQAEDVA VFYCHQYYST .PLTFGGGTK VAIK (SEQ ID NO:115)
U2-31 ISSLQAEDVA VFYCHQYYST .PLTFGGGTK VAIK (SEQ ID NO:115)
U2-32 ISSLQAEDVA VYFCQQYFIT .PLTFGGGTK VEIK (SEQ ID NO:116)
U2-33 ISSLQAEDVA VYFCQQYFIT .PLTFGGGTK VEIK (SEQ ID NO:116)
U2-34 ISSLQPEDFA TYYCQQYNNY .PFTFGPGTK VDIK (SEQ ID NO:117)
U2-35 ISSLQPEDFA TYYCQQYNTY .PFTFGPGTK MDIK (SEQ ID NO:118)
U2-36 ISSLQSEDFA VYYCQQHNNW PPWTFGQGTK VEIK (SEQ ID NO:119)
U2-37 ISSLQSEDFA VYYCQQHNNW PPWTFGQGTK VEIK (SEQ ID NO:119)
U2-38 ISSLQPEDFA TYYCQQANSF .PPTFGQGTK VEFK (SEQ ID NO:120)
U2-39 ISSLQPEDFA AYYCQQSHSA .PFTFGPGTK VDIK (SEQ ID NO:121)
U2-40 ISSLQPEDFA TYYCQQSYST ..LTFGGGTK VEIK (SEQ ID NO:122)
U2-41 IRSLQPEDFA TYYCQQSYSI .PLTFGGGTK VEIK (SEQ ID NO:123)
U2-42 LSSLQPEDFA TYYCQQIYST .SITFGQGTR LEIK (SEQ ID NO:124)
U2-43 ISSLQPEDFA TYYCQQSYIT .PITFGQGTR LEII (SEQ ID NO:125)
U2-44 ISSLQPENFA TYYCQQSYFT .PITFGQGTR LEIK (SEQ ID NO:126)
U2-45 FSSLQPEDFA TYYCQQSYFS .PITFGQGTR LEIK (SEQ ID NO:127)
U2-46 LSSLQPEDFA SYYCQQSFYT .PITFGQGTR LEIK (SEQ ID NO:128)
U2-47 LSSLQPEDFA SYYCQQSFYT .PITFGQGTR LEIK (SEQ ID NO:128)
U2-48 ISSLQPEDFA TYYCQQSYFT .PITFGQGTR LEIK (SEQ ID NO:129)
U2-49 ISSLQPEDFA TYYCQQSYFT .PITFGQGTR LEIK (SEQ ID NO:129)
U2-50 ISSLQPEDFA TYYCQQSYFT .PITFGQGTR LEIK (SEQ ID NO:129)
U2-51 ISSLQPEDFA SYYCQQSFYA .PITFGQGTR LEIK (SEQ ID NO:130)
U2-52 ISSLQPEDFA SYYCQQSFYA .PITFGQGTR LEIK (SEQ ID NO:130)
U2-53 ISSLQPEDFA TYYCQQSYFT .PITFGQGTR LEIK (SEQ ID NO:131)
U2-54 ISSLQPEDIA TYYCQQYDYL .PFTFGPGTK VDIK (SEQ ID NO:132)
U2-55 ISSLQPEDIA TYYCQQYDYL .PFTFGPGTK VDIK (SEQ ID NO:132)
U2-56 ISSLQPEDIA TYYCQQCDDL .PLTFGGGTK VEIK (SEQ ID NO:133)
U2-57 ISSLQPEDIA TYYCQHYDNL .PLTFGGGTK VEIK (SEQ ID NO:134)
U2-58 ISSLQPEDIA TYYCQQYDNL .PLTFGGGTK VEIK (SEQ ID NO:135)
U2-59 ISSLQPEDIA TYYCQQYDNL .PLTFGGGTK VEIK (SEQ ID NO:135)
U2-60 ISSLQPEDIA TYYCQQCDIL .PLSFGGGTK VEIK (SEQ ID NO:136)
U2-61 ISSLQPEDIA TYYCQQYDNL .PLAFGGGTK VEIR (SEQ ID NO:137)
U2-62 ISSLQPEDIA TYYCQQYDSL .PITFGQGTR LEIK (SEQ ID NO:138)
U2-63 ISSLQPEDIA TYYCQQYDNL .PITFGQGTR LEIK (SEQ ID NO:139)
U2-64 ISSLQPEDIA TYYCQHYDNL .PITFGQGTR LEIK (SEQ ID NO:140)
U2-65 ISSLQPEDIA TYYCQHYDNL .PITFGQGTR LEIK (SEQ ID NO:141)
CDR3

FIGURA 11A: Regiones Variables de la Cadena Pesada

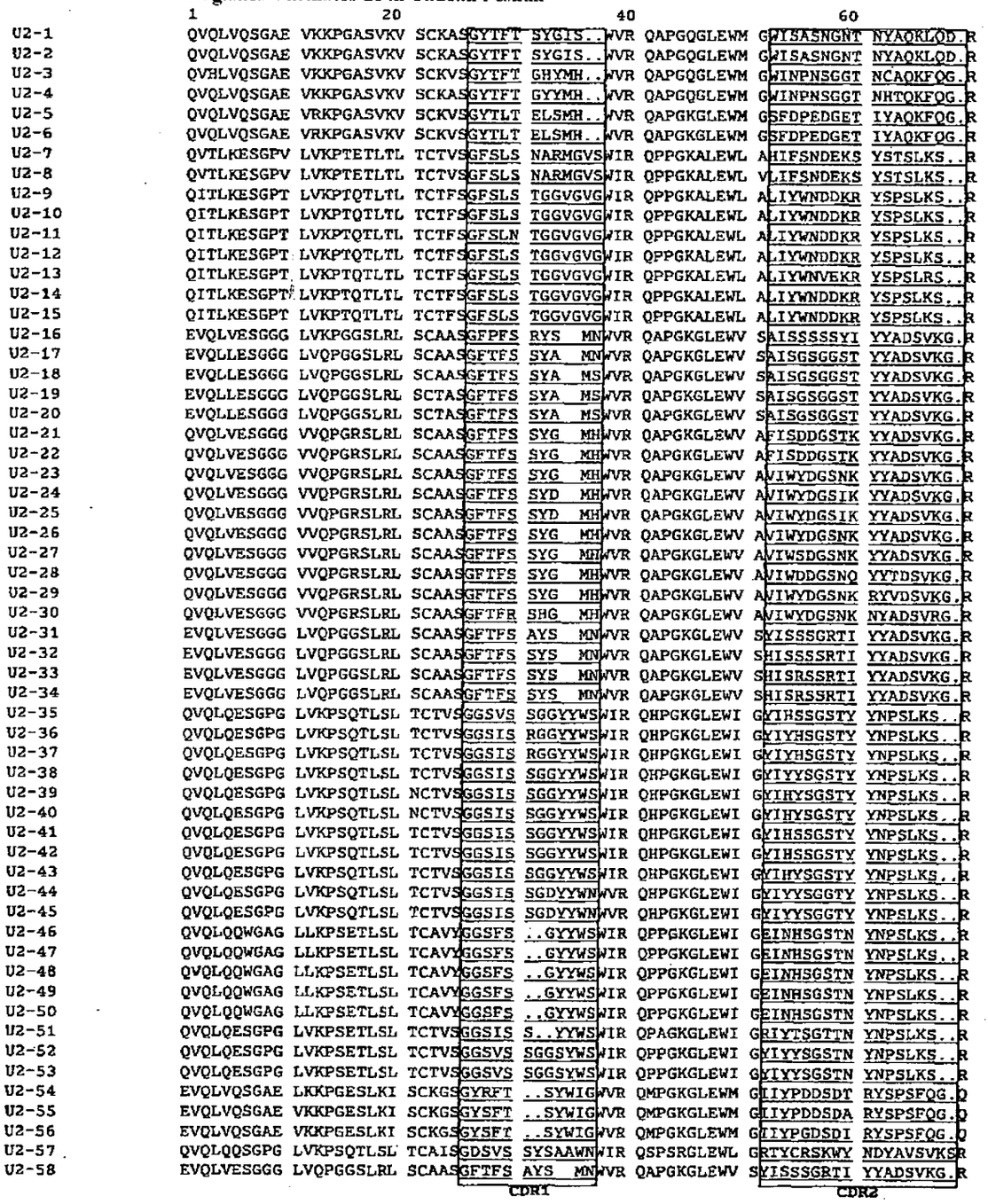
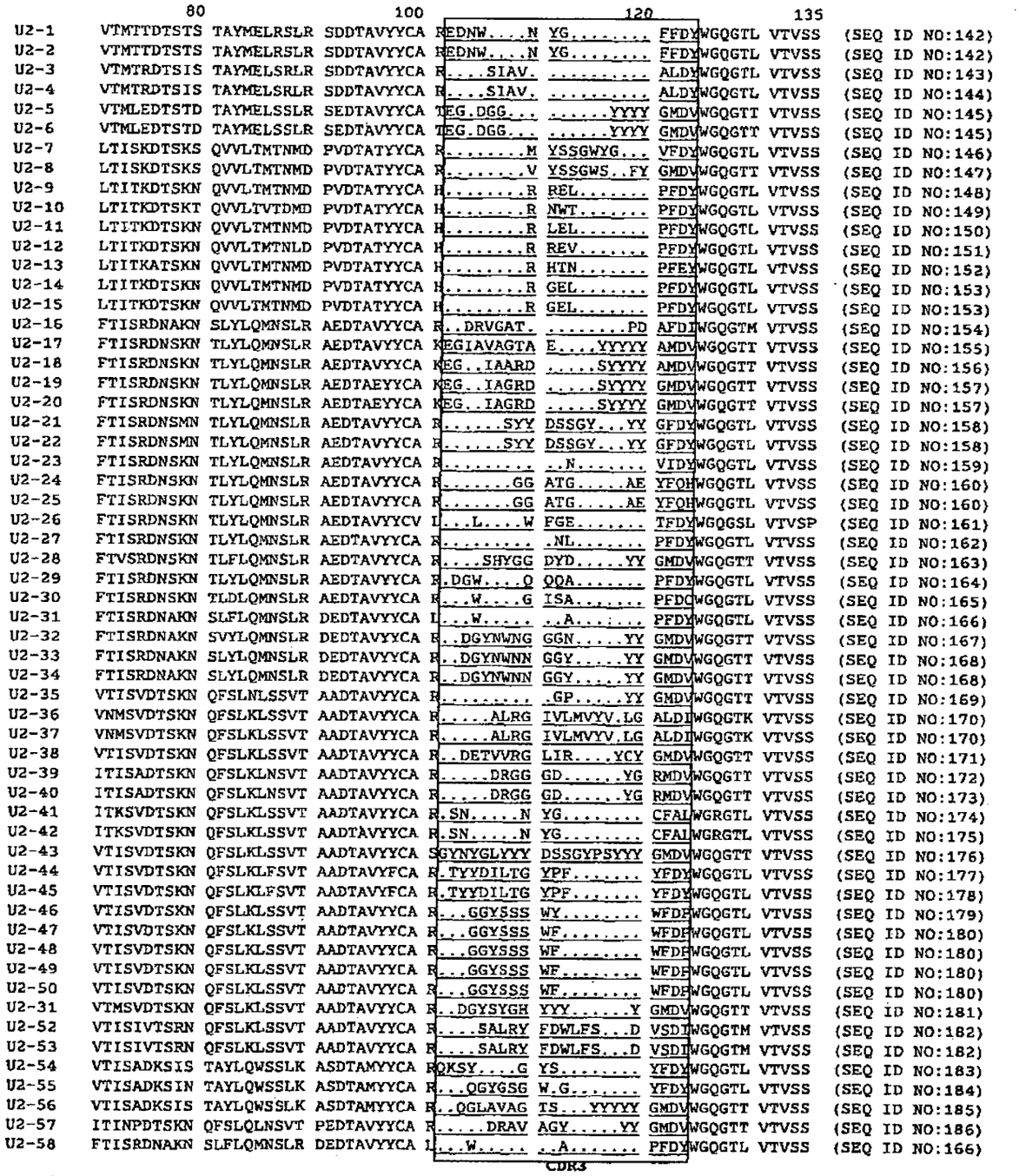


FIGURA 11B


80
100
120
135
CDR3
U2-1 VTMTTDTSTS TAYMELRSLR SDDTAVYYCA REDNW....N YG..... FFDYWGQGTL VTVSS (SEQ ID NO:142)
U2-2 VTMTTDTSTS TAYMELRSLR SDDTAVYYCA REDNW....N YG..... FFDYWGQGTL VTVSS (SEQ ID NO:142)
U2-3 VTMTRDTSIS TAYMELSRLR SDDTAVYYCA R....SIAV. ..... ALDYWGQGTL VTVSS (SEQ ID NO:143)
U2-4 VTMTRDTSIS TAYMELSRLR SDDTAVYYCA R....SIAV. ..... ALDYWGQGTL VTVSS (SEQ ID NO:144)
U2-5 VTMLEDTSTD TAYMELSSLR SEDTAVYYCA TEG.DGG... .....YYYY GMDVWGQGTT VTVSS (SEQ ID NO:145)
U2-6 VTMLEDTSTD TAYMELSSLR SEDTAVYYCA TEG.DGG... .....YYYY GMDVWGQGTT VTVSS (SEQ ID NO:145)
U2-7 LTISKDTSKS QVVLTMTNMD PVDTATYYCA R.....M YSSGWYG... VFDYWGQGTL VTVSS (SEQ ID NO:146)
U2-8 LTISKDTSKS QVVLTMTNMD PVDTATYYCA R.....V YSSGWS..FY GMDVWGQGTT VTVSS (SEQ ID NO:147)
U2-9 LTITKDTSKN QVVLTMTNMD PVDTATYYCA H.....R REL..... PFDYWGQGTL VTVSS (SEQ ID NO:148)
U2-10 LTITKDTSKT QVVLTVTDMD PVDTATYYCA H.....R NWT..... PFDYWGQGTL VTVSS (SEQ ID NO:149)
U2-11 LTITKDTSKN QVVLTMTNMD PVDTATYYCA H.....R LEL..... PFDYWGQGTL VTVSS (SEQ ID NO:150)
U2-12 LTITKDTSKN QVVLTMTNLD PVDTATYYCA H.....R REV..... PFDYWGQGTL VTVSS (SEQ ID NO:151)
U2-13 LTITKATSKN QVVLTMTNMD PVDTATYYCA H.....R HTN..... PFEYWGQGTL VTVSS (SEQ ID NO:152)
U2-14 LTITKDTSKN QVVLTMTNMD PVDTATYYCA H.....R GEL..... PFDYWGQGTL VTVSS (SEQ ID NO:153)
U2-15 LTITKDTSKN QVVLTMTNMD PVDTATYYCA H.....R GEL..... PFDYWGQGTL VTVSS (SEQ ID NO:153)
U2-16 FTISRDNAKN SLYLQMNSLR AEDTAVYYCA R..DRVGAT. .....PD AFDIWGQGTM VTVSS (SEQ ID NO:154)
U2-17 FTISRDNSKN TLYLQMNSLR AEDTAVYYCA KEGIAVAGTA E....YYYYY AMDVWGQGTT VTVSS (SEQ ID NO:155)
U2-18 FTISRDNSKN TLYLQMNSLR AEDTAVYYCA KEG..IAARD .....SYYYY AMDVWGQGTT VTVSS (SEQ ID NO:156)
U2-19 FTISRDNSKN TLYLQMNSLR AEDTAEYYCA KEG..IAGRD .....SYYYY GMDVWGQGTT VTVSS (SEQ ID NO:157)
U2-20 FTISRDNSKN TLYLQMNSLR AEDTAEYYCA KEG..IAGRD .....SYYYY GMDVWGQGTT VTVSS (SEQ ID NO:157)
U2-21 FTISRDNSMN TLYLQMNSLR AEDTAVYYCA R.....SYY DSSGY...YY GFDYWGQGTL VTVSS (SEQ ID NO:158)
U2-22 FTISRDNSMN TLYLQMNSLR AEDTAVYYCA R.....SYY DSSGY...YY GFDYWGQGTL VTVSS (SEQ ID NO:158)
U2-23 FTISRDNSKN TLYLQMNSLR AEDTAVYYCA R..... ..N..... VIDYWGQGTL VTVSS (SEQ ID NO:159)
U2-24 FTISRDNSKN TLYLQMNSLR AEDTAVYYCA R.....GG ATG.....AE YFQHWGQGTL VTVSS (SEQ ID NO:160)
U2-25 FTISRDNSKN TLYLQMNSLR AEDTAVYYCA R.....GG ATG.....AE YFQHWGQGTL VTVSS (SEQ ID NO:160)
U2-26 FTISRDNSKN TLYLQMNSLR AEDTAVYYCV L...L....W FGE..... TFDYWGQGSL VTVSP (SEQ ID NO:161)
U2-27 FTISRDNSKN TLYLQMNSLR AEDTAVYYCA R..... .NL..... PFDYWGQGTL VTVSS (SEQ ID NO:162)
U2-28 FTVSRDNSKN TLFLQMNSLR AEDTAVYYCA R....SHYGG DYD.....YY GMDVWGQGTT VTVSS (SEQ ID NO:163)
U2-29 FTISRDNSKN TLYLQMNSLR AEDTAVYYCA R.DGW....Q QQA..... PFDYWGQGTL VTVSS (SEQ ID NO:164)
U2-30 FTISRDNSKN TLDLQMNSLR AEDTAVYYCA R...W....G ISA..... PFDQWGQGTL VTVSS (SEQ ID NO:165)
U2-31 FTISRDNAKN SLFLQMNSLR DEDTAVYYCA L...W..... ..A..... PFDYWGQGTL VTVSS (SEQ ID NO:166)
U2-32 FTISRDNAKN SVYLQMNSLR DEDTAVYYCA R..DGYNWNG GGN.....YY GMDVWGQGTT VTVSS (SEQ ID NO:167)
U2-33 FTISRDNAKN SLYLQMNSLR DEDTAVYYCA R..DGYNWNN GGY.....YY GMDVWGQGTT VTVSS (SEQ ID NO:168)
U2-34 FTISRDNAKN SLYLQMNSLR DEDTAVYYCA R..DGYNWNN GGY.....YY GMDVWGQGTT VTVSS (SEQ ID NO:168)
U2-35 VTISVDTSKN QFSLNLSSVT AADTAVYYCA R..... .GP.....YY GMDVWGQGTT VTVSS (SEQ ID NO:169)
U2-36 VNMSVDTSKN QFSLKLSSVT AADTAVYYCA R.....ALRG IVLMVYV.LG ALDIWGQGTK VTVSS (SEQ ID NO:170)
U2-37 VNMSVDTSKN QFSLKLSSVT AADTAVYYCA R.....ALRG IVLMVYV.LG ALDIWGQGTK VTVSS (SEQ ID NO:170)
U2-38 VTISVDTSKN QFSLKLSSVT AADTAVYYCA R..DETVVRG LIR....YCY GMDVWGQGTT VTVSS (SEQ ID NO:171)
U2-39 ITISADTSKN QFSLKLNSVT AADTAVYYCA R.....DRGG GD.....YG RMDVWGQGTT VTVSS (SEQ ID NO:172)
U2-40 ITISADTSKN QFSLKLNSVT AADTAVYYCA R.....DRGG GD.....YG RMDVWGQGTT VTVSS (SEQ ID NO:173)
U2-41 ITKSVDTSKN QFSLKLSSVT AADTAVYYCA R.SN.....N YG..... CFALWGRGTL VTVSS (SEQ ID NO:174)
U2-42 ITKSVDTSKN QFSLKLSSVT AADTAVYYCA R.SN.....N YG..... CFALWGRGTL VTVSS (SEQ ID NO:175)
U2-43 VTISVDTSKN QFSLKLSSVT AADTAVYYCA SGYNYGLYYY DSSGYPSYYY GMDVWGQGTT VTVSS (SEQ ID NO:176)
U2-44 VTISVDTSKN QFSLKLFSVT AADTAVYFCA R.TYYDILTG YPF..... YFDYWGQGTL VTVSS (SEQ ID NO:177)
U2-45 VTISVDTSKN QFSLKLFSVT AADTAVYFCA R.TYYDILTG YPF..... YFDYWGQGTL VTVSS (SEQ ID NO:178)
U2-46 VTISVDTSKN QFSLKLSSVT AADTAVYYCA R...GGYSSS WY..... WFDPWGQGTL VTVSS (SEQ ID NO:179)
U2-47 VTISVDTSKN QFSLKLSSVT AADTAVYYCA R...GGYSSS WF..... WFDPWGQGTL VTVSS (SEQ ID NO:180)
U2-48 VTISVDTSKN QFSLKLSSVT AADTAVYYCA R...GGYSSS WF..... WFDPWGQGTL VTVSS (SEQ ID NO:180)
U2-49 VTISVDTSKN QFSLKLSSVT AADTAVYYCA R...GGYSSS WF..... WFDPWGQGTL VTVSS (SEQ ID NO:180)
U2-50 VTISVDTSKN QFSLKLSSVT AADTAVYYCA R...GGYSSS WF..... WFDPWGQGTL VTVSS (SEQ ID NO:180)
U2-31 VTMSVDTSKN QFSLKLSSVT AADTAVYYCA R..DGYSYGH YYY.....Y GMDVWGQGTT VTVSS (SEQ ID NO:181)
U2-52 VTISIVTSRN QFSLKLSSVT AADTAVYYCA R....SALRY FDWLFS...D VSDIWGQGTM VTVSS (SEQ ID NO:182)
U2-53 VTISIVTSRN QFSLKLSSVT AADTAVYYCA R....SALRY FDWLFS...D VSDIWGQGTM VTVSS (SEQ ID NO:182)
U2-54 VTISADKSIS TAYLQWSSLK ASDTAMYYCA RQKSY....G YS..... YFDYWGQGTL VTVSS (SEQ ID NO:183)
U2-55 VTISADKSIN TAYLQWSSLK ASDTAMYYCA R...QGYGSG W.G..... YFDYWGQGTL VTVSS (SEQ ID NO:184)
U2-56 VTISADKSIS TAYLQWSSLK ASDTAMYYCA R..QGLAVAG TS...YYYYY GMDVWGQGTT VTVSS (SEQ ID NO:185)
U2-57 ITINPDTSKN QFSLQLNSVT PEDTAVYYCA R.....DRAV AGY.....YY GMDVWGQGTT VTVSS (SEQ ID NO:186)
U2-58 FTISRDNAKN SLFLQMNSLR DEDTAVYYCA L...W..... ..A..... PFDYWGQGTL VTVSS (SEQ ID NO:166)

Cladograma de las Regiones Variables de la Cadena Ligera

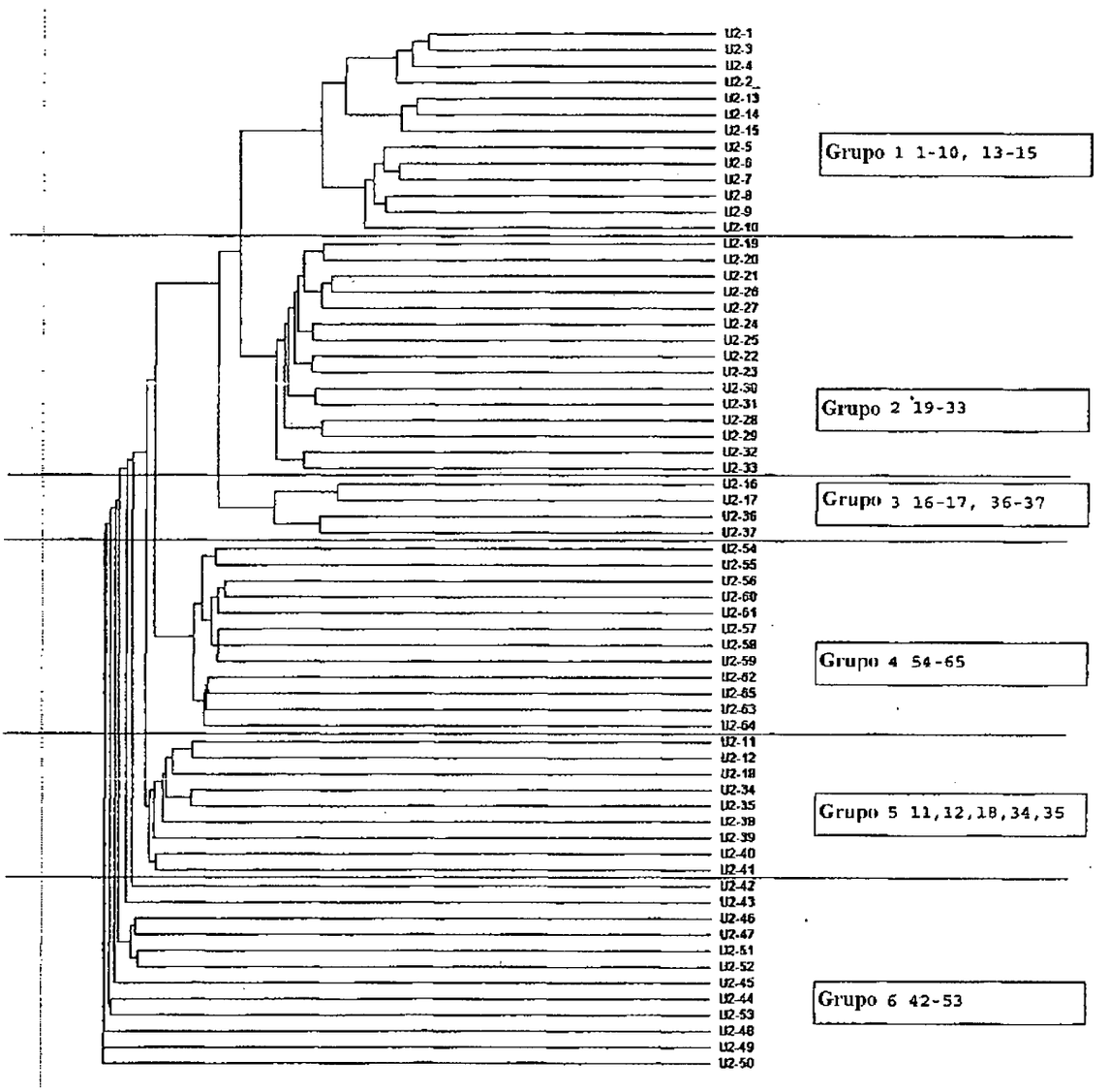


FIGURA 12A

CDRL3- Cladograma

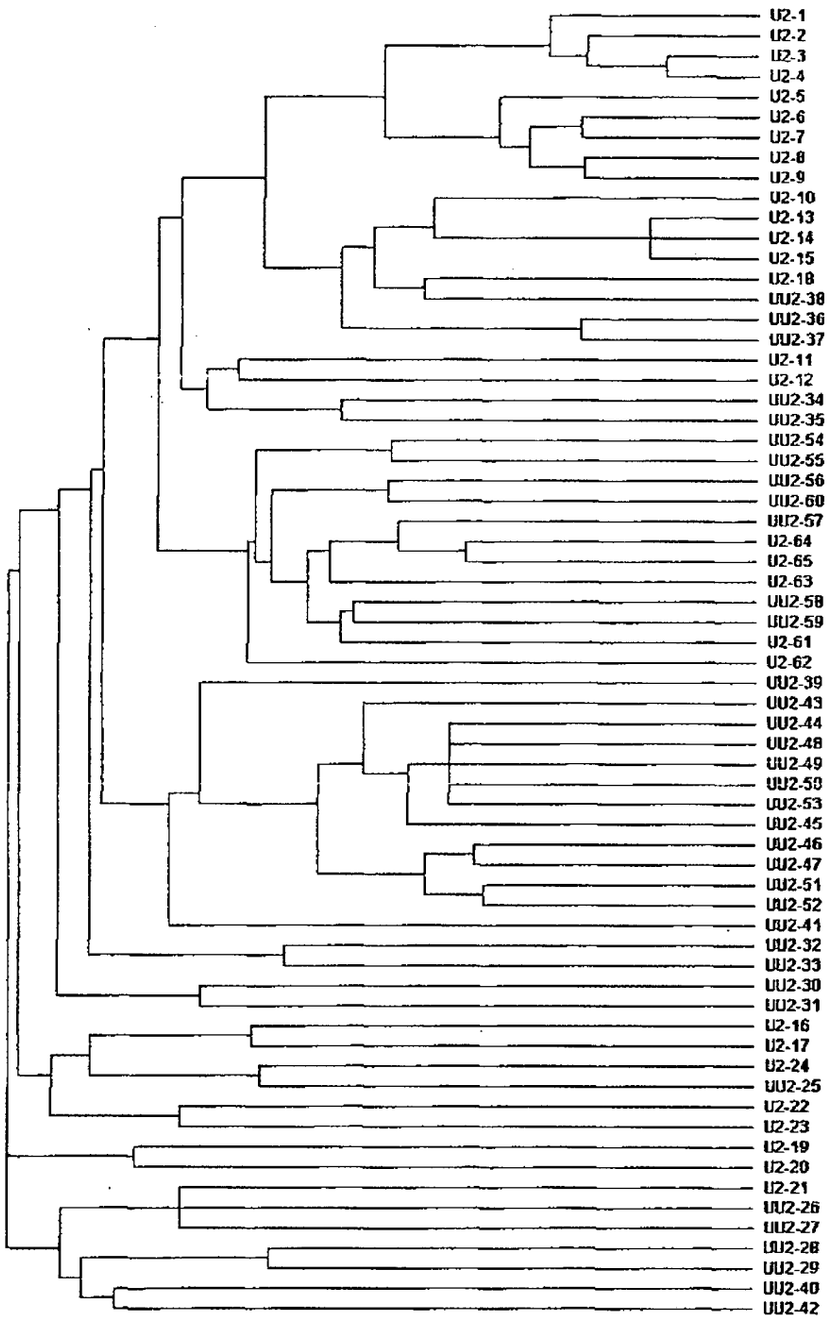


FIGURA 12B

Cladograma de las Regiones Variables de la Cadena Pesada

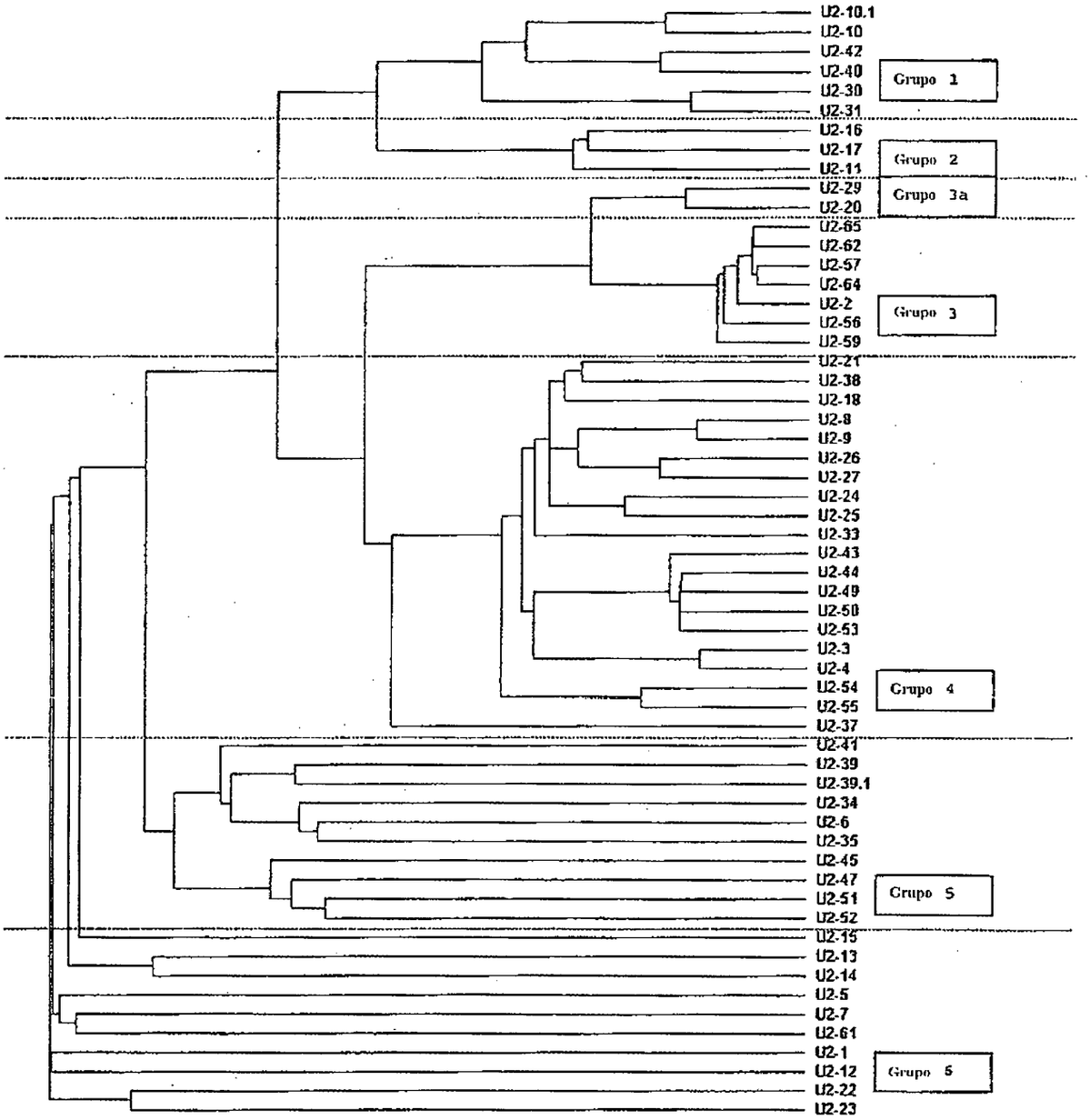


FIGURA 12C

U_L-1: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:532)

gaygtngtnatgacncarwsnccnmtnwsnmtnccngtnacnmtnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnmtngtntaywsngayggnaayacntaymtnaaytggttycarca
rmgnccnggncarwsnccnmgnmgnmtnathtayaargtnwsnaaytgggaywsnggngtnccn
gaymgnttyaayggnwsnggnwsnggnacngayttyacnmtnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarwsnacncaytggccnathacnttyggncarggnac
nmgnmtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygar
carmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcna
argtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarca
rgaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygar
aarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnt
tyaaymgnggngartgy

U_L-2: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:533)

gaygtngtnatgacncarwsnccnmtnwsnmtnccngtnacnmtnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnmtngtntaywsngayggnaayacntaymtnaaytggttycarca
rmgnccnggncarwsnccnmgnmgnmtnathtayaargtnwsnaaytgggaywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyathcarggnacncaytggccnacnacnttyggncarggnac
nmgnmtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygar
carmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcna
argtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarca
rgaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygar
aarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnt
tyaaymgnggngartgy

U_L-3: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:534)

gaygtngtnatgacncarwsnccnmtnwsnmtnccngtnacnmtnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnmtngtntaywsngayggnaayacntaymtnaaytggmtncarca
rmgnccnggncarwsnccnmgnmgnmtnathtayaargtnwsnaaytgggaywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarggnacncaytggccnathacnttyggncarggnac
nmgnmtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygar
carmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcna
argtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarca
rgaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygar
aarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnt
tyaaymgnggngartgy

FIGURA 13A

U_L-4: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:534)

gaygtngtnatgacncarwsnccnmtnwsnmtnccngtnacnmtnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnmtngtntaywsngayggnaayacntaymtnaaytggmtncarca
rmgnccnggncarwsnccnmgnmgnmtnathtayaargtnwsnaaytgggaywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarggnacncaytggccnathacnttyggncarggnac
nmgnmtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygar
carmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcna
argtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarca
rgaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygar
aarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnt
tyaaymgnggngartgy

U_L-5: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:535)

gayathgtnatgacncaracnccnmtnwsnmtnwsngtnacnccnggncarccngcnwsnathw
sntgyaarwsnwsncarwsnmtnmtncaywsngayggnaaracntaymtntaytggtaymtnca
raarccnggncarccnccncarmtnmtnathtaygargtnwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarggnathcarmtnccntgywsnttyggncarggnac
naarmtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygar
carmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcna
argtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarca
rgaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygar
aarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnt
tyaaymgnggngartgy

U_L-6: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:536)

gayathgtnatgacncaracnccnmtnwsnmtnwsngtnacnccnggncarccngcnwsnathw
sntgyaarwsnwsncarwsnmtnmtncaywsngayggnaaracntaymtntaytggtaymtnca
raarccnggncarccnccncarmtnmtnathtaygargtnwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarwsnathcarmtnccnmtnacnttyggnggnggnac
naargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygar
carmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcna
argtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarca
rgaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygar
aarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnt
tyaaymgnggngartgy

FIGURA 13B

U_L-7: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:536)

gayathgtnatgacncaracnccnmtnwsnmtnwsngtnacnccnggncarccngcnwsnathw
sntgyaarwsnwsncarwsnmtnmtncaywsngayggnaaracntaymtntaytggtaymtnca
raarccnggncarccnccncarmtnmtnathtaygargtnwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarwsnathcarmtnccnmtnacnttyggnggnggnac
naargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygar
carmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcna
argtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarca
rgaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygar
aarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnt
tyaaymgnggngartgy

U_L-8: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:537)

gayathgtnatgacncaracnccnmtnwsnmtnwsngtnacnccnggncarccngcnwsnathw
sntgyaarwsnwsncarwsnmtnmtncaywsngayggnaaracntaymtntaytggttymtnca
raarccnggncarccnccncarccnmtnathtaygargtnwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarwsnathcarmtnccnathacnttyggncayggnac
nmgnmtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygar
carmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcna
argtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarca
rgaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygar
aarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnt
tyaaymgnggngartgy

U_L-9: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:537)

gayathgtnatgacncaracnccnmtnwsnmtnwsngtnacnccnggncarccngcnwsnathw
sntgyaarwsnwsncarwsnmtnmtncaywsngayggnaaracntaymtntaytggttymtnca
raarccnggncarccnccncarccnmtnathtaygargtnwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarwsnathcarmtnccnathacnttyggncayggnac
nmgnmtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygar
carmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcna
argtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarca
rgaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygar
aarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnt
tyaaymgnggngartgy

FIGURA 13C

U_L-11: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:538)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarggnathgcnaaytaymtngcntggtaycarcaraarccnggnaargt
nccnaarmtnmtnathtaygtngcnwsnacnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargaygtngcnacnt
aytaytgycaraaytayaaywsngcnccnttyacnttyggnccnggnacnaargtngayathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-12: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:539)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
thtgymgngcnwsncarggnathwsnaaygaymtngcntggtaycarcaraarccnggnaargt
nccnaarmtnmtnathtaygcngcnwsnacnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargaygtngcnacnt
aytaytgycaraartayaaywsngtnccnmtnacnttyggnggnggnacnaargtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-13: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:540)

aayathgtnatgacncaracnccnmtnwsnwsnccngtnacnmtnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnmtngtncaywsngayggnaayacntaymtnwsntggmtncarca
rmgnccnggncarccnccnmgnmtnmtnathtayaarathwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggngcnggnacngayttyacnmtnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcargcnacncarttyccncayacnttyggnccnggnac
naargtngayathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygar
carmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcna
argtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarca
rgaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygar
aarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnt
tyaaymgnggngartgy

FIGURA 13D

U_L-14: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:540)

aayathgtnatgacncaracnccnmtnwsnwsnccngtnacnmtnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnmtngtncaywsngayggnaayacntaymtnwsntggmtncarca
rmgnccnggncarccnccnmgnmtnmtnathtayaarathwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggngcnggnacngayttyacnmtnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcargcnacncarttyccncayacnttyggnccnggnac
naargtngayathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygar
carmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcna
argtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarca
rgaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygar
aarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnt
tyaaymgnggngartgy

U_L-15: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:541)

garathgtnatgacncaracnccnmtnwsnwsnccngtnacnmtnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnmtngtncaywsngayggnaayacntaymtnwsntggmtncarca
rmgnccnggncarccnccnmgnmtnmtnathtayaarathwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnacnggngcnggnacngayttyacnmtnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcargcnacncarttyccncayacnttyggnggnggnac
naargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygar
carmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcna
argtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarca
rgaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygar
aarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnt
tyaaymgnggngartgy

U_L-16: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:542)

garathgtnmtnacncarwsnccnggnacnmtnwsnmtnwsnccnggngarmgngcnacnmtnw
sntgymgngcnwsncaracngtnathwsnwsntaymtngcntggtaycarcaraarccnggnca
rgcnccnmgnmtnmtnathwsnggngcnwsnwsnmgngcnacnggnathccngaymgnttywsn
ggnwsnggnwsnggnacngayttyacnmtnacnathwsnmgnmtngarccngargayttygcng
tntaytaytgycarcartayggnwsnwsnccnmgnacnttyggncarggnacnaargtngarat
haarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsn
ggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartgga
argtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaarga
ywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtn
taygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggng
artgy

FIGURA 13E

U_L-17: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:543)

garathgtnmtnacncarwsnccnggnacnmtnwsnmtnwsnccnggngarmgngcnacnmtnw
sntgymgngcnwsncarwsngtnwsnmgnmtngcntggtaycarcaraarccnggncargcncc
nmgnmtnmtnathtayggngcnwsnmgnmgngcnacnggnathccngaymgnttywsnggnwsn
ggnwsnggnacngayttyacnmtnacnathwsnmgnmtngarccngargayttygcngtntayt
aytgycarcartayggnwsnwsnccnmgnwsnttyggncarggnacnaarmtngarathaarmg
nacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggnacn
gcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaargtng
ayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargaywsnac
ntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntaygcn
tgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngartgy

U_L-18: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:544)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarggnathmgnaaygaymtnggntggtaycarcaraarccnggnaargc
nccnaarmgnmtnathtaygcngcnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngarttyacnmtnacnathwsnwsnmtncarccngargayttygcnacnt
aytaytgymtncarcayaaywsntayccnccnacnttyggncarggnacnaargtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-19: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:545)

gayathgtnatgacncarwsnccngaywsnmtngcngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncarwsngtnmtntaywsnwsnaayaayaaraaytaymtngtntggtayca
rcaraarccnggncarccnccnaarmtnttyathtaytgggcnwsnacnmgngarwsnggngtn
ccngaymgnttyacnggnwsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarg
cngargaygtngcngtntaytaytgycarcartaytaywsnttyccntggacnttyggncargg
nacnaargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

FIGURA 13F

U_L-20: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:545)

gayathgtnatgacncarwsnccngaywsnmtngcngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncarwsngtnmtntaywsnwsnaayaayaaraaytaymtngtntggtayca
rcaraarccnggncarccnccnaarmtnttyathtaytgggcnwsnacnmgngarwsnggngtn
ccngaymgnttyacnggnwsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarg
cngargaygtngcngtntaytaytgycarcartaytaywsnttyccntggacnttyggncargg
nacnaargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

U_L-21: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:546)

gayathgtnatgacncarwsnccngaywsnmtngcngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncarwsngtnmtntaywsnwsnaayaayaaraaytaymtngcntggtayca
rcaraarccnggncarccnccnaarmtnmtnathtaytgggcnwsnacnmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarg
cngargaygtngcngtntaytaytgycarcartaytaywsnacnacntggacnttyggncargg
nacnaargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

U_L-22: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:547)

gayathgtnatgacncarwsnccngaywsnmtngcngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncaraaygtnmtntaywsnwsnaayaayaaraaytaymtngcntggtayca
rcaraarccnggncarccnccnaarmtnmtnathtaytgggcnwsnacnmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarg
cngargaygtngcngtntayttytgycarcartaytayggnacnccnmgnacnttyggncargg
nacnaargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

FIGURA 13G

U_L-23: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:548)

gayathgtnatgacncarwsnccngaywsnmtngcngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncaraaygtnmtntaywsnwsnaayaayaaraaytaymtngcntggtayca
rcaraarccnggncarccnccnaarmtnmtnathtaytgggcnwsnacnmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarg
cngargaygtngcngtntayttytgycarcartaytayggnacnccnmgnacnttyggncargg
nacnaargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

U_L-24: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:549)

gayathgtnatgacncarwsnccngaywsnmtnacngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncarwsngtnmtntaywsnwsnaayaayaaraaytaymtngcntggtayca
rcaraarccnggncarccnccnaarmtnmtnathtaytgggcnwsnacnmgngarwsnggngtn
ccngaymgnttyggnggnwsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarg
cngargaygtngcngtntaytaytgycarcartaytaywsnathwsnmgnacnttyggncargg
nacnaargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

U_L-25: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:549)

gayathgtnatgacncarwsnccngaywsnmtnacngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncarwsngtnmtntaywsnwsnaayaayaaraaytaymtngcntggtayca
rcaraarccnggncarccnccnaarmtnmtnathtaytgggcnwsnacnmgngarwsnggngtn
ccngaymgnttyggnggnwsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarg
cngargaygtngcngtntaytaytgycarcartaytaywsnathwsnmgnacnttyggncargg
nacnaargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

FIGURA 13H

U_L-26: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:550)

gayathgtnatgacncarwsnccngaywsnmtngcngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncarwsngtnmtntayaaywsnaayaayaaraaytaymtngcntggtayca
rcaraarccnggncarccnccnaarmtnmtnathtaytgggcnwsnacnmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarg
cngaygaygtngcngtntaytaytgycarcartaytaywsnacnacntggacnttyggnccngg
nacnaargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

U_L-27: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:551)

gayathgtnatgacncarwsnccngaywsnmtngcngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncarwsngtnmtntayaaywsnaayaayaaraaytaymtngcntggtayca
rcaraarccnggncarccnccnaarmtnmtnathtaytgggcnwsnacnmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarg
cngaygaygtngcngtntaytaytgycarcartaytaywsnacnacntggacnttyggnccngg
nacnaargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

U_L-28: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:552)

gayathgtnatgacncarwsnccngaywsnmtngcngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncarwsngtnmtntaywsnwsnaayaayaaraaytaymtngcntggtayca
rcaraarccnggncarccnccnaargtnmtnathtaytgggcnwsnacnmgnaarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnacnathwsnggnmtncarg
cngargaygtngcnmtntaytaytgycarcartaytaywsnacnatgttywsnttyggncargg
nacnaarmtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

FIGURA 13I

$_L$-29: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:552)

gayathgtnatgacncarwsnccngaywsnmtngcngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncarwsngtnmtntaywsnwsnaayaayaaraaytaymtngcntggtayca
rcaraarccnggncarccnccnaargtnmtnathtaytgggcnwsnacnmgnaarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnacnathwsnggnmtncarg
cngargaygtngcnmtntaytaytgycarcartaytaywsnacnatgttywsnttyggncargg
nacnaarmtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

U_L-30: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:553)

gayathgtnatgacncarwsnccngaywsnmtngcngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncarwsngtnmtngaywsnwsnaayaayaaraaytaymtngcntggtayca
rcaraarccnggncarccnccnaarmtnmtnathtaytgggcnwsnacnmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarg
cngargaygtngcngtnttytaytgycaycartaytaywsnacnccnmtnacnttyggnggngg
nacnaargtngcnathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

U_L-31: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:553)

gayathgtnatgacncarwsnccngaywsnmtngcngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncarwsngtnmtngaywsnwsnaayaayaaraaytaymtngcntggtayca
rcaraarccnggncarccnccnaarmtnmtnathtaytgggcnwsnacnmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarg
cngargaygtngcngtnttytaytgycaycartaytaywsnacnccnmtnacnttyggnggngg
nacnaargtngcnathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

FIGURA 13J

U_L-32: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:554)

gayathgtnatgacncarwsnccngaywsnmtngcngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncarwsnathmtntaymgnwsnaayaayaaraaytaymtngcntggtayca
rcaraarccnggncarccnccnaarmtnmtnathtaytgggcnwsngcnmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarg
cngargaygtngcngtntayttytgycarcartayttyathacnccnmtnacnttyggnggngg
nacnaargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

U_L-33: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:554)

gayathgtnatgacncarwsnccngaywsnmtngcngtnwsnmtnggngarmgngcnacnatha
aytgyaarwsnwsncarwsnathmtntaymgnwsnaayaayaaraaytaymtngcntggtayca
rcaraarccnggncarccnccnaarmtnmtnathtaytgggcnwsngcnmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarg
cngargaygtngcngtntayttytgycarcartayttyathacnccnmtnacnttyggnggngg
nacnaargtngarathaarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngay
garcarmtnaarwsnggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngarg
cnaargtncartggaargtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacnga
rcargaywsnaargaywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytay
garaarcayaargtntaygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarw
snttyaaymgnggngartgy

U_L-34: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:555)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncargayathwsncaytaymtngcntggttycarcaraarccnggnaargc
nccnaarwsnmtnathtaygcngcnwsnwsnmtncarwsnggngtnccnwsnaarttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargayttygcnacnt
aytaytgycarcartayaayaaytayccnttyacnttyggnccnggnacnaargtngayathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

FIGURA 13K

U_L-35: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:556)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtngcnatha
cntgymgngcnwsncargayathwsnaaytaymtngcntggmtncarcaraarccnggnaargc
nccnaarwsnmtnathtaygcngcnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargayttygcnacnt
aytaytgycarcartayaayacntayccnttyacnttyggnccnggnacnaaratggayathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-36: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:557)

garathgtnatgacncarwsnccngcnacnmtnwsngtnwsnccnggngarmgngcnacnmtnw
sntgymgngcnwsncarwsngtnwsnwsnaaymtngcntggtaycarcargayccnggncargc
nccnmgnmtnmtnathtayggngcnwsnmgnmgngcnacnggnathccngcnmgnttywsnggn
wsnggnwsnggnacngarttyacnmtnacnathwsnwsnmtncarwsngargayttygcngtnt
aytaytgycarcarcayaayaaytggccnccntggacnttyggncarggnacnaargtngarat
haarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsn
ggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartgga
argtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaarga
ywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtn
taygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggng
artgy

U_L-37: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:557)

garathgtnatgacncarwsnccngcnacnmtnwsngtnwsnccnggngarmgngcnacnmtnw
sntgymgngcnwsncarwsngtnwsnwsnaaymtngcntggtaycarcargayccnggncargc
nccnmgnmtnmtnathtayggngcnwsnmgnmgngcnacnggnathccngcnmgnttywsnggn
wsnggnwsnggnacngarttyacnmtnacnathwsnwsnmtncarwsngargayttygcngtnt
aytaytgycarcarcayaayaaytggccnccntggacnttyggncarggnacnaargtngarat
haarmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsn
ggnacngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartgga
argtngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaarga
ywsnacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtn
taygcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggng
artgy

FIGURA 13L

U_L-38: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:558)

gayathcaratgacncarwsnccnwsnwsngtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncargayathwsnmgntggmtngcntggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtaygcngcnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargayttygcnacnt
aytaytgycarcargcnaaywsnttyccnccnacnttyggncarggnacnaargtngarttyaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-39: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:559)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarwsnathwsnacntaymtnaaytggtaycarcaraarccnggnaargc
nccnaarttymtnathtaygcngcnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargayttygcngcnt
aytaytgycarcarwsncaywsngcnccnttyacnttyggnccnggnacnaargtngayathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-40: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:560)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsnmtnggngaymgngtnacnatha
cntgymgngcnwsncaracnathwsnathtaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtaygcngcnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargayttygcnacnt
aytaytgycarcarwsntaywsnacnmtnacnttyggnggnggnacnaargtngarathaarmg
nacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggnacn
gcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaargtng
ayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargaywsnac
ntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntaygcn
tgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngartgy

FIGURA 13M

U_L-41: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:561)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarwsnathmgnwsntaymtnaaytggtaycarcarmgnccnggnaaygc
nccnaarmtnmtnathtaygcngcnwsnwsnmtncarwsnggngtnccnwsnmgngtnwsnggn
wsnggnwsnggnacngayttyacnmtnacnathmgnwsnmtncarccngargayttygcnacnt
aytaytgycarcarwsntaywsnathccnmtnacnttyggnggnggnacnaargtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-42 : Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:562)

gayathcaratgacncarwsnccnwsnwsnmgnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncaracnathwsnmgntaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtaygcngcnwsnacnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnmtnwsnwsnmtncarccngargayttygcnacnt
aytaytgycarcarathtaywsnacnwsnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-43 : Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:563)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarmgnathwsnwsntaymtnaaytggtaycarcaraarccnggnaargc
nccnaargtnmtnathtaygcngarwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargayttygcnacnt
aytaytgycarcarwsntayathacnccnathacnttyggncarggnacnmgnmtngarathat
hmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

FIGURA 13N

U_L-44: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:564)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarwsnathwsnmgntaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtayacngcnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngaraayttygcnacnt
aytaytgycarcarwsntayttyacnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-45: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:565)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarwsnathwsnwsntaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtayacngcnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnttywsnwsnmtncarccngargayttygcnacnt
aytaytgycarcarwsntayttywsnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-46: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:566)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarwsnathwsnwsntaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtayacngcnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnmtnwsnwsnmtncarccngargayttygcnwsnt
aytaytgycarcarwsnttytayacnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

FIGURA 13O

U_L-47: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:566)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarwsnathwsnwsntaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtayacngcnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnmtnwsnwsnmtncarccngargayttygcnwsnt
aytaytgycarcarwsnttytayacnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargaywss
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-48: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:567)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarwsnathwsnwsntaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtayacngtnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargayttygcnacnt
aytaytgycarcarwsntayttyacnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargaywss
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-49: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:567)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarwsnathwsnwsntaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtayacngtnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargayttygcnacnt
aytaytgycarcarwsntayttyacnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargaywss
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

FIGURA 13P

U_L-50: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:567)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarwsnathwsnwsntaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtayacngtnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargayttygcnacnt
aytaytgycarcarwsntayttyacnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-51: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:568)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarwsnathwsnwsntaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtayacngcnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargayttygcnwsnt
aytaytgycarcarwsnttytaygcnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-52: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:568)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarwsnathwsnwsntaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtayacngcnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargayttygcnwsnt
aytaytgycarcarwsnttytaygcnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

FIGURA 13Q

U_L-53: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:569)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgymgngcnwsncarwsnathwsnwsntaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtayacngcnwsnwsnmtncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnmtnacnathwsnwsnmtncarccngargayttygcnacnt
aytaytgycarcarwsntayttyacnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-54: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:570)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgycargcnwsncargayathwsnaaytaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtaygaygcnwsnaaymtngaracnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnttyacnathwsnwsnmtncarccngargayathgcnacnt
aytaytgycarcartaygaytaymtnccnttyacnttyggnccnggnacnaargtngayathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-55: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:570)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgycargcnwsncargayathwsnaaytaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtaygaygcnwsnaaymtngaracnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnttyacnathwsnwsnmtncarccngargayathgcnacnt
aytaytgycarcartaygaytaymtnccnttyacnttyggnccnggnacnaargtngayathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

FIGURA 13R

U_L-56: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:571)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgycargcnwsncargayathwsnaaywsnmtnaaytggtaycarcaraarccnggnaargc
nccngarmtnmtnathtaygaygcnwsnaaymtngaracnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnttyacnathwsnwsnmtncarccngargayathgcnacnt
aytaytgycarcartgygaygaymtnccnmtnacnttyggnggnggnacnaargtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-57: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:572)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgycargcnwsncargayathwsngaytaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtaygaygcnwsnaaymtngaracnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnttyacnathwsnwsnmtncarccngargayathgcnacnt
aytaytgycarcaytaygayaaymtnccnmtnacnttyggnggnggnacnaargtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-58: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:573)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtngcnatha
cntgycargcnwsncargayathwsnaaytaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtaygaygcnwsnaaymtngaracnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnttyacnathwsnwsnmtncarccngargayathgcnacnt
aytaytgycarcartaygayaaymtnccnmtnacnttyggnggnggnacnaargtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

FIGURA 13S

U_L-59: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:573)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtngcnatha
cntgycargcnwsncargayathwsnaaytaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtaygaygcnwsnaaymtngaracnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnttyacnathwsnwsnmtncarccngargayathgcnacnt
aytaytgycarcartaygayaaymtnccnmtnacnttyggnggnggnacnaargtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-60: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:574)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgycargcnwsncargayathwsnaaywsnmtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtaygaygcnwsnathmtngaracnggngtnccnwsnmgnttywsnggn
wsnggnwsngaracngayttyacnttyacnathwsnwsnmtncarccngargayathgcnacnt
aytaytgycarcartgygayathmtnccnmtnwsnttyggnggnggnacnaargtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-61: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:575)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgycargcnwsncargayathwsnaaywsnmtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtaygaygcnwsnaaymtngaracnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnttyacnathwsnwsnmtncarccngargayathgcnacnt
aytaytgycarcartaygayaaymtnccnmtngcnttyggnggnggnacnaargtngarathmg
nmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

FIGURA 13T

U_L-62: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:576)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngayggngtnacnatha
cntgycargcnwsncargayathacnaaytaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtaygaygcnwsnaaymtngaracnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnttyacnathwsnwsnmtncarccngargayathgcnacnt
aytaytgycarcartaygaywsnmtnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-63: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:577)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgycargcnwsncargayathwsnaaytaymtnaaytggtaycarcaraarmtnggnaargc
nccnaarmtnmtnathcaygaygcnwsnaaymtngaracnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnttyacnathwsnwsnmtncarccngargayathgcnacnt
aytaytgycarcartaygayaaymtnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

U_L-64: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:578)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgycargcnwsncargayathwsngaytaymtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtaygaygcnwsnaaymtngaracnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnttyacnathwsnwsnmtncarccngargayathgcnacnt
aytaytgycarcaytaygayaaymtnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

FIGURA 13U

U_L-65: Secuencia de nucleótidos de la cadena ligera (SEQ ID NO:579)

gayathcaratgacncarwsnccnwsnwsnmtnwsngcnwsngtnggngaymgngtnacnatha
cntgycargcnwsncargayathwsnaaywsnmtnaaytggtaycarcaraarccnggnaargc
nccnaarmtnmtnathtaygaygcnwsnaaymtngaracnggngtnccnwsnmgnttywsnggn
wsnggnwsnggnacngayttyacnttyacnathwsnwsnmtncarccngargayathgcnacnt
aytaytgycarcaytaygayaaymtnccnathacnttyggncarggnacnmgnmtngarathaa
rmgnacngtngcngcnccnwsngtnttyathttyccnccnwsngaygarcarmtnaarwsnggn
acngcnwsngtngtntgymtnmtnaayaayttytayccnmgngargcnaargtncartggaarg
tngayaaygcnmtncarwsnggnaaywsncargarwsngtnacngarcargaywsnaargayws
nacntaywsnmtnwsnwsnacnmtnacnmtnwsnaargcngaytaygaraarcayaargtntay
gcntgygargtnacncaycarggnmtnwsnwsnccngtnacnaarwsnttyaaymgnggngart
gy

FIGURA 13V

U_H-1 : Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:580)

cargtncarmtngtncarwsnggngcngargtnaaraarccnggngcnwsngtnaargtnwsnt
gyaargcnwsnggntayacnttyacnwsntayggnathwsntgggtnmgncargcnccnggnca
rggnmtngartggatgggntggathwsngcnwsnaayggnaayacnaaytaygcncaraarmtn
cargaymgngtnacnatgacnacngayacnwsnacnwsnacngcntayatggarmtnmgnwsnm
tnmgnwsngaygayacngcngtntaytaytgygcnmgngargayaaytggaaytayggnttytt
ygaytaytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtn
ttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtna
argaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtnca
yacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccn
wsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaarg
tngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngc
nggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccn
gargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtayg
tngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacntt
ymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgy
aargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarc
cnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnws
nmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggn
carccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtnt
aywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnat
gcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_H-2 : Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:580)

cargtncarmtngtncarwsnggngcngargtnaaraarccnggngcnwsngtnaargtnwsnt
gyaargcnwsnggntayacnttyacnwsntayggnathwsntgggtnmgncargcnccnggnca
rggnmtngartggatgggntggathwsngcnwsnaayggnaayacnaaytaygcncaraarmtn
cargaymgngtnacnatgacnacngayacnwsnacnwsnacngcntayatggarmtnmgnwsnm
tnmgnwsngaygayacngcngtntaytaytgygcnmgngargayaaytggaaytayggnttytt
ygaytaytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtn
ttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtna
argaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtnca
yacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccn
wsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaarg
tngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngc
nggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccn
gargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtayg
tngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacntt
ymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgy
aargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarc
cnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnws
nmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggn
carccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtnt
aywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnat
gcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURA 14A

U_H-3: Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:581)

cargtncaymtngtncarwsnggngcngargtnaaraarccnggngcnwsngtnaargtnwsnt
gyaargtnwsnggntayacnttyacnggncaytayatgcaytgggtnmgncargcnccnggnca
rggnmtngartggatgggntggathaayccnaaywsnggnggnacnaaytgygcncaraartty
carggnmgngtnacnatgacnmgngayacnwsnathwsnacngcntayatggarmtnwsnmgnm
tnmgnwsngaygayacngcngtntaytaytgygcnmgnwsnathgcngtngcnmtngaytaytg
gggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccnmtn
gcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargaytayt
tyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacnttycc
ngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsnaay
ttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngayaara
cngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggnccnws
ngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtnacn
tgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayggng
tngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngtngt
nwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtnwsn
aayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgngarc
cncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnacntg
ymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccngar
aayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsnaarm
tnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcaygargc
nmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_H-4: Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:582)

cargtncarmtngtncarwsnggngcngargtnaaraarccnggngcnwsngtnaargtnwsnt
gyaargcnwsnggntayacnttyacnggntaytayatgcaytgggtnmgncargcnccnggnca
rggnmtngartggatgggntggathaayccnaaywsnggnggnacnaaycayacncaraartty
carggnmgngtnacnatgacnmgngayacnwsnathwsnacngcntayatggarmtnwsnmgnm
tnmgnwsngaygayacngcngtntaytaytgygcnmgnwsnathgcngtngcnmtngaytaytg
gggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccnmtn
gcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargaytayt
tyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacnttycc
ngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsnaay
ttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngayaara
cngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggnccnws
ngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtnacn
tgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayggng
tngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngtngt
nwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtnwsn
aayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgngarc
cncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnacntg
ymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccngar
aayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsnaarm
tnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcaygargc
nmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURA 14B

U_H-5 : Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:583)

cargtncarmtngtncarwsnggngcngargtnmgnaarccnggngcnwsngtnaargtnwsnt
gyaargtnwsnggntayacnmtnacngarmtnwsnatgcaytgggtnmgncargcnccnggnaa
rggnmtngartggatgggnwsnttygayccngargayggngaracnathtaygcncaraartty
carggnmgngtnacnatgmtngargayacnwsnacngayacngcntayatggarmtnwsnwsnm
tnmgnwsngargayacngcngtntaytaytgygcnacngarggngayggnggntaytaytayta
yggnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacnaarggnccn
wsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgym
tngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsngg
ngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacn
gtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaaya
cnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccncc
ngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgn
acnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaayt
ggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywss
nacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartay
aartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarg
gncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraayca
rgtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsn
aayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyt
tymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgyws
ngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_H-6 : Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:583)

cargtncarmtngtncarwsnggngcngargtnmgnaarccnggngcnwsngtnaargtnwsnt
gyaargtnwsnggntayacnmtnacngarmtnwsnatgcaytgggtnmgncargcnccnggnaa
rggnmtngartggatgggnwsnttygayccngargayggngaracnathtaygcncaraartty
carggnmgngtnacnatgmtngargayacnwsnacngayacngcntayatggarmtnwsnwsnm
tnmgnwsngargayacngcngtntaytaytgygcnacngarggngayggnggntaytaytayta
yggnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacnaarggnccn
wsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgym
tngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsngg
ngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacn
gtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaaya
cnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccncc
ngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgn
acnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaayt
ggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywss
nacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartay
aartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarg
gncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraayca
rgtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsn
aayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyt
tymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgyws
ngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURA 14C

U_H-7: Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:584)

cargtnacnmtnaargarwsnggnccngtnmtngtnaarccnacngaracnmtnacnmtnacnt
gyacngtnwsnggnttywsnmtnwsnaaygcnmgnatgggngtnwsntggathmgncarccncc
nggnaargcnmtngartggmtngcncayathttywsnaaygaygaraarwsntaywsnacnwsn
mtnaarwsnmgnmtnacnathwsnaargayacnwsnaarwsncargtngtnmtnacnatgacna
ayatggayccngtngayacngcnacntaytaytgygcnmgnatgtaywsnwsnggntggtaygg
ngtnttygaytaytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccn
wsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgym
tngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsngg
ngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacn
gtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaaya
cnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccncc
ngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgn
acnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaayt
ggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaayws
nacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartay
aartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarg
gncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraayca
rgtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsn
aaygggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyt
tymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgyws
ngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_H-8: Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:585)

cargtnacnmtnaargarwsnggnccngtnmtngtnaarccnacngaracnmtnacnmtnacnt
gyacngtnwsnggnttywsnmtnwsnaaygcnmgnatgggngtnwsntggathmgncarccncc
nggnaargcnmtngartggmtngtnmtnathttywsnaaygaygaraarwsntaywsnacnwsn
mtnaarwsnmgnmtnacnathwsnaargayacnwsnaarwsncargtngtnmtnacnatgacna
ayatggayccngtngayacngcnacntaytaytgygcnmgngtntaywsnwsnggntggwsntt
ytayggnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacnaarggn
ccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggnt
gymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnws
nggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtn
acngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsna
ayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcncc
nccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsn
mgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttya
aytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaa
ywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargar
tayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracna
arggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraa
ycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggar
wsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnt
tyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntg
ywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggn
aar

FIGURA 14D

U_B-9 : Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:586)

carathacnmtnaargarwsnggnccnacnmtngtnaarccnacncaracnmtnacnmtnacnt
gyacnttywsnggnttywsnmtnwsnacnggnggngtnggngtnggntggathmgncarccncc
nggnaargcnmtngartggmtngcnmtnathtaytggaaygaygayaarmgntaywsnccnwsn
mtnaarwsnmgnmtnacnathacnaargayacnwsnaaraaycargtngtnmtnacnatgacna
ayatggayccngtngayacngcnacntaytaytgygcncaymgnmgngarmtnccnttygayta
ytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccn
mtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargayt
ayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacntt
yccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsn
aayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngaya
aracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggncc
nwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtn
acntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayg
gngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngt
ngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtn
wsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgng
arccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnac
ntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccn
garaayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsna
armtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcayga
rgcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_B-10 : Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:587)

carathacnmtnaargarwsnggnccnacnmtngtnaarccnacncaracnmtnacnmtnacnt
gyacnttywsnggnttywsnmtnwsnacnggnggngtnggngtnggntggathmgncarccncc
nggnaargcnmtngartggmtngcnmtnathtaytggaaygaygayaarmgntaywsnccnwsn
mtnaarwsnmgnmtnacnathacnaargayacnwsnaaracncargtngtnmtnacngtnacng
ayatggayccngtngayacngcnacntaytaytgygcncaymgnaaytggacnccnttygayta
ytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccn
mtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargayt
ayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacntt
yccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsn
aayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngaya
aracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggncc
nwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtn
acntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayg
gngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngt
ngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtn
wsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgng
arccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnac
ntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccn
garaayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsna
armtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcayga
rgcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURA 14E

U_H-11: Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:588)

carathacnmtnaargarwsnggnccnacnmtngtnaarccnacncaracnmtnacnmtnacnt
gyacnttywsnggnttywsnmtnaayacnggnggngtnggngtnggntggathmgncarccncc
nggnaargcnmtngartggmtngcnmtnathtaytggaaygaygayaarmgntaywsnccnwsn
mtnaarwsnmgnmtnacnathacnaargayacnwsnaaraaycargtngtnmtnacnatgacna
ayatggayccngtngayacngcnacntaytaytgygcncaymgnmtngarmtnccnttygayta
ytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccn
mtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargayt
ayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacntt
yccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsn
aayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngaya
aracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggncc
nwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtn
acntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayg
gngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngt
ngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtn
wsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgng
arccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnac
ntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccn
garaayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsna
armtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcayga
rgcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_H-12: Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:589)

carathacnmtnaargarwsnggnccnacnmtngtnaarccnacncaracnmtnacnmtnacnt
gyacnttywsnggnttywsnmtnwsnacnggnggngtnggngtnggntggathmgncarccncc
nggnaargcnmtngartggmtngcnmtnathtaytggaaygaygayaarmgntaywsnccnwsn
mtnaarwsnmgnmtnacnathacnaargayacnwsnaaraaycargtngtnmtnacnatgacna
aymtngayccngtngayacngcnacntaytaytgygcncaymgnmgngargtnccnttygayta
ytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccn
mtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargayt
ayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacntt
yccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsn
aayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngaya
aracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggncc
nwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtn
acntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayg
gngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngt
ngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtn
wsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgng
arccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnac
ntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccn
garaayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsna
armtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcayga
rgcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURA 14F

U_B-13 : Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:590)

carathacnmtnaargarwsnggnccnacnmtngtnaarccnacncaracnmtnacnmtnacnt
gyacnttywsnggnttywsnmtnwsnacnggnggngtnggngtnggntggathmgncarccncc
nggnaargcnmtngartggmtngcnmtnathtaytggaaygtngaraarmgntaywsnccnwsn
mtnmgnwsnmgnmtnacnathacnaargcnacnwsnaaraaycargtngtnmtnacnatgacna
ayatggayccngtngayacngcnacntaytaytgygcncaymgncayacnaayccnttygarta
ytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccn
mtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargayt
ayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacntt
yccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsn
aayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngaya
aracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggncc
nwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtn
acntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayg
gngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngt
ngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtn
wsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgng
arccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnac
ntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccn
garaayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsna
armtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcayga
rgcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_B-14 : Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:591)

carathacnmtnaargarwsnggnccnacnmtngtnaarccnacncaracnmtnacnmtnacnt
gyacnttywsnggnttywsnmtnwsnacnggnggngtnggngtnggntggathmgncarccncc
nggnaargcnmtngartggmtngcnmtnathtaytggaaygaygayaarmgntaywsnccnwsn
mtnaarwsnmgnmtnacnathacnaargayacnwsnaaraaycargtngtnmtnacnatgacna
ayatggayccngtngayacngcnacntaytaytgygcncaymgnggngarmtnccnttygayta
ytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccn
mtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargayt
ayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacntt
yccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsn
aayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngaya
aracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggncc
nwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtn
acntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayg
gngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngt
ngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtn
wsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgng
arccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnac
ntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccn
garaayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsna
armtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcayga
rgcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURA 14G

UH-15 : Secuencia de nucleótidos de la cadena pesada **(SEQ ID NO:591)**

carathacnmtnaargarwsnggnccnacnmtngtnaarccnacncaracnmtnacnmtnacnt
gyacnttywsnggnttywsnmtnwsnacnggnggngtnggngtnggntggathmgncarccncc
nggnaargcnmtngartggmtngcnmtnathtaytggaaygaygayaarmgntaywsnccnwsn
mtnaarwsnmgnmtnacnathacnaargayacnwsnaaraaycargtngtnmtnacnatgacna
ayatggayccngtngayacngcnacntaytaytgygcncaymgnggngarmtnccnttygayta
ytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccn
mtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargayt
ayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacntt
yccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsn
aayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngaya
aracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggncc
nwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtn
acntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayg
gngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngt
ngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtn
wsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgng
arccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnac
ntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccn
garaayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsna
armtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcayga
rgcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_H-16 : Secuencia de nucleótidos de la cadena pesada **(SEQ ID NO:592)**

gargtncarmtngtngarwsnggnggnggnmtngtnaarccnggnggnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyccnttywsnmgntaywsnatgaaytgggtnmgncargcnccnggnaa
rggnmtngartgggtnwsngcnathwsnwsnwsnwsnwsntayathtaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaygcnaaraaywsnmtntaymtncaratgaaywsnm
tnmgngcngargayacngcngtntaytaytgygcnmgngaymgngtnggngcnacnccngaygc
nttygayathtggggncarggnacnatggtnacngtnwsnwsngcnwsnacnaarggnccnwsn
gtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtng
tnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngt
ncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtn
ccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacna
argtngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngt
ngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacn
ccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggt
aygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnac
nttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaar
tgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggnc
arccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargt
nwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaay
ggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttym
tntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngt
natgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURA 14H

U_H-17: Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:593)

gargtncarmtnmtngarwsnggnggnggnmtngtncarccnggnggnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntaygcnatgaaytgggtnmgncargcnccnggnaa
rggnmtngartgggtnwsngcnathwsnggnwsnggnggnwsnacntaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaywsnaaraayacnmtntaymtncaratgaaywsnm
tnmgngcngargayacngcngtntaytaytgygcnaargarggnathgcngtngcnggnacngc
ngartaytaytaytaytaygcnatggaygtntggggncarggnacnacngtnacngtnwsnwsn
gcnwsnacnaarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsna
cngcngcnmtnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaayws
nggngcnmtnacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsn
mtnwsnwsngtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtng
aycayaarccnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgycc
nccntgyccngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargay
acnmtnatgathwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayc
cngargtncarttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmg
ngargarcarttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytgg
mtnaayggnaargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraara
cnathwsnaaracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgnga
rgaratgacnaaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayath
gcngtngartgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtng
aywsngayggnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcargg
naaygtnttywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtn
wsnmtnwsnccnggnaar

U_H-18: Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:594)

gargtncarmtnmtngarwsnggnggnggnmtngtncarccnggnggnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntaygcnatgwsntgggtnmgncargcnccnggnaa
rggnmtngartgggtnwsngcnathwsnggnwsnggnggnwsnacntaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaywsnaaraayacnmtntaymtncaratgaaywsnm
tnmgngcngargayacngcngtntaytaytgygcnaargarggnathgcngcnmgngaywsnta
ytaytaytaygcnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacn
aarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnm
tnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmt
nacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsn
gtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarc
cnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgycc
ngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatg
athwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtnc
arttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarca
rttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggn
aargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsna
aracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgac
naaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngar
tgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayg
gnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtntt
ywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsn
ccnggnaar

FIGURA 14I

U_R-19: Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:595)

gargtncarmtnmtngarwsnggnggnggnmtngtncarccnggnggnwsnmtnmgnmtnwsnt
gyacngcnwsnggnttyacnttywsnwsntaygcnatgwsntgggtnmgncargcnccnggnaa
rggnmtngartgggtnwsngcnathwsnggnwsnggnggnwsnacntaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaywsnaaraayacnmtntaymtncaratgaaywsnm
tnmgngcngargayacngcngartaytaytgygcnaargarggnathgcnggnmgngaywsnta
ytaytaytayggnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacn
aarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnm
tnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmt
nacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsn
gtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarc
cnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgycc
ngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatg
athwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtnc
arttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarca
rttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggn
aargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsna
aracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgac
naaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngar
tgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayg
gnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtntt
ywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsn
ccnggnaar

U_R-20: Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:595)

gargtncarmtnmtngarwsnggnggnggnmtngtncarccnggnggnwsnmtnmgnmtnwsnt
gyacngcnwsnggnttyacnttywsnwsntaygcnatgwsntgggtnmgncargcnccnggnaa
rggnmtngartgggtnwsngcnathwsnggnwsnggnggnwsnacntaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaywsnaaraayacnmtntaymtncaratgaaywsnm
tnmgngcngargayacngcngartaytaytgygcnaargarggnathgcnggnmgngaywsnta
ytaytaytayggnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacn
aarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnm
tnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmt
nacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsn
gtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarc
cnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgycc
ngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatg
athwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtnc
arttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarca
rttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggn
aargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsna
aracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgac
naaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngar
tgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayg
gnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtntt
ywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsn
ccnggnaar

FIGURA 14J

U_B-21: Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:596)

cargtncarmtngtngarwsnggnggnggngtngtncarccnggnmgnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnmtngartgggtngcnttyathwsngaygayggnwsnacnaartaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaywsnatgaayacnmtntaymtncaratgaaywsnm
tnmgngcngargayacngcngtntaytaytgygcnmgnwsntaytaygaywsnwsnggntayta
ytayggnttygaytaytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggn
ccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggnt
gymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnws
nggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtn
acngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsna
ayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcncc
nccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsn
mgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttya
aytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaa
ywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargar
tayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracna
arggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraa
ycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggar
wsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnt
tyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntg
ywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggn
aar

U_B-22: Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:596)

cargtncarmtngtngarwsnggnggnggngtngtncarccnggnmgnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnmtngartgggtngcnttyathwsngaygayggnwsnacnaartaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaywsnatgaayacnmtntaymtncaratgaaywsnm
tnmgngcngargayacngcngtntaytaytgygcnmgnwsntaytaygaywsnwsnggntayta
ytayggnttygaytaytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggn
ccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggnt
gymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnws
nggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtn
acngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsna
ayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcncc
nccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsn
mgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttya
aytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaa
ywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargar
tayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracna
arggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraa
ycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggar
wsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnt
tyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntg
ywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggn
aar

FIGURA 14K

U_H-23 : Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:597)

cargtncarmtngtngarwsnggnggnggngtngtncarccnggnmgnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnmtngartgggtngcngtnathtggtaygayggnwsnaayaartaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaywsnaaraayacnmtntaymtncaratgaaywsnm
tnmgngcngargayacngcngtntaytaytgygcnmgnaaygtnathgaytaytggggncargg
nacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccnmtngcnccntgy
wsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargaytayttyccngarc
cngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacnttyccngcngtnmt
ncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsnaayttyggnacn
caracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngayaaracngtngarm
gnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggnccnwsngtnttymt
nttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtnacntgygtngtn
gtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayggngtngargtnc
ayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngtngtnwsngtnmt
nacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtnwsnaayaarggn
mtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgngarccncargtnt
ayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnacntgymtngtnaa
rggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccngaraayaaytay
aaracnacnccnccnatgmtngaywsngayggnwsnttytttymtntaywsnaarmtnacngtng
ayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcaygargcnmtncayaa
ycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_H-24 : Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:598)

cargtncarmtngtngarwsnggnggnggngtngtncarccnggnmgnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntaygayatgcaytgggtnmgncargcnccnggnaa
rggnmtngartgggtngcngtnathtggtaygayggnwsnathaartaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaywsnaaraayacnmtntaymtncaratgaaywsnm
tnmgngcngargayacngcngtntaytaytgygcnmgnggnggngcnacnggngcngartaytt
ycarcaytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtn
ttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtna
argaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtnca
yacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccn
wsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaarg
tngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngc
nggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccn
gargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtayg
tngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacntt
ymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgy
aargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarc
cnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnws
nmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggn
carccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtnt
aywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnat
gcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURA 14L

U_R-25 : Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:598)

cargtncarmtngtngarwsnggnggnggngtngtncarccnggnmgnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntaygayatgcaytgggtnmgncargcnccnggnaa
rggnmtngartgggtngcngtnathtggtaygayggnwsnathaartaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaywsnaaraayacnmtntaymtncaratgaaywsnm
tnmgngcngargayacngcngtntaytaytgygcnmgnggnggngcnacnggngcngartaytt
ycarcaytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtn
ttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtna
argaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtnca
yacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccn
wsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaarg
tngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngc
nggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccn
gargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtayg
tngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacntt
ymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgy
aargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarc
cnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnws
nmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggn
carccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtnt
aywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnat
gcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_R-26: Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:599)

cargtncarmtngtngarwsnggnggnggngtngtncarccnggnmgnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnmtngartgggtngcngtnathtggtaygayggnwsnaayaartaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaywsnaaraayacnmtntaymtncaratgaaywsnm
tnmgngcngargayacngcngtntaytaytgygtnmtnmtntggttyggngaracnttygayta
ytggggncarggnwsnmtngtnacngtnwsnccngcnwsnacnaarggnccnwsngtnttyccn
mtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargayt
ayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacntt
yccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsn
aayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngaya
aracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggncc
nwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtn
acntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayg
gngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngt
ngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtn
wsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgng
arccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnac
ntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccn
garaayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsna
armtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcayga
rgcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURA 14M

U_R-27: Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:600)

cargtncarmtngtngarwsnggnggnggngtngtncarccnggnmgnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnmtngartgggtngcngtnathtggwsngayggnwsnaayaartaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaywsnaaraayacnmtntaymtncaratgaaywsnm
tnmgngcngargayacngcngtntaytaytgygcnmgnaaymtnccnttygaytaytggggnca
rggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccnmtngcnccn
tgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargaytayttyccng
arccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacnttyccngcngt
nmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsnaayttyggn
acncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngayaaracngtng
armgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggnccnwsngtntt
ymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtnacntgygtn
gtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayggngtngarg
tncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngtngtnwsngt
nmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtnwsnaayaar
ggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgngarccncarg
tntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnacntgymtngt
naarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccngaraayaay
tayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsnaarmtnacng
tngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcaygargcnmtnca
yaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_R-28: Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:601)

cargtncarmtngtngarwsnggnggnggngtngtncarccnggnmgnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnmtngartgggtngcngtnathtgggaygayggnwsnaaycartaytayacngaywsngtn
aarggnmgnttyacngtnwsnmgngayaaywsnaaraayacnmtnttymtncaratgaaywsnm
tnmgngcngargayacngcngtntaytaytgygcnmgnwsncaytayggnggngaytaygayta
ytayggnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacnaarggn
ccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggnt
gymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnws
nggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtn
acngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsna
ayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcncc
nccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsn
mgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttya
aytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaa
ywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargar
tayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracna
arggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraa
ycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggar
wsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnt
tyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntg
ywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggn
aar

FIGURA 14N

U_B-29: Secuencia de nucleótidos de la cadena pesada **(SEQ ID NO:602)**

cargtncarmtngtngarwsnggnggnggngtngtncarccnggnmgnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnmtngartgggtngcngtnathtggtaygayggnwsnaayaarmgntaygtngaywsngtn
aarggnmgnttyacnathwsnmgngayaaywsnaaraayacnmtntaymtncaratgaaywsnm
tnmgngcngargayacngcngtntaytaytgygcnmgngaygggntggcarcarcargcnccntt
ygaytaytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtn
ttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtna
argaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtnca
yacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccn
wsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaarg
tngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngc
nggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccn
gargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtayg
tngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacntt
ymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgy
aargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarc
cnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnws
nmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggn
carccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtnt
aywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnat
gcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_B-30: Secuencia de nucleótidos de la cadena pesada **(SEQ ID NO:603)**

cargtncarmtngtngarwsnggnggnggngtngtncarccnggnmgnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttymgnwsncayggnatgcaytgggtnmgncargcnccnggnaa
rggnmtngartgggtngcngtnathtggtaygayggnwsnaayaaraaytaygcngaywsngtn
mgnggnmgnttyacnathwsnmgngayaaywsnaaraayacnmtngaymtncaratgaaywsnm
tnmgngcngargayacngcngtntaytaytgygcnmgntggggnathwsngcnccnttygaytg
ytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccn
mtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargayt
ayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacntt
yccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsn
aayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngaya
aracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggncc
nwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtn
acntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayg
gngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngt
ngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtn
wsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgng
arccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnac
ntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccn
garaayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsna
armtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcayga
rgcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURA 14O

U_B-31: Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:604)

gargtncarmtngtngarwsnggnggnggnmtngtncarccnggnggnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsngcntaywsnatgaaytgggtnmgncargcnccnggnaa
rggnmtngartgggtnwsntayathwsnwsnwsnggnmgnacnathtaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaygcnaaraaywsnmtnttymtncaratgaaywsnm
tnmgngaygargayacngcngtntaytaytgygcnmtntgggcnccnttygaytaytggggnca
rggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccnmtngcnccn
tgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargaytayttyccng
arccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacnttyccngcngt
nmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsnaayttyggn
acncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngayaaracngtng
armgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggnccnwsngtntt
ymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtnacntgygtn
gtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayggngtngarg
tncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngtngtnwsngt
nmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtnwsnaayaar
ggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgngarccncarg
tntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnacntgymtngt
naarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccngaraayaay
tayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsnaarmtnacng
tngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcaygargcnmtnca
yaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_B-32: Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:605)

gargtncarmtngtngarwsnggnggnggnmtngtncarccnggnggnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntaywsnatgaaytgggtnmgncargcnccnggnaa
rggnmtngartgggtnwsncayathwsnwsnwsnwsnmgnacnathtaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaygcnaaraaywsngtntaymtncaratgaaywsnm
tnmgngaygargayacngcngtntaytaytgygcnmgngayggntayaaytggaayggnggngg
naaytaytayggnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacn
aarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnm
tnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmt
nacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsn
gtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarc
cnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgycc
ngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatg
athwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtnc
arttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarca
rttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggn
aargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsna
aracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgac
naaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngar
tgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayg
gnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtntt
ywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsn
ccnggnaar

FIGURA 14P

U_B-33 : Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:606)

gargtncarmtngtngarwsnggnggnggnmtngtncarccnggnggnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntaywsnatgaaytgggtnmgncargcnccnggnaa
rggnmtngartgggtnwsncayathwsnmgnwsnwsnmgnacnathtaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaygcnaaraaywsnmtntaymtncaratgaaywsnm
tnmgngaygargayacngcngtntaytaytgygcnmgngayggntayaaytggaayaayggngg
ntaytaytayggnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacn
aarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnm
tnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmt
nacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsn
gtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarc
cnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgycc
ngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatg
athwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtnc
arttyaaytggtaygtngaygggngtngargtncayaaygcnaaracnaarccnmgngargarca
rttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggn
aargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsna
aracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgac
naaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngar
tgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayg
gnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtntt
ywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsn
ccnggnaar

U_B-34 : Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:606)

gargtncarmtngtngarwsnggnggnggnmtngtncarccnggnggnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsnwsntaywsnatgaaytgggtnmgncargcnccnggnaa
rggnmtngartgggtnwsncayathwsnmgnwsnwsnmgnacnathtaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaygcnaaraaywsnmtntaymtncaratgaaywsnm
tnmgngaygargayacngcngtntaytaytgygcnmgngayggntayaaytggaayaayggngg
ntaytaytayggnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacn
aarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnm
tnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmt
nacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsn
gtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarc
cnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgycc
ngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatg
athwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtnc
arttyaaytggtaygtngaygggngtngargtncayaaygcnaaracnaarccnmgngargarca
rttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggn
aargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsna
aracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgac
naaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngar
tgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayg
gnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtntt
ywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsn
ccnggnaar

FIGURA 14Q

U_R-35 : Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:607)

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsncaracnmtnwsnmtnacnt
gyacngtnwsnggnggnwsngtnwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnmtngartggathggntayathcaywsnwsnggnwsnacntaytayaayccnwsn
mtnaarwsnmgngtnacnathwsngtngayacnwsnaaraaycarttywsnmtnaaymtnwsnw
sngtnacngcngcngayacngcngtntaytaytgygcnmgnggnccntaytayggnatggaygt
ntggggncarggnacnacngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccn
mtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargayt
aytttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacntt
yccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsn
aayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngaya
aracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggncc
nwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtn
acntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayg
gngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngt
ngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtn
wsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgng
arccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnac
ntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccn
garaayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsna
armtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcayga
rgcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_R-36 : Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:608)

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsncaracnmtnwsnmtnacnt
gyacngtnwsnggnggnwsnathwsnmgnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnmtngartggathggntayathtaycaywsnggnwsnacntaytayaayccnwsn
mtnaarwsnmgngtnaayatgwsngtngayacnwsnaaraaycarttywsnmtnaarmtnwsnw
sngtnacngcngcngayacngcngtntaytaytgygcnmgngcnmtnmgnggnathgtnmtnat
ggtntaygtnmtnggngcnmtngayathtggggncarggnacnaargtnacngtnwsnwsngcn
wsnacnaarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacng
cngcnmtnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsngg
ngcnmtnacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtn
wsnwsngtngtnacngtnccnwsnwsnaaytttyggnacncaracntayacntgyaaygtngayc
ayaarccnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccncc
ntgyccngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacn
mtnatgathwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccng
argtncarttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgnga
rgarcarttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtn
aayggnaargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracna
thwsnaaracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngarga
ratgacnaaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcn
gtngartgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngayw
sngayggnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaa
ygtnttywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsn
mtnwsnccnggnaar

FIGURA 14R

U_H-37 : Secuencia de nucleótidos de la cadena pesada **(SEQ ID NO:608)**

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsncaracnmtnwsnmtnacnt
gyacngtnwsnggnggnwsnathwsnmgnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnmtngartggathggntayathtaycaywsnggnwsnacntaytayaayccnwsn
mtnaarwsnmgngtnaayatgwsngtngayacnwsnaaraaycarttywsnmtnaarmtnwsnw
sngtnacngcngcngayacngcngtntaytaytgygcnmgngcnmtnmgnggnathgtnmtnat
ggtntaygtnmtnggngcnmtngayathtggggncarggnacnaargtnacngtnwsnwsngcn
wsnacnaarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacng
cngcnmtnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsngg
ngcnmtnacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtn
wsnwsngtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngayc
ayaarccnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccncc
ntgyccngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacn
mtnatgathwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccng
argtncarttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgnga
rgarcarttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtn
aayggnaargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracna
thwsnaaracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngarga
ratgacnaaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcn
gtngartgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngayw
sngayggnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaa
ygtnttywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsn
mtnwsnccnggnaar

U_H-38 : Secuencia de nucleótidos de la cadena pesada **(SEQ ID NO:609)**

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsncaracnmtnwsnmtnacnt
gyacngtnwsnggnggnwsnathwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnmtngartggathggntayathtaytaywsnggnwsnacntaytayaayccnwsn
mtnaarwsnmgngtnacnathwsngtngayacnwsnaaraaycarttywsnmtnaarmtnwsnw
sngtnacngcngcngayacngcngtntaytaytgygcnmgngaygaracngtngtnmgnggnmt
nathmgntaytgytayggnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcn
wsnacnaarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacng
cngcnmtnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsngg
ngcnmtnacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtn
wsnwsngtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngayc
ayaarccnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccncc
ntgyccngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacn
mtnatgathwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccng
argtncarttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgnga
rgarcarttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtn
aayggnaargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracna
thwsnaaracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngarga
ratgacnaaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcn
gtngartgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngayw
sngayggnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaa
ygtnttywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsn
mtnwsnccnggnaar

FIGURA 14S

U_H-39: Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:610)

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsncaracnmtnwsnmtnaayt
gyacngtnwsnggnggnwsnathwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnmtngartggathggntayathcaytaywsnggnwsnacntaytayaayccnwsn
mtnaarwsnmgnathacnathwsngcngayacnwsnaaraaycarttywsnmtnaarmtnaayw
sngtnacngcngcngayacngcngtntaytaytgygcnmgngaymgnggnggnggngaytaygg
nmgnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacnaarggnccn
wsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgym
tngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsngg
ngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacn
gtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaaya
cnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccncc
ngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgn
acnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaayt
ggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaayws
nacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartay
aartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarg
gncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraayca
rgtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsn
aayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyt
tymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgyws
ngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_H-40 : Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:611)

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsncaracnmtnwsnmtnaayt
gyacngtnwsnggnggnwsnathwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnmtngartggathggntayathcaytaywsnggnwsnacntaytayaayccnwsn
mtnaarwsnmgnathacnathwsngcngayacnwsnaaraaycarttywsnmtnaarmtnaayw
sngtnacngcngcngayacngcngtntaytaytgygcnmgngaymgnggnggnggngaytaygg
nmgnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacnaarggnccn
wsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgym
tngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsngg
ngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacn
gtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaaya
cnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccncc
ngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgn
acnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaayt
ggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaayws
nacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartay
aartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarg
gncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraayca
rgtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsn
aayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyt
tymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgyws
ngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURA 14T

U_H-41 : Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:612)

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsncaracnmtnwsnmtnacnt
gyacngtnwsnggnggnwsnathwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnmtngartggathggntayathcaywsnwsnggnwsnacntaytayaayccnwsn
mtnaarwsnmgnathacnaarwsngtngayacnwsnaaraaycarttywsnmtnaarmtnwsnw
sngtnacngcngcngayacngcngtntaytaytgygcnmgnwsnaayaaytayggntgyttygc
nmtntggggnmgnggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtntty
ccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaarg
aytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayac
nttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsn
wsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtng
ayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcngg
nccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngar
gtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtng
ayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymg
ngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaar
gtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnm
gngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmt
nacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncar
ccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntayw
snaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgca
ygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_H-42 : Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:613)

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsncaracnmtnwsnmtnacnt
gyacngtnwsnggnggnwsnathwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnmtngartggathggntayathcaywsnwsnggnwsnacntaytayaayccnwsn
mtnaarwsnmgnathacnaarwsngtngayacnwsnaaraaycarttywsnmtnaarmtnwsnw
sngtnacngcngcngayacngcngtntaytaytgygcnmgnwsnaayaaytayggntgyttygc
nmtntggggnmgnggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtntty
ccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaarg
aytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayac
nttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsn
wsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtng
ayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcngg
nccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngar
gtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtng
ayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymg
ngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaar
gtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnm
gngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmt
nacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggncar
ccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntayw
snaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgca
ygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURA 14U

U_B-43 : Secuencia de nucleótidos de la cadena pesada **(SEQ ID NO:614)**

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsncaracnmtnwsnmtnacnt
gyacngtnwsnggnggnwsnathwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnmtngartggathggntayathcaytaywsnggnwsnacntaytayaayccnwsn
mtnaarwsnmgngtnacnathwsngtngayacnwsnaaraaycarttywsnmtnaarmtnwsnw
sngtnacngcngcngayacngcngtntaytaytgygcnwsnggntayaaytayggnmtntayta
ytaygaywsnwsnggntayccnwsntaytaytayggnatggaygtntggggncarggnacnacn
gtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccnmtngcnccntgywsnmgnw
snacnwsngarwsnacngcngcnmtnggntgymtngtnaargaytayttyccngarccngtnac
ngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacnttyccngcngtnmtncarwsn
wsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsnaayttyggnacncaracnt
ayacntgyaaygtngaycayaarccnwsnaayacnaargtngayaaracngtngarmgnaartg
ytgygtngartgyccnccntgyccngcnccnccngtngcnggnccnwsngtnttymtnttyccn
ccnaarccnaargayacnmtnatgathwsnmgnacnccngargtnacntgygtngtngtngayg
tnwsncaygargayccngargtncarttyaaytggtaygtngayggngtngargtncayaaygc
naaracnaarccnmgngargarcarttyaaywsnacnttymgngtngtnwsngtnmtnacngtn
gtncaycargaytggmtnaayggnaargartayaartgyaargtnwsnaayaarggnmtnccng
cnccnathgaraaracnathwsnaaracnaarggncarccnmgngarccncargtntayacnmt
nccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnacntgymtngtnaarggntty
tayccnwsngayathgcngtngartgggarwsnaayggncarccngaraayaaytayaaracna
cnccnccnatgmtngaywsngayggnwsnttyttymtntaywsnaarmtnacngtngayaarws
nmgntggcarcarggnaaygtnttywsntgywsngtnatgcaygargcnmtncayaaycaytay
acncaraarwsnmtnwsnmtnwsnccnggnaar

U_B-44 : Secuencia de nucleótidos de la cadena pesada **(SEQ ID NO:615)**

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsncaracnmtnwsnmtnacnt
gyacngtnwsnggnggnwsnathwsnwsnggngaytaytaytggaaytgggtnmgncarcaycc
nggnaarggnmtngartggathggntayathtaytaywsnggnggnacntaytayaayccnwsn
mtnaarwsnmgngtnacnathwsngtngayacnwsnaaraaycarttywsnmtnaarmtnttyw
sngtnacngcngcngayacngcngtntayttytgygcnmgnacntaytaygayathmtnacngg
ntayccnttytayttygaytaytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacn
aarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnm
tnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmt
nacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsn
gtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarc
cnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgycc
ngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatg
athwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtnc
arttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarca
rttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggn
aargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsna
aracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgac
naaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngar
tgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayg
gnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtntt
ywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsn
ccnggnaar

FIGURA 14V

U_H-45 : Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:616)

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsncaracnmtnwsnmtnacnt
gyacngtnwsnggnggnwsnathwsnwsnggngaytaytaytggaaytgggtnmgncarcaycc
nggnaarggnmtngartggathggntayathtaytaywsnggnggnacntaytayaayccnwsn
mtnaarwsnmgngtnacnathwsngtngayacnwsnaaraaycarttywsnmtnaarmtnttyw
sngtnacngcngcngayacngcngtntayttytgygcnmgnacntaytaygayathmtnacngg
ntayccnttytayttygaytaytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacn
aarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnm
tnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmt
nacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsn
gtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarc
cnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgycc
ngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatg
athwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtnc
arttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarca
rttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggn
aargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsna
aracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgac
naaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngar
tgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayg
gnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtntt
ywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsn
ccnggnaar

U_H-46 : Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:617)

cargtncarmtncarcartggggngcnggnmtnmtnaarccnwsngaracnmtnwsnmtnacnt
gygcngtntayggnggnwsnttywsnggntaytaytggwsntggathmgncarccnccnggnaa
rggnmtngartggathggngarathaaycaywsnggnwsnacnaaytayaayccnwsnmtnaar
wsnmgngtnacnathwsngtngayacnwsnaaraaycarttywsnmtnaarmtnwsnwsngtna
cngcngcngayacngcngtntaytaytgygcnmgnggnggntaywsnwsnwsntggtaytggtt
ygayccntggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtn
ttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtna
argaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtnca
yacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccn
wsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaarg
tngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngc
nggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccn
gargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtayg
tngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacntt
ymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgy
aargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarc
cnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnws
nmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggn
carccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtnt
aywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnat
gcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURA 14W

U_B-47: Secuencia de nucleótidos de la cadena pesada **(SEQ ID NO:618)**

cargtncarmtncarcartggggngcnggnmtnmtnaarccnwsngaracnmtnwsnmtnacnt
gygcngtntayggnggnwsnttywsnggntaytaytggwsntggathmgncarccnccnggnaa
rggnmtngartggathggngarathaaycaywsnggnwsnacnaaytayaayccnwsnmtnaar
wsnmgngtnacnathwsngtngayacnwsnaaraaycarttywsnmtnaarmtnwsnwsngtna
cngcngcngayacngcngtntaytaytgygcnmgnggnggntaywsnwsnwsntggttytggtt
ygayccntggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtn
ttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtna
argaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtnca
yacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccn
wsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaarg
tngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngc
nggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccn
gargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtayg
tngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacntt
ymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgy
aargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarc
cnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnws
nmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggn
carccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtnt
aywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnat
gcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_B-48: Secuencia de nucleótidos de la cadena pesada **(SEQ ID NO:618)**

cargtncarmtncarcartggggngcnggnmtnmtnaarccnwsngaracnmtnwsnmtnacnt
gygcngtntayggnggnwsnttywsnggntaytaytggwsntggathmgncarccnccnggnaa
rggnmtngartggathggngarathaaycaywsnggnwsnacnaaytayaayccnwsnmtnaar
wsnmgngtnacnathwsngtngayacnwsnaaraaycarttywsnmtnaarmtnwsnwsngtna
cngcngcngayacngcngtntaytaytgygcnmgnggnggntaywsnwsnwsntggttytggtt
ygayccntggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtn
ttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtna
argaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtnca
yacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccn
wsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaarg
tngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngc
nggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccn
gargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtayg
tngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacntt
ymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgy
aargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarc
cnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnws
nmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggn
carccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtnt
aywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnat
gcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURA 14X

U_H-49 : Secuencia de nucleótidos de la cadena pesada **(SEQ ID NO:618)**

cargtncarmtncarcartggggngcnggnmtnmtnaarccnwsngaracnmtnwsnmtnacnt
gygcngtntayggnggnwsnttywsnggntaytaytggwsntggathmgncarccnccnggnaa
rggnmtngartggathggngarathaaycaywsnggnwsnacnaaytayaayccnwsnmtnaar
wsnmgngtnacnathwsngtngayacnwsnaaraaycarttywsnmtnaarmtnwsnwsngtna
cngcngcngayacngcngtntaytaytgygcnmgnggnggntaywsnwsnwsntggttytggtt
ygayccntggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtn
ttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtna
argaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtnca
yacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccn
wsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaarg
tngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngc
nggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccn
gargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtayg
tngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacntt
ymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgy
aargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarc
cnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnws
nmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggn
carccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtnt
aywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnat
gcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_H-50 : Secuencia de nucleótidos de la cadena pesada **(SEQ ID NO:618)**

cargtncarmtncarcartggggngcnggnmtnmtnaarccnwsngaracnmtnwsnmtnacnt
gygcngtntayggnggnwsnttywsnggntaytaytggwsntggathmgncarccnccnggnaa
rggnmtngartggathggngarathaaycaywsnggnwsnacnaaytayaayccnwsnmtnaar
wsnmgngtnacnathwsngtngayacnwsnaaraaycarttywsnmtnaarmtnwsnwsngtna
cngcngcngayacngcngtntaytaytgygcnmgnggnggntaywsnwsnwsntggttytggtt
ygayccntggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtn
ttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtna
argaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtnca
yacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccn
wsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaarg
tngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngc
nggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccn
gargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtayg
tngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacntt
ymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgy
aargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarc
cnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnws
nmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggn
carccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtnt
aywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnat
gcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURA 14Y

U_B-51 : Secuencia de nucleótidos de la cadena pesada **(SEQ ID NO:619)**

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsngaracnmtnwsnmtnacnt
gyacngtnwsnggnggnwsnathwsnwsntaytaytggwsntggathmgncarccngcnggnaa
rggnmtngartggathggnmgnathtayacnwsnggnacnacnaaytayaayccnwsnmtnaar
wsnmgngtnacnatgwsngtngayacnwsnaaraaycarttywsnmtnaarmtnwsnwsngtna
cngcngcngayacngcngtntaytaytgygcnmgngayggntaywsntayggncaytaytayta
ytayggnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacnaarggn
ccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggnt
gymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnws
nggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtn
acngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsna
ayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcncc
nccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsn
mgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttya
aytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaa
ywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargar
tayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracna
arggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraa
ycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggar
wsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnt
tyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntg
ywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggn
aar

U_B-52 : Secuencia de nucleótidos de la cadena pesada **(SEQ ID NO:620)**

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsngaracnmtnwsnmtnacnt
gyacngtnwsnggnggnwsngtnwsnwsnggnggnwsntaytggwsntggathmgncarccncc
nggnaarggnmtngartggathggntayathtaytaywsnggnwsnacnaaytayaayccnwsn
mtnaarwsnmgngtnacnathwsnathgtnacnwsnmgnaaycarttywsnmtnaarmtnwsnw
sngtnacngcngcngayacngcngtntaytaytgygcnmgnwsngcnmtnmgntayttygaytg
gmtnttywsngaygtnwsngayathtggggncarggnacnatggtnacngtnwsnwsngcnwsn
acnaarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcng
cnmtnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngc
nmtnacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsn
wsngtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycaya
arccnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntg
yccngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtn
atgathwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngarg
tncarttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngarga
rcarttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaay
ggnaargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathw
snaaracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargarat
gacnaaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtn
gartgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsng
ayggnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygt
nttywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtn
wsnccnggnaar

FIGURA 14Z

U_H-53: Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:620)

cargtncarmtncargarwsnggnccnggnmtngtnaarccnwsngaracnmtnwsnmtnacnt
gyacngtnwsnggnggnwsngtnwsnwsnggnggnwsntaytggwsntggathmgncarccncc
nggnaarggnmtngartggathggntayathtaytaywsnggnwsnacnaaytayaayccnwsn
mtnaarwsnmgngtnacnathwsnathgtnacnwsnmgnaaycarttywsnmtnaarmtnwsnw
sngtnacngcngcngayacngcngtntaytaytgygcnmgnwsngcnmtnmgntayttygaytg
gmtnttywsngaygtnwsngayathtggggncarggnacnatggtnacngtnwsnwsngcnwsn
acnaarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcng
cnmtnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngc
nmtnacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsn
wsngtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycaya
arccnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntg
yccngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtn
atgathwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngarg
tncarttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngarga
rcarttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaay
ggnaargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathw
snaaracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargarat
gacnaaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtn
gartgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsng
ayggnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygt
nttywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtn
wsnccnggnaar

U_H-54: Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:621)

gargtncarmtngtncarwsnggngcngarmtnaaraarccnggngarwsnmtnaarathwsnt
gyaarggnwsnggntaymgnttyacnwsntaytggathggntgggtnmgncaratgccnggnaa
rggnmtngartggatgggnathathtayccngaygaywsngayacnmgntaywsnccnwsntty
carggncargtnacnathwsngcngayaarwsnathwsnacngcntaymtncartggwsnwsnm
tnaargcnwsngayacngcnatgtaytaytgygcnmgncaraarwsntayggntaywsntaytt
ygaytaytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtn
ttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtna
argaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtnca
yacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccn
wsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacnaarg
tngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngtngc
nggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccn
gargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggtayg
tngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacntt
ymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaartgy
aargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarc
cnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnws
nmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaayggn
carccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtnt
aywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnat
gcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURA 14AA

U_B-55: Secuencia de nucleótidos de la cadena pesada **(SEQ ID NO:622)**

gargtncarmtngtncarwsnggngcngargtnaaraarccnggngarwsnmtnaarathwsnt
gyaarggnwsnggntaywsnttyacnwsntaytggathggntgggtnmgncaratgccnggnaa
rggnmtngartggatgggnathathtayccngaygaywsngaygcnmgntaywsnccnwsntty
carggncargtnacnathwsngcngayaarwsnathaayacngcntaymtncartggwsnwsnm
tnaargcnwsngayacngcnatgtaytaytgygcnmgncarggntayggnwsnggntggggnta
yttygaytaytggggncarggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsn
gtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtng
tnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngt
ncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtn
ccnwsnwsnaayttyggnacncaracntayacntgyaaygtngaycayaarccnwsnaayacna
argtngayaaracngtngarmgnaartgytgygtngartgyccnccntgyccngcnccnccngt
ngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacn
ccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtncarttyaaytggt
aygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarcarttyaaywsnac
nttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggnaargartayaar
tgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsnaaracnaarggnc
arccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgacnaaraaycargt
nwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngartgggarwsnaay
ggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayggnwsnttyttym
tntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngt
natgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

U_B-56 : Secuencia de nucleótidos de la cadena pesada **(SEQ ID NO:623)**

gargtncarmtngtncarwsnggngcngargtnaaraarccnggngarwsnmtnaarathwsnt
gyaarggnwsnggntaywsnttyacnwsntaytggathggntgggtnmgncaratgccnggnaa
rggnmtngartggatgggnathathtayccnggngaywsngayathmgntaywsnccnwsntty
carggncargtnacnathwsngcngayaarwsnathwsnacngcntaymtncartggwsnwsnm
tnaargcnwsngayacngcnatgtaytaytgygcnmgncarggnmtngcngtngcnggnacnws
ntaytaytaytaytayggnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcn
wsnacnaarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacng
cngcnmtnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsngg
ngcnmtnacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtn
wsnwsngtngtnacngtnccnwsnwsnaayttyggnacncaracntayacntgyaaygtngayc
ayaarccnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccncc
ntgyccngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacn
mtnatgathwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccng
argtncarttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgnga
rgarcarttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtn
aayggnaargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracna
thwsnaaracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngarga
ratgacnaaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcn
gtngartgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngayw
sngayggnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaa
ygtnttywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsn
mtnwsnccnggnaar

FIGURA **14AB**

U_H-57 : Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:624)

cargtncarmtncarcarwsnggnccnggnmtngtnaarccnwsncaracnmtnwsnmtnacnt
gygcnathwsnggngaywsngtnwsnwsntaywsngcngcntggaaytggathmgncarwsncc
nwsnmgnggnmtngartggmtnggnmgnacntaytgymgnwsnaartggtayaaygaytaygcn
gtnwsngtnaarwsnmgnathacnathaayccngayacnwsnaaraaycarttywsnmtncarm
tnaaywsngtnacnccngargayacngcngtntaytaytgygcnmgngaymgngcngtngcngg
ntaytaytayggnatggaygtntggggncarggnacnacngtnacngtnwsnwsngcnwsnacn
aarggnccnwsngtnttyccnmtngcnccntgywsnmgnwsnacnwsngarwsnacngcngcnm
tnggntgymtngtnaargaytayttyccngarccngtnacngtnwsntggaaywsnggngcnmt
nacnwsnggngtncayacnttyccngcngtnmtncarwsnwsnggnmtntaywsnmtnwsnwsn
gtngtnacngtnccnwsnwsnaaytttyggnacncaracntayacntgyaaygtngaycayaarc
cnwsnaayacnaargtngayaaracngtngarmgnaartgytgygtngartgyccnccntgycc
ngcnccnccngtngcnggnccnwsngtnttymtnttyccnccnaarccnaargayacnmtnatg
athwsnmgnacnccngargtnacntgygtngtngtngaygtnwsncaygargayccngargtnc
arttyaaytggtaygtngayggngtngargtncayaaygcnaaracnaarccnmgngargarca
rttyaaywsnacnttymgngtngtnwsngtnmtnacngtngtncaycargaytggmtnaayggn
aargartayaartgyaargtnwsnaayaarggnmtnccngcnccnathgaraaracnathwsna
aracnaarggncarccnmgngarccncargtntayacnmtnccnccnwsnmgngargaratgac
naaraaycargtnwsnmtnacntgymtngtnaarggnttytayccnwsngayathgcngtngar
tgggarwsnaayggncarccngaraayaaytayaaracnacnccnccnatgmtngaywsngayg
gnwsnttyttymtntaywsnaarmtnacngtngayaarwsnmgntggcarcarggnaaygtntt
ywsntgywsngtnatgcaygargcnmtncayaaycaytayacncaraarwsnmtnwsnmtnwsn
ccnggnaar

U_H-58 : Secuencia de nucleótidos de la cadena pesada (SEQ ID NO:604)

gargtncarmtngtngarwsnggnggnggnmtngtncarccnggnggnwsnmtnmgnmtnwsnt
gygcngcnwsnggnttyacnttywsngcntaywsnatgaaytgggtnmgncargcnccnggnaa
rggnmtngartgggtnwsntayathwsnwsnwsnggnmgnacnathtaytaygcngaywsngtn
aarggnmgnttyacnathwsnmgngayaaygcnaaraaywsnmtnttymtncaratgaaywsnm
tnmgngaygargayacngcngtntaytaytgygcnmtntgggcnccnttygaytaytggggnca
rggnacnmtngtnacngtnwsnwsngcnwsnacnaarggnccnwsngtnttyccnmtngcnccn
tgywsnmgnwsnacnwsngarwsnacngcngcnmtnggntgymtngtnaargaytayttyccng
arccngtnacngtnwsntggaaywsnggngcnmtnacnwsnggngtncayacnttyccngcngt
nmtncarwsnwsnggnmtntaywsnmtnwsnwsngtngtnacngtnccnwsnwsnaayttyggn
acncaracntayacntgyaaygtngaycayaarccnwsnaayacnaargtngayaaracngtng
armgnaartgytgygtngartgyccnccntgyccngcnccnccngtngcnggnccnwsngtntt
ymtnttyccnccnaarccnaargayacnmtnatgathwsnmgnacnccngargtnacntgygtn
gtngtngaygtnwsncaygargayccngargtncarttyaaytggtaygtngayggngtngarg
tncayaaygcnaaracnaarccnmgngargarcarttyaaywsnacnttymgngtngtnwsngt
nmtnacngtngtncaycargaytggmtnaayggnaargartayaartgyaargtnwsnaayaar
ggnmtnccngcnccnathgaraaracnathwsnaaracnaarggncarccnmgngarccncarg
tntayacnmtnccnccnwsnmgngargaratgacnaaraaycargtnwsnmtnacntgymtngt
naarggnttytayccnwsngayathgcngtngartgggarwsnaayggncarccngaraayaay
tayaaracnacnccnccnatgmtngaywsngayggnwsnttyttymtntaywsnaarmtnacng
tngayaarwsnmgntggcarcarggnaaygtnttywsntgywsngtnatgcaygargcnmtnca
yaaycaytayacncaraarwsnmtnwsnmtnwsnccnggnaar

FIGURA 14AC

U-V_L-1 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:625)

gaygtngtnatgcancarwsnccnytnwsnytnccngtncanytnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnytngtntaywsngayggnaaycantayytnaaytggttycarca
rmgnccnggncarwsnccnmgnmgnytnathtayaargtnwsnaaytgggaywsnggngtnccn
gaymgnttyaayggnwsnggnwsnggncangayttycanytnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarwsncancaytggccnathcanttyggncarggnca
nmgnytngarathaar

U-V_L-2 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:626)

gaygtngtnatgcancarwsnccnytnwsnytnccngtncanytnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnytngtntaywsngayggnaaycantayytnaaytggttycarca
rmgnccnggncarwsnccnmgnmgnytnathtayaargtnwsnaaytgggaywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggncangayttycanytnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyathcarggncancaytggccncancanttyggncarggnca
nmgnytngarathaar

U-V_L-3 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:627)

gaygtngtnatgcancarwsnccnytnwsnytnccngtncanytnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnytngtntaywsngayggnaaycantayytnaaytggytncarca
rmgnccnggncarwsnccnmgnmgnytnathtayaargtnwsnaaytgggaywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggncangayttycanytnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarggncancaytggccnathcanttyggncarggnca
nmgnytngarathaar

U-V_L-4 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:627)

gaygtngtnatgcancarwsnccnytnwsnytnccngtncanytnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnytngtntaywsngayggnaaycantayytnaaytggytncarca
rmgnccnggncarwsnccnmgnmgnytnathtayaargtnwsnaaytgggaywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggncangayttycanytnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarggncancaytggccnathcanttyggncarggnca
nmgnytngarathaar

U-V_L-5 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:628)

Gayathgtnatgcancarcanccnytnwsnytnwsngtncanccnggncarccngcnwsnathw
sntgyaarwsnwsncarwsnytnytncaywsngayggnaarcantayytntaytggtayytnca
raarccnggncarccncncncarytnytnathtaygargtnwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggncangayttycanytnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarggnathcarytnccntgywsnttyggncarggnca
naarytngarathaar

FIGURA 15A

U-V_L-6 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:629)

gayathgtnatgcancarcanccnytnwsnytnwsngtncanccnggncarccngcnwsnathw
sntgyaarwsnwsncarwsnytnytncaywsngayggnaarcantayytntaytggtayytnca
raarccnggncarccnccncarytnytnathtaygargtnwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggncangayttycanytnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarwsnathcarytnccnytncanttyggnggnggnca
naargtngarathaar

U-V_L-7 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:629)

gayathgtnatgcancarcanccnytnwsnytnwsngtncanccnggncarccngcnwsnathw
sntgyaarwsnwsncarwsnytnytncaywsngayggnaarcantayytntaytggtayytnca
raarccnggncarccnccncarytnytnathtaygargtnwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggncangayttycanytnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarwsnathcarytnccnytncanttyggnggnggnca
naargtngarathaar

U-V_L-8 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:630)

gayathgtnatgcancarcanccnytnwsnytnwsngtncanccnggncarccngcnwsnathw
sntgyaarwsnwsncarwsnytnytncaywsngayggnaarcantayytntaytggttyytnca
raarccnggncarccnccncarccnytnathtaygargtnwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggncangayttycanytnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarwsnathcarytnccnathcanttyggncayggnca
nmgnytngarathaar

U-V_L-9 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:630)

gayathgtnatgcancarcanccnytnwsnytnwsngtncanccnggncarccngcnwsnathw
sntgyaarwsnwsncarwsnytnytncaywsngayggnaarcantayytntaytggttyytnca
raarccnggncarccnccncarccnytnathtaygargtnwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggnwsnggncangayttycanytnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcarwsnathcarytnccnathcanttyggncayggnca
nmgnytngarathaar

U-V_L-11 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:631)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarggnathgcnaaytayytngcntggtaycarcaraarccnggnaargt
nccnaarytnytnathtaygtngcnwsncanytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargaygtngcncant
aytaytgycaraaytayaaywsngcnccnttycanttyggnccnggncanaargtngayathaar

FIGURA 15B

U-V_L-12 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:632)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanatha
thtgymgngcnwsncarggnathwsnaaygayytngcntggtaycarcaraarccnggnaargt
nccnaarytnytnathtaygcngcnwsncanytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargaygtngcncant
aytaytgycaraartayaaywsngtnccnytncanttyggnggnggncanaargtngarathaar

U-V_L-13 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:633)

aayathgtnatgcancarcanccnytnwsnwsnccngtncanytnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnytngtncaywsngayggnaaycantayytnwsntggytncarca
rmgnccnggncarccnccnmgnytnytnathtayaarathwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggngcnggncangayttycanytnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcargcncancarttyccncaycanttyggnccnggnca
naargtngayathaar

U-V_L-14 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:633)

aayathgtnatgcancarcanccnytnwsnwsnccngtncanytnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnytngtncaywsngayggnaaycantayytnwsntggytncarca
rmgnccnggncarccnccnmgnytnytnathtayaarathwsnaaymgnttywsnggngtnccn
gaymgnttywsnggnwsnggngcnggncangayttycanytnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcargcncancarttyccncaycanttyggnccnggnca
naargtngayathaar

U-V_L-15 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:634)

garathgtnatgcancarcanccnytnwsnwsnccngtncanytnggncarccngcnwsnathw
sntgymgnwsnwsncarwsnytngtncaywsngayggnaaycantayytnwsntggytncarca
rmgnccnggncarccnccnmgnytnytnathtayaarathwsnaaymgnttywsnggngtnccn
gaymgnttywsnggncanggngcnggncangayttycanytnaarathwsnmgngtngargcng
argaygtnggngtntaytaytgyatgcargcncancarttyccncaycanttyggnggnggnca
naargtngarathaar

U-V_L-16 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:635)

garathgtnytncancarwsnccnggncanytnwsnytnwsnccnggngarmgngcncanytnw
sntgymgngcnwsncarcangtnathwsnwsntayytngcntggtaycarcaraarccnggnca
rgcnccnmgnytnytnathwsnggngcnwsnwsnmgngcncanggnathccngaymgnttywsn
ggnwsnggnwsnggncangayttycanytncanathwsnmgnytngarccngargayttygcng
tntaytaytgycarcartayggnwsnwsnccnmgncanttyggncarggncanaargtngarat
haar

FIGURA 15C

U-V_L-17 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:636)

garathgtnytncancarwsnccnggncanytnwsnytnwsnccnggngarmgngcncanytnw
sntgymgngcnwsncarwsngtnwsnmgnytngcntggtaycarcaraarccnggncargcncc
nmgnytnytnathtayggngcnwsnmgnmgngcncanggnathccngaymgnttywsnggnwsn
ggnwsnggncangayttycanytncanathwsnmgnytngarccngargayttygcngtntayt
aytgycarcartayggnwsnwsnccnmgnwsnttyggncarggncanaarytngarathaar

U-V_L-18 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:637)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarggnathmgnaaygayytnggntggtaycarcaraarccnggnaargc
nccnaarmgnytnathtaygcngcnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangarttycanytncanathwsnwsnytncarccngargayttygcncant
aytaytgyytncarcayaaywsntayccnccncanttyggncarggncanaargtngarathaar

U-V_L-19 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:638)

gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngtntggtayca
rcaraarccnggncarccnccnaarytnttyathtaytgggcnwsncanmgngarwsnggngtn
ccngaymgnttycanggnwsnggnwsnggncangayttycanytncanathwsnwsnytncarg
cngargaygtngcngtntaytaytgycarcartaytaywsnttyccntggcanttyggncargg
ncanaargtngarathaar

U-V_L-20 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:638)

gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngtntggtayca
rcaraarccnggncarccnccnaarytnttyathtaytgggcnwsncanmgngarwsnggngtn
ccngaymgnttycanggnwsnggnwsnggncangayttycanytncanathwsnwsnytncarg
cngargaygtngcngtntaytaytgycarcartaytaywsnttyccntggcanttyggncargg
ncanaargtngarathaar

U-V_L-21 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:639)

gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngcntggtayca
rcaraarccnggncarccnccnaarytnytnathtaytgggcnwsncanmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggncangayttycanytncanathwsnwsnytncarg
cngargaygtngcngtntaytaytgycarcartaytaywsncancantggcanttyggncargg
ncanaargtngarathaar

FIGURA 15D

U-V_L-22 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:640)

gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncaraaygtnytntaywsnwsnaayaayaaraaytayytngcntggtayca
rcaraarccnggncarccnccnaarytnytnathtaytgggcnwsncanmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggncangayttycanytncanathwsnwsnytncarg
cngargaygtngcngtntayttytgycarcartaytayggncanccnmgncanttyggncargg
ncanaargtngarathaar

U-V_L-23 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:641)

gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncaraaygtnytntaywsnwsnaayaayaaraaytayytngcntggtayca
rcaraarccnggncarccnccnaarytnytnathtaytgggcnwsncanmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggncangayttycanytncanathwsnwsnytncarg
cngargaygtngcngtntayttytgycarcartaytayggncanccnmgncanttyggncargg
ncanaargtngarathaar

U-V_L-24 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:642)

gayathgtnatgcancarwsnccngaywsnytncangtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngcntggtayca
rcaraarccnggncarccnccnaarytnytnathtaytgggcnwsncanmgngarwsnggngtn
ccngaymgnttyggnggnwsnggnwsnggncangayttycanytncanathwsnwsnytncarg
cngargaygtngcngtntaytaytgycarcartaytaywsnathwsnmgncanttyggncargg
ncanaargtngarathaar

U-V_L-25 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:642)

gayathgtnatgcancarwsnccngaywsnytncangtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngcntggtayca
rcaraarccnggncarccnccnaarytnytnathtaytgggcnwsncanmgngarwsnggngtn
ccngaymgnttyggnggnwsnggnwsnggncangayttycanytncanathwsnwsnytncarg
cngargaygtngcngtntaytaytgycarcartaytaywsnathwsnmgncanttyggncargg
ncanaargtngarathaar

U-V_L-26 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:643)

gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncarwsngtnytntayaaywsnaayaayaaraaytayytngcntggtayca
rcaraarccnggncarccnccnaarytnytnathtaytgggcnwsncanmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggncangayttycanytncanathwsnwsnytncarg
cngaygaygtngcngtntaytaytgycarcartaytaywsncancantggcanttyggnccngg
ncanaargtngarathaar

FIGURA 15E

U-V_L-27: Secuencia de nucleótidos de la región variable de la cadena ligera **(SEQ ID NO:644)**

gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncarwsngtnytntayaaywsnaayaayaaraaytayytngcntggtayca
rcaraarccnggncarccnccnaarytnytnathtaytgggcnwsncanmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggncangayttycanytncanathwsnwsnytncarg
cngaygaygtngcngtntaytaytgycarcartaytaywsncancantggcanttyggnccngg
ncanaargtngarathaar

U-V_L-28: Secuencia de nucleótidos de la región variable de la cadena ligera **(SEQ ID NO:645)**

gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngcntggtayca
rcaraarccnggncarccnccnaargtnytnathtaytgggcnwsncanmgnaarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggncangayttycanytncanathwsnggnytncarg
cngargaygtngcnytntaytaytgycarcartaytaywsncanatgttywsnttyggncargg
ncanaarytngarathaar

U-V_L-29: Secuencia de nucleótidos de la región variable de la cadena ligera **(SEQ ID NO:645)**

gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngcntggtayca
rcaraarccnggncarccnccnaargtnytnathtaytgggcnwsncanmgnaarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggncangayttycanytncanathwsnggnytncarg
cngargaygtngcnytntaytaytgycarcartaytaywsncanatgttywsnttyggncargg
ncanaarytngarathaar

U-V_L-30: Secuencia de nucleótidos de la región variable de la cadena ligera **(SEQ ID NO:646)**

gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncarwsngtnytngaywsnwsnaayaayaaraaytayytngcntggtayca
rcaraarccnggncarccnccnaarytnytnathtaytgggcnwsncanmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggncangayttycanytncanathwsnwsnytncarg
cngargaygtngcngtnttytaytgycaycartaytaywsncanccnytncanttyggnggngg
ncanaargtngcnathaar

U-V_L-31: Secuencia de nucleótidos de la región variable de la cadena ligera **(SEQ ID NO:646)**

gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncarwsngtnytngaywsnwsnaayaayaaraaytayytngcntggtayca
rcaraarccnggncarccnccnaarytnytnathtaytgggcnwsncanmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggncangayttycanytncanathwsnwsnytncarg
cngargaygtngcngtnttytaytgycaycartaytaywsncanccnytncanttyggnggngg
ncanaargtngcnathaar

FIGURA 15F

U-V_L-32 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:647)

gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncarwsnathytntaymgnwsnaayaayaaraaytayytngcntggtayca
rcaraarccnggncarccnccnaarytnytnathtaytgggcnwsngcnmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggncangayttycanytncanathwsnwsnytncarg
cngargaygtngcngtntayttytgycarcartayttyathcanccnytncanttyggnggngg
ncanaargtngarathaar

U-V_L-33 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:647)

gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggngarmgngcncanatha
aytgyaarwsnwsncarwsnathytntaymgnwsnaayaayaaraaytayytngcntggtayca
rcaraarccnggncarccnccnaarytnytnathtaytgggcnwsngcnmgngarwsnggngtn
ccngaymgnttywsnggnwsnggnwsnggncangayttycanytncanathwsnwsnytncarg
cngargaygtngcngtntayttytgycarcartayttyathcanccnytncanttyggnggngg
ncanaargtngarathaar

U-V_L-34 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:648)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncargayathwsncaytayytngcntggttycarcaraarccnggnaargc
nccnaarwsnytnathtaygcngcnwsnwsnytncarwsnggngtnccnwsnaarttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargayttygcncant
aytaytgycarcartayaayaaytayccnttycanttyggnccnggncanaargtngayathaar

U-V_L-35 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:649)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtngcnathc
antgymgngcnwsncargayathwsnaaytayytngcntggytncarcaraarccnggnaargc
nccnaarwsnytnathtaygcngcnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargayttygcncant
aytaytgycarcartayaaycantayccnttycanttyggnccnggncanaaratggayathaar

U-V_L-36 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:650)

garathgtnatgcancarwsnccngcncanytnwsngtnwsnccnggngarmgngcncanytnw
sntgymgngcnwsncarwsngtnwsnwsnaayytngcntggtaycarcargayccnggncargc
nccnmgnytnytnathtayggngcnwsnmgnmgngcncanggnathccngcnmgnttywsnggn
wsnggnwsnggncangarttycanytncanathwsnwsnytncarwsngargayttygcngtnt
aytaytgycarcarcayaayaaytggccnccntggcanttyggncarggncanaargtngarat
haar

FIGURA 15G

U-V_L-37 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:650)

garathgtnatgcancarwsnccngcncanytnwsngtnwsnccnggngarmgngcncanytnw
sntgymgngcnwsncarwsngtnwsnwsnaayytngcntggtaycarcargayccnggncargc
nccnmgnytnytnathtayggngcnwsnmgnmgngcncanggnathccngcnmgnttywsnggn
wsnggnwsnggncangarttycanytncanathwsnwsnytncarwsngargayttygcngtnt
aytaytgycarcarcayaayaaytggccnccntggcanttyggncarggncanaargtngarat
haar

U-V_L-38 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:651)

Gayathcaratgcancarwsnccnwsnwsngtnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncargayathwsnmgntggytngcntggtaycarcaraarccnggnaargc
nccnaarytnytnathtaygcngcnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargayttygcncant
aytaytgycarcargcnaaywsnttyccnccncanttyggncarggncanaargtngarttyaar

U-V_L-39 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:652)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarwsnathwsncantayytnaaytggtaycarcaraarccnggnaargc
nccnaarttyytnathtaygcngcnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargayttygcngcnt
aytaytgycarcarwsncaywsngcnccnttycanttyggnccnggncanaargtngayathaar

U-V_L-40 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:653)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsnytnggngaymgngtncanathc
antgymgngcnwsncarcanathwsnathtayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaygcngcnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargayttygcncant
aytaytgycarcarwsntaywsncanytncanttyggnggnggncanaargtngarathaar

U-V_L-41 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:654)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarwsnathmgnwsntayytnaaytggtaycarcarmgnccnggnaaygc
nccnaarytnytnathtaygcngcnwsnwsnytncarwsnggngtnccnwsnmgngtnwsnggn
wsnggnwsnggncangayttycanytncanathmgnwsnytncarccngargayttygcncant
aytaytgycarcarwsntaywsnathccnytncanttyggnggnggncanaargtngarathaar

FIGURA 15H

U-V_L-42 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:655)

gayathcaratgcancarwsnccnwsnwsnmgnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarcanathwsnmgntayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaygcngcnwsncanytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanytnwsnwsnytncarccngargayttygcncant
aytaytgycarcarathtaywsncanwsnathcanttyggncarggncanmgnytngarathaar

U-V_L-43 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:656)

Gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarmgnathwsnwsntayytnaaytggtaycarcaraarccnggnaargc
nccnaargtnytnathtaygcngarwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargayttygcncant
aytaytgycarcarwsntayathcanccnathcanttyggncarggncanmgnytngarathath

U-V_L-44 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:657)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarwsnathwsnmgntayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaycangcnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngaraayttygcncant
aytaytgycarcarwsntayttycanccnathcanttyggncarggncanmgnytngarathaar

U-V_L-45 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:658)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarwsnathwsnwsntayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaycangcnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanttywsnwsnytncarccngargayttygcncant
aytaytgycarcarwsntayttywsnccnathcanttyggncarggncanmgnytngarathaar

U-V_L-46 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:659)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarwsnathwsnwsntayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaycangcnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanytnwsnwsnytncarccngargayttygcnwsnt
aytaytgycarcarwsnttytaycanccnathcanttyggncarggncanmgnytngarathaar

FIGURA 15I

U-V_L-47 : Secuencia de nucléotidos de la región variable de la cadena ligera **(SEQ ID NO:659)**

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarwsnathwsnwsntayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaycangcnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanytnwsnwsnytncarccngargayttygcnwsnt
aytaytgycarcarwsnttytaycanccnathcanttyggncarggncanmgnytngarathaar

U-V_L-48 : Secuencia de nucléotidos de la región variable de la cadena ligera **(SEQ ID NO:660)**

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarwsnathwsnwsntayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaycangtnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargayttygcncant
aytaytgycarcarwsntayttycanccnathcanttyggncarggncanmgnytngarathaar

U-V_L-49 : Secuencia de nucléotidos de la región variable de la cadena ligera **(SEQ ID NO:660)**

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarwsnathwsnwsntayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaycangtnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargayttygcncant
aytaytgycarcarwsntayttycanccnathcanttyggncarggncanmgnytngarathaar

U-V_L-50 : Secuencia de nucléotidos de la región variable de la cadena ligera **(SEQ ID NO:660)**

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarwsnathwsnwsntayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaycangtnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargayttygcncant
aytaytgycarcarwsntayttycanccnathcanttyggncarggncanmgnytngarathaar

U-V_L-51 : Secuencia de nucléotidos de la región variable de la cadena ligera **(SEQ ID NO:661)**

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarwsnathwsnwsntayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaycangcnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargayttygcnwsnt
aytaytgycarcarwsnttytaygcnccnathcanttyggncarggncanmgnytngarathaar

FIGURA 15J

U-V_L-52 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:661)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarwsnathwsnwsntayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaycangcnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargayttygcnwsnt
aytaytgycarcarwsnttytaygcnccnathcanttyggncarggncanmgnytngarathaar

U-V_L-53 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:662)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgymgngcnwsncarwsnathwsnwsntayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaycangcnwsnwsnytncarwsnggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanytncanathwsnwsnytncarccngargayttygcncant
aytaytgycarcarwsntayttycanccnathcanttyggncarggncanmgnytngarathaar

U-V_L-54 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:663)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgycargcnwsncargayathwsnaaytayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaygaygcnwsnaayytngarcanggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanttycanathwsnwsnytncarccngargayathgcncant
aytaytgycarcartaygaytayytnccnttycanttyggnccnggncanaargtngayathaar

U-V_L-55 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:663)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgycargcnwsncargayathwsnaaytayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaygaygcnwsnaayytngarcanggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanttycanathwsnwsnytncarccngargayathgcncant
aytaytgycarcartaygaytayytnccnttycanttyggnccnggncanaargtngayathaar

U-V_L-56 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:664)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgycargcnwsncargayathwsnaaywsnytnaaytggtaycarcaraarccnggnaargc
nccngarytnytnathtaygaygcnwsnaayytngarcanggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanttycanathwsnwsnytncarccngargayathgcncant
aytaytgycarcartgygaygayytnccnytncanttyggnggnggncanaargtngarathaar

FIGURA 15K

U-V_L-57 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:665)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgycargcnwsncargayathwsngaytayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaygaygcnwsnaayytngarcanggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanttycanathwsnwsnytncarccngargayathgcncant
aytaytgycarcaytaygayaayytnccnytncanttyggnggnggncanaargtngarathaar

U-V_L-58 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:666)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtngcnathc
antgycargcnwsncargayathwsnaaytayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaygaygcnwsnaayytngarcanggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanttycanathwsnwsnytncarccngargayathgcncant
aytaytgycarcartaygayaayytnccnytncanttyggnggnggncanaargtngarathaar

U-V_L-59 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:666)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtngcnathc
antgycargcnwsncargayathwsnaaytayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaygaygcnwsnaayytngarcanggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanttycanathwsnwsnytncarccngargayathgcncant
aytaytgycarcartaygayaayytnccnytncanttyggnggnggncanaargtngarathaar

U-V_L-60 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:667)

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgycargcnwsncargayathwsnaaywsnytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaygaygcnwsnathytngarcanggngtnccnwsnmgnttywsnggn
wsnggnwsngarcangayttycanttycanathwsnwsnytncarccngargayathgcncant
aytaytgycarcartgygayathytnccnytnwsnttyggnggnggncanaargtngarathaar

U-V_L-61 : Secuencia de nucléotidos de la región variable de la cadena ligera (SEQ ID NO:668)

Gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgycargcnwsncargayathwsnaaywsnytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaygaygcnwsnaayytngarcanggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanttycanathwsnwsnytncarccngargayathgcncant
aytaytgycarcartaygayaayytnccnytngcnttyggnggnggncanaargtngarathmgn

FIGURA 15L

U-V_L-62 : Secuencia de nucléotidos de la región variable de la cadena ligera **(SEQ ID NO:669)**

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngayggngtncanathc
antgycargcnwsncargayathcanaaytayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaygaygcnwsnaayytngarcanggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanttycanathwsnwsnytncarccngargayathgcncant
aytaytgycarcartaygaywsnytnccnathcanttyggncarggncanmgnytngarathaar

U-V_L-63 : Secuencia de nucléotidos de la región variable de la cadena ligera **(SEQ ID NO:670)**

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgycargcnwsncargayathwsnaaytayytnaaytggtaycarcaraarytnggnaargc
nccnaarytnytnathcaygaygcnwsnaayytngarcanggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanttycanathwsnwsnytncarccngargayathgcncant
aytaytgycarcartaygayaayytnccnathcanttyggncarggncanmgnytngarathaar

U-V_L-64 : Secuencia de nucléotidos de la región variable de la cadena ligera **(SEQ ID NO:671)**

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgycargcnwsncargayathwsngaytayytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaygaygcnwsnaayytngarcanggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanttycanathwsnwsnytncarccngargayathgcncant
aytaytgycarcaytaygayaayytnccnathcanttyggncarggncanmgnytngarathaar

U-V_L-65 : Secuencia de nucléotidos de la región variable de la cadena ligera **(SEQ ID NO:672)**

gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggngaymgngtncanathc
antgycargcnwsncargayathwsnaaywsnytnaaytggtaycarcaraarccnggnaargc
nccnaarytnytnathtaygaygcnwsnaayytngarcanggngtnccnwsnmgnttywsnggn
wsnggnwsnggncangayttycanttycanathwsnwsnytncarccngargayathgcncant
aytaytgycarcaytaygayaayytnccnathcanttyggncarggncanmgnytngarathaar

FIGURA 15M

U-V_H-1 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:673)

cargtncarytngtncarwsnggngcngargtnaaraarccnggngcnwsngtnaargtnwsnt
gyaargcnwsnggntaycanttycanwsntayggnathwsntgggtnmgncargcnccnggnca
rggnytngartggatgggntggathwsngcnwsnaayggnaaycanaaytaygcncaraarytn
cargaymgngtncanatgcancangaycanwsncanwsncangcntayatggarytnmgnwsny
tnmgnwsngaygaycangcngtntaytaytgygcnmgngargayaaytggaaytayggnttytt
ygaytaytggggncarggncanytngtncangtnwsnwsn

U-V_H-2 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:673)

cargtncarytngtncarwsnggngcngargtnaaraarccnggngcnwsngtnaargtnwsnt
gyaargcnwsnggntaycanttycanwsntayggnathwsntgggtnmgncargcnccnggnca
rggnytngartggatgggntggathwsngcnwsnaayggnaaycanaaytaygcncaraarytn
cargaymgngtncanatgcancangaycanwsncanwsncangcntayatggarytnmgnwsny
tnmgnwsngaygaycangcngtntaytaytgygcnmgngargayaaytggaaytayggnttytt
ygaytaytggggncarggncanytngtncangtnwsnwsn

U-V_H-3 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:674)

cargtncayytngtncarwsnggngcngargtnaaraarccnggngcnwsngtnaargtnwsnt
gyaargtnwsnggntaycanttycanggncaytayatgcaytgggtnmgncargcnccnggnca
rggnytngartggatgggntggathaayccnaaywsnggnggncanaaytgygcncaraartty
carggnmgngtncanatgcanmgngaycanwsnathwsncangcntayatggarytnwsnmgny
tnmgnwsngaygaycangcngtntaytaytgygcnmgnwsnathgcngtngcnytngaytaytg
gggncarggncanytngtncangtnwsnwsn

U-V_H-4 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:675)

cargtncarytngtncarwsnggngcngargtnaaraarccnggngcnwsngtnaargtnwsnt
gyaargcnwsnggntaycanttycanggntaytayatgcaytgggtnmgncargcnccnggnca
rggnytngartggatgggntggathaayccnaaywsnggnggncanaaycaycancaraartty
carggnmgngtncanatgcanmgngaycanwsnathwsncangcntayatggarytnwsnmgny
tnmgnwsngaygaycangcngtntaytaytgygcnmgnwsnathgcngtngcnytngaytaytg
gggncarggncanytngtncangtnwsnwsn

U-V_H-5 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:676)

cargtncarytngtncarwsnggngcngargtnmgnaarccnggngcnwsngtnaargtnwsnt
gyaargtnwsnggntaycanytncangarytnwsnatgcaytgggtnmgncargcnccnggnaa
rggnytngartggatgggnwsnttygayccngargayggngarcanathtaygcncaraartty
carggnmgngtncanatgytngargaycanwsncangaycangcntayatggarytnwsnwsny
tnmgnwsngargaycangcngtntaytaytgygcncangarggngayggnggntaytaytayta
yggnatggaygtntggggncarggncancangtncangtnwsnwsn

FIGURA 16A

U-V_H-6 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:676)

cargtncarytngtncarwsnggngcngargtnmgnaarccnggngcnwsngtnaargtnwsnt
gyaargtnwsnggntaycanytncangarytnwsnatgcaytgggtnmgncargcnccnggnaa
rggnytngartggatgggnwsnttygayccngargayggngarcanathtaygcncaraartty
carggnmgngtncanatgytngargaycanwsncangaycangcntayatggarytnwsnwsny
tnmgnwsngargaycangcngtntaytaytgygcncangarggngayggnggntaytaytayta
yggnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_H-7 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:677)

cargtncanytnaargarwsnggnccngtnytngtnaarccncangarcanytncanytncant
gycangtnwsnggnttywsnytnwsnaaygcnmgnatgggngtnwsntggathmgncarccncc
nggnaargcnytngartggytngcncayathttywsnaaygaygaraarwsntaywsncanwsn
ytnaarwsnmgnytncanathwsnaargaycanwsnaarwsncargtngtnytncanatgcana
ayatggayccngtngaycangcncantaytaytgygcnmgnatgtaywsnwsnggntggtaygg
ngtnttygaytaytggggncarggncanytngtncangtnwsnwsn

U-V_H-8 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:678)

cargtncanytnaargarwsnggnccngtnytngtnaarccncangarcanytncanytncant
gycangtnwsnggnttywsnytnwsnaaygcnmgnatgggngtnwsntggathmgncarccncc
nggnaargcnytngartggytngtnytnathttywsnaaygaygaraarwsntaywsncanwsn
ytnaarwsnmgnytncanathwsnaargaycanwsnaarwsncargtngtnytncanatgcana
ayatggayccngtngaycangcncantaytaytgygcnmgngtntaywsnwsnggntggwsntt
ytayggnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_H-9 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:679)

carathcanytnaargarwsnggnccncanytngtnaarccncancarcanytncanytncant
gycanttywsnggnttywsnytnwsncanggnggngtnggngtnggntggathmgncarccncc
nggnaargcnytngartggytngcnytnathtaytggaaygaygayaarmgntaywsnccnwsn
ytnaarwsnmgnytncanathcanaargaycanwsnaaraaycargtngtnytncanatgcana
ayatggayccngtngaycangcncantaytaytgygcncaymgnmgngarytnccnttygayta
ytggggncarggncanytngtncangtnwsnwsn

U-V_H-10 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:680)

carathcanytnaargarwsnggnccncanytngtnaarccncancarcanytncanytncant
gycanttywsnggnttywsnytnwsncanggnggngtnggngtnggntggathmgncarccncc
nggnaargcnytngartggytngcnytnathtaytggaaygaygayaarmgntaywsnccnwsn
ytnaarwsnmgnytncanathcanaargaycanwsnaarcancargtngtnytncangtncang
ayatggayccngtngaycangcncantaytaytgygcncaymgnaaytggcanccnttygayta
ytggggncarggncanytngtncangtnwsnwsn

FIGURA 16B

U-V_H-11 : Secuencia de nucleótidos de la región variable de la cadena pesada (SEQ ID NO:681)

carathcanytnaargarwsnggnccncanytngtnaarccncancarcanytncanytncant
gycanttywsnggnttywsnytnaaycanggnggngtnggngtnggntggathmgncarccncc
nggnaargcnytngartggytngcnytnathtaytggaaygaygayaarmgntaywsnccnwsn
ytnaarwsnmgnytncanathcanaargaycanwsnaaraaycargtngtnytncanatgcana
ayatggayccngtngaycangcncantaytaytgygcncaymgnytngarytnccnttygayta
ytggggncarggncanytngtncangtnwsnwsn

U-V_H-12 : Secuencia de nucleótidos de la región variable de la cadena pesada (SEQ ID NO:682)

carathcanytnaargarwsnggnccncanytngtnaarccncancarcanytncanytncant
gycanttywsnggnttywsnytnwsncanggnggngtnggngtnggntggathmgncarccncc
nggnaargcnytngartggytngcnytnathtaytggaaygaygayaarmgntaywsnccnwsn
ytnaarwsnmgnytncanathcanaargaycanwsnaaraaycargtngtnytncanatgcana
ayytngayccngtngaycangcncantaytaytgygcncaymgnmgngargtnccnttygayta
ytggggncarggncanytngtncangtnwsnwsn

U-V_H-13 : Secuencia de nucleótidos de la región variable de la cadena pesada (SEQ ID NO:683)

carathcanytnaargarwsnggnccncanytngtnaarccncancarcanytncanytncant
gycanttywsnggnttywsnytnwsncanggnggngtnggngtnggntggathmgncarccncc
nggnaargcnytngartggytngcnytnathtaytggaaygtngaraarmgntaywsnccnwsn
ytnmgnwsnmgnytncanathcanaargcncanwsnaaraaycargtngtnytncanatgcana
ayatggayccngtngaycangcncantaytaytgygcncaymgncaycanaayccnttygarta
ytggggncarggncanytngtncangtnwsnwsn

U-V_H-14 : Secuencia de nucleótidos de la región variable de la cadena pesada (SEQ ID NO:684)

carathcanytnaargarwsnggnccncanytngtnaarccncancarcanytncanytncant
gycanttywsnggnttywsnytnwsncanggnggngtnggngtnggntggathmgncarccncc
nggnaargcnytngartggytngcnytnathtaytggaaygaygayaarmgntaywsnccnwsn
ytnaarwsnmgnytncanathcanaargaycanwsnaaraaycargtngtnytncanatgcana
ayatggayccngtngaycangcncantaytaytgygcncaymgnggngarytnccnttygayta
ytggggncarggncanytngtncangtnwsnwsn

U-V_H-15 : Secuencia de nucleótidos de la región variable de la cadena pesada (SEQ ID NO:684)

carathcanytnaargarwsnggnccncanytngtnaarccncancarcanytncanytncant
gycanttywsnggnttywsnytnwsncanggnggngtnggngtnggntggathmgncarccncc
nggnaargcnytngartggytngcnytnathtaytggaaygaygayaarmgntaywsnccnwsn
ytnaarwsnmgnytncanathcanaargaycanwsnaaraaycargtngtnytncanatgcana
ayatggayccngtngaycangcncantaytaytgygcncaymgnggngarytnccnttygayta
ytggggncarggncanytngtncangtnwsnwsn

FIGURA 16C

U-V_H-16 : Secuencia de nucléotidos de la región variable de la cadena pesada **(SEQ ID NO:685)**

gargtncarytngtngarwsnggnggnggnytngtnaarccnggnggnwsnytnmgnytnwsnt
gygcngcnwsnggnttyccnttywsnmgntaywsnatgaaytgggtnmgncargcnccnggnaa
rggnytngartgggtnwsngcnathwsnwsnwsnwsnwsntayathtaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaygcnaaraaywsnytntayytncaratgaaywsny
tnmgngcngargaycangcngtntaytaytgygcnmgngaymgngtnggngcncanccngaygc
nttygayathtggggncarggncanatggtncangtnwsnwsn

U-V_H-17 : Secuencia de nucléotidos de la región variable de la cadena pesada **(SEQ ID NO:686)**

gargtncarytnytngarwsnggnggnggnytngtncarccnggnggnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntaygcnatgaaytgggtnmgncargcnccnggnaa
rggnytngartgggtnwsngcnathwsnggnwsnggnggnwsncantaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaywsnaaraaycanytntayytncaratgaaywsny
tnmgngcngargaycangcngtntaytaytgygcnaargarggnathgcngtngcnggncangc
ngartaytaytaytaytaygcnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_H-18 : Secuencia de nucléotidos de la región variable de la cadena pesada **(SEQ ID NO:687)**

gargtncarytnytngarwsnggnggnggnytngtncarccnggnggnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntaygcnatgwsntgggtnmgncargcnccnggnaa
rggnytngartgggtnwsngcnathwsnggnwsnggnggnwsncantaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaywsnaaraaycanytntayytncaratgaaywsny
tnmgngcngargaycangcngtntaytaytgygcnaargarggnathgcngcnmgngaywsnta
ytaytaytaygcnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_H-19 : Secuencia de nucléotidos de la región variable de la cadena pesada **(SEQ ID NO:688)**

gargtncarytnytngarwsnggnggnggnytngtncarccnggnggnwsnytnmgnytnwsnt
gycangcnwsnggnttycanttywsnwsntaygcnatgwsntgggtnmgncargcnccnggnaa
rggnytngartgggtnwsngcnathwsnggnwsnggnggnwsncantaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaywsnaaraaycanytntayytncaratgaaywsny
tnmgngcngargaycangcngartaytaytgygcnaargarggnathgcnggnmgngaywsnta
ytaytaytayggnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_H-20 : Secuencia de nucléotidos de la región variable de la cadena pesada **(SEQ ID NO:688)**

gargtncarytnytngarwsnggnggnggnytngtncarccnggnggnwsnytnmgnytnwsnt
gycangcnwsnggnttycanttywsnwsntaygcnatgwsntgggtnmgncargcnccnggnaa
rggnytngartgggtnwsngcnathwsnggnwsnggnggnwsncantaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaywsnaaraaycanytntayytncaratgaaywsny
tnmgngcngargaycangcngartaytaytgygcnaargarggnathgcnggnmgngaywsnta
ytaytaytayggnatggaygtntggggncarggncancangtncangtnwsnwsn

FIGURA 16D

U-V_H-21 : Secuencia de nucléotidos de la región variable de la cadena pesada **(SEQ ID NO:689)**

cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnytngartgggtngcnttyathwsngaygayggnwsncanaartaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaywsnatgaaycanytntayytncaratgaaywsny
tnmgngcngargaycangcngtntaytaytgygcnmgnwsntaytaygaywsnwsnggntayta
ytayggnttygaytaytggggncarggncanytngtncangtnwsnwsn

U-V_H-22 : Secuencia de nucléotidos de la región variable de la cadena pesada **(SEQ ID NO:689)**

cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnytngartgggtngcnttyathwsngaygayggnwsncanaartaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaywsnatgaaycanytntayytncaratgaaywsny
tnmgngcngargaycangcngtntaytaytgygcnmgnwsntaytaygaywsnwsnggntayta
ytayggnttygaytaytggggncarggncanytngtncangtnwsnwsn

U-V_H-23 : Secuencia de nucléotidos de la región variable de la cadena pesada **(SEQ ID NO:690)**

cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnytngartgggtngcngtnathtggtaygayggnwsnaayaartaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaywsnaaraaycanytntayytncaratgaaywsny
tnmgngcngargaycangcngtntaytaytgygcnmgnaaygtnathgaytaytggggncargg
ncanytngtncangtnwsnwsn

U-V_H-24 : Secuencia de nucléotidos de la región variable de la cadena pesada **(SEQ ID NO:691)**

cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntaygayatgcaytgggtnmgncargcnccnggnaa
rggnytngartgggtngcngtnathtggtaygayggnwsnathaartaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaywsnaaraaycanytntayytncaratgaaywsny
tnmgngcngargaycangcngtntaytaytgygcnmgnggnggngcncanggngcngartaytt
ycarcaytggggncarggncanytngtncangtnwsnwsn

U-V_H-25 : Secuencia de nucléotidos de la región variable de la cadena pesada **(SEQ ID NO:691)**

cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntaygayatgcaytgggtnmgncargcnccnggnaa
rggnytngartgggtngcngtnathtggtaygayggnwsnathaartaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaywsnaaraaycanytntayytncaratgaaywsny
tnmgngcngargaycangcngtntaytaytgygcnmgnggnggngcncanggngcngartaytt
ycarcaytggggncarggncanytngtncangtnwsnwsn

FIGURA 16E

U-V_H-26 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:692)

Cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnytngartgggtngcngtnathtggtaygayggnwsnaayaartaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaywsnaaraaycanytntayytncaratgaaywsny
tnmgngcngargaycangcngtntaytaytgygtnytnytntggttyggngarcanttygayta
ytggggncarggnwsnytngtncangtnwsnccn

U-V_H-27 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:693)

cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnytngartgggtngcngtnathtggwsngayggnwsnaayaartaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaywsnaaraaycanytntayytncaratgaaywsny
tnmgngcngargaycangcngtntaytaytgygcnmgnaayytnccnttygaytaytggggnca
rggncanytngtncangtnwsnwsn

U-V_H-28 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:694)

cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnytngartgggtngcngtnathtgggaygayggnwsnaaycartaytaycangaywsngtn
aarggnmgnttycangtnwsnmgngayaaywsnaaraaycanytnttyytncaratgaaywsny
tnmgngcngargaycangcngtntaytaytgygcnmgnwsncaytayggnggngaytaygayta
ytayggnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_H-29 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:695)

cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntayggnatgcaytgggtnmgncargcnccnggnaa
rggnytngartgggtngcngtnathtggtaygayggnwsnaayaarmgntaygtngaywsngtn
aarggnmgnttycanathwsnmgngayaaywsnaaraaycanytntayytncaratgaaywsny
tnmgngcngargaycangcngtntaytaytgygcnmgngayggntggcarcarcargcnccntt
ygaytaytggggncarggncanytngtncangtnwsnwsn

U-V_H-30 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:696)

cargtncarytngtngarwsnggnggnggngtngtncarccnggnmgnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttymgnwsncayggnatgcaytgggtnmgncargcnccnggnaa
rggnytngartgggtngcngtnathtggtaygayggnwsnaayaaraaytaygcngaywsngtn
mgnggnmgnttycanathwsnmgngayaaywsnaaraaycanytngayytncaratgaaywsny
tnmgngcngargaycangcngtntaytaytgygcnmgntggggnathwsngcnccnttygaytg
ytggggncarggncanytngtncangtnwsnwsn

FIGURA 16F

U-V_H-31 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:697)

gargtncarytngtngarwsnggnggnggnytngtncarccnggnggnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsngcntaywsnatgaaytgggtnmgncargcnccnggnaa
rggnytngartgggtnwsntayathwsnwsnwsnggnmgncanathtaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaygcnaaraaywsnytnttyytncaratgaaywsny
tnmgngaygargaycangcngtntaytaytgygcnytntgggcnccnttygaytaytggggnca
rggncanytngtncangtnwsnwsn

U-V_H-32 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:698)

gargtncarytngtngarwsnggnggnggnytngtncarccnggnggnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntaywsnatgaaytgggtnmgncargcnccnggnaa
rggnytngartgggtnwsncayathwsnwsnwsnwsnmgncanathtaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaygcnaaraaywsngtntayytncaratgaaywsny
tnmgngaygargaycangcngtntaytaytgygcnmgngayggntayaaytggaayggnggngg
naaytaytayggnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_H-33 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:699)

gargtncarytngtngarwsnggnggnggnytngtncarccnggnggnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntaywsnatgaaytgggtnmgncargcnccnggnaa
rggnytngartgggtnwsncayathwsnmgnwsnwsnmgncanathtaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaygcnaaraaywsnytntayytncaratgaaywsny
tnmgngaygargaycangcngtntaytaytgygcnmgngayggntayaaytggaayaayggngg
ntaytaytayggnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_H-34 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:699)

gargtncarytngtngarwsnggnggnggnytngtncarccnggnggnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsnwsntaywsnatgaaytgggtnmgncargcnccnggnaa
rggnytngartgggtnwsncayathwsnmgnwsnwsnmgncanathtaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaygcnaaraaywsnytntayytncaratgaaywsny
tnmgngaygargaycangcngtntaytaytgygcnmgngayggntayaaytggaayaayggngg
ntaytaytayggnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_H-35 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:700)

cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncant
gycangtnwsnggnggnwsngtnwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnytngartggathggntayathcaywsnwsnggnwsncantaytayaayccnwsn
ytnaarwsnmgngtncanathwsngtngaycanwsnaaraaycarttywsnytnaayytnwsnw
sngtncangcngcngaycangcngtntaytaytgygcnmgnggnccntaytayggnatggaygt
ntggggncarggncancangtncangtnwsnwsn

FIGURA 16G

U-V_H-36 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:701)

cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncant
gycangtnwsnggnggnwsnathwsnmgnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnytngartggathggntayathtaycaywsnggnwsncantaytayaayccnwsn
ytnaarwsnmgngtnaayatgwsngtngaycanwsnaaraaycarttywsnytnaarytnwsnw
sngtncangcngcngaycangcngtntaytaytgygcnmgngcnytnmgnggnathgtnytnat
ggtntaygtnytnggngcnytngayathtggggncarggncanaargtncangtnwsnwsn

U-V_H-37 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:701)

cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncant
gycangtnwsnggnggnwsnathwsnmgnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnytngartggathggntayathtaycaywsnggnwsncantaytayaayccnwsn
ytnaarwsnmgngtnaayatgwsngtngaycanwsnaaraaycarttywsnytnaarytnwsnw
sngtncangcngcngaycangcngtntaytaytgygcnmgngcnytnmgnggnathgtnytnat
ggtntaygtnytnggngcnytngayathtggggncarggncanaargtncangtnwsnwsn

U-V_H-38 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:702)

cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncant
gycangtnwsnggnggnwsnathwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnytngartggathggntayathtaytaywsnggnwsncantaytayaayccnwsn
ytnaarwsnmgngtncanathwsngtngaycanwsnaaraaycarttywsnytnaarytnwsnw
sngtncangcngcngaycangcngtntaytaytgygcnmgngaygarcangtngtnmgnggnyt
nathmgntaytgytayggnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_H-39 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:703)

cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytnaayt
gycangtnwsnggnggnwsnathwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnytngartggathggntayathcaytaywsnggnwsncantaytayaayccnwsn
ytnaarwsnmgnathcanathwsngcngaycanwsnaaraaycarttywsnytnaarytnaayw
sngtncangcngcngaycangcngtntaytaytgygcnmgngaymgnggnggnggngaytaygg
nmgnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_H-40 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:704)

cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytnaayt
gycangtnwsnggnggnwsnathwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnytngartggathggntayathcaytaywsnggnwsncantaytayaayccnwsn
ytnaarwsnmgnathcanathwsngcngaycanwsnaaraaycarttywsnytnaarytnaayw
sngtncangcngcngaycangcngtntaytaytgygcnmgngaymgnggnggnggngaytaygg
nmgnatggaygtntggggncarggncancangtncangtnwsnwsn

FIGURA 16H

U-V_H-41 : Secuencia de nucléotidos de la región variable de la cadena pesada **(SEQ ID NO:705)**

cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncant
gycangtnwsnggnggnwsnathwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnytngartggathggntayathcaywsnwsnggnwsncantaytayaayccnwsn
ytnaarwsnmgnathcanaarwsngtngaycanwsnaaraaycarttywsnytnaarytnwsnw
sngtncangcngcngaycangcngtntaytaytgygcnmgnwsnaayaaytayggntgyttygc
nytntggggnmgnggncanytngtncangtnwsnwsn

U-V_H-42 : Secuencia de nucléotidos de la región variable de la cadena pesada **(SEQ ID NO:706)**

cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncant
gycangtnwsnggnggnwsnathwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnytngartggathggntayathcaywsnwsnggnwsncantaytayaayccnwsn
ytnaarwsnmgnathcanaarwsngtngaycanwsnaaraaycarttywsnytnaarytnwsnw
sngtncangcngcngaycangcngtntaytaytgygcnmgnwsnaayaaytayggntgyttygc
nytntggggnmgnggncanytngtncangtnwsnwsn

U-V_H-43 : Secuencia de nucléotidos de la región variable de la cadena pesada **(SEQ ID NO:707)**

cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncant
gycangtnwsnggnggnwsnathwsnwsnggnggntaytaytggwsntggathmgncarcaycc
nggnaarggnytngartggathggntayathcaytaywsnggnwsncantaytayaayccnwsn
ytnaarwsnmgngtncanathwsngtngaycanwsnaaraaycarttywsnytnaarytnwsnw
sngtncangcngcngaycangcngtntaytaytgygcnwsnggntayaaytayggnytntayta
ytaygaywsnwsnggntayccnwsntaytaytayggnatggaygtntggggncarggncancan
gtncangtnwsnwsn

U-V_H-44 : Secuencia de nucléotidos de la región variable de la cadena pesada **(SEQ ID NO:708)**

cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncant
gycangtnwsnggnggnwsnathwsnwsnggngaytaytaytggaaytgggtnmgncarcaycc
nggnaarggnytngartggathggntayathtaytaywsnggnggncantaytayaayccnwsn
ytnaarwsnmgngtncanathwsngtngaycanwsnaaraaycarttywsnytnaarytnttyw
sngtncangcngcngaycangcngtntayttytgygcnmgncantaytaygayathytncangg
ntayccnttytayttygaytaytggggncarggncanytngtncangtnwsnwsn

U-V_H-45 : Secuencia de nucléotidos de la región variable de la cadena pesada **(SEQ ID NO:709)**

cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncant
gycangtnwsnggnggnwsnathwsnwsnggngaytaytaytggaaytgggtnmgncarcaycc
nggnaarggnytngartggathggntayathtaytaywsnggnggncantaytayaayccnwsn
ytnaarwsnmgngtncanathwsngtngaycanwsnaaraaycarttywsnytnaarytnttyw
sngtncangcngcngaycangcngtntayttytgygcnmgncantaytaygayathytncangg
ntayccnttytayttygaytaytggggncarggncanytngtncangtnwsnwsn

FIGURA 16I

U-V_H-46 : Secuencia de nucleótidos de la región variable de la cadena pesada (SEQ ID NO:710)

cargtncarytncarcartggggngcnggnytnytnaarccnwsngarcanytnwsnytncant
gygcngtntayggnggnwsnttywsnggntaytaytggwsntggathmgncarccnccnggnaa
rggnytngartggathggngarathaaycaywsnggnwsncanaaytayaayccnwsnytnaar
wsnmgngtncanathwsngtngaycanwsnaaraaycarttywsnytnaarytnwsnwsngtnc
angcngcngaycangcngtntaytaytgygcnmgnggnggntaywsnwsnwsntggtaytggtt
ygayccntggggncarggncanytngtncangtnwsnwsn

U-V_H-47 : Secuencia de nucleótidos de la región variable de la cadena pesada (SEQ ID NO:711)

cargtncarytncarcartggggngcnggnytnytnaarccnwsngarcanytnwsnytncant
gygcngtntayggnggnwsnttywsnggntaytaytggwsntggathmgncarccnccnggnaa
rggnytngartggathggngarathaaycaywsnggnwsncanaaytayaayccnwsnytnaar
wsnmgngtncanathwsngtngaycanwsnaaraaycarttywsnytnaarytnwsnwsngtnc
angcngcngaycangcngtntaytaytgygcnmgnggnggntaywsnwsnwsntggttytggtt
ygayccntggggncarggncanytngtncangtnwsnwsn

U-V_H-48 : Secuencia de nucleótidos de la región variable de la cadena pesada (SEQ ID NO:711)

cargtncarytncarcartggggngcnggnytnytnaarccnwsngarcanytnwsnytncant
gygcngtntayggnggnwsnttywsnggntaytaytggwsntggathmgncarccnccnggnaa
rggnytngartggathggngarathaaycaywsnggnwsncanaaytayaayccnwsnytnaar
wsnmgngtncanathwsngtngaycanwsnaaraaycarttywsnytnaarytnwsnwsngtnc
angcngcngaycangcngtntaytaytgygcnmgnggnggntaywsnwsnwsntggttytggtt
ygayccntggggncarggncanytngtncangtnwsnwsn

U-V_H-49 : Secuencia de nucleótidos de la región variable de la cadena pesada (SEQ ID NO:711)

cargtncarytncarcartggggngcnggnytnytnaarccnwsngarcanytnwsnytncant
gygcngtntayggnggnwsnttywsnggntaytaytggwsntggathmgncarccnccnggnaa
rggnytngartggathggngarathaaycaywsnggnwsncanaaytayaayccnwsnytnaar
wsnmgngtncanathwsngtngaycanwsnaaraaycarttywsnytnaarytnwsnwsngtnc
angcngcngaycangcngtntaytaytgygcnmgnggnggntaywsnwsnwsntggttytggtt
ygayccntggggncarggncanytngtncangtnwsnwsn

U-V_H-50 : Secuencia de nucleótidos de la región variable de la cadena pesada (SEQ ID NO:711)

cargtncarytncarcartggggngcnggnytnytnaarccnwsngarcanytnwsnytncant
gygcngtntayggnggnwsnttywsnggntaytaytggwsntggathmgncarccnccnggnaa
rggnytngartggathggngarathaaycaywsnggnwsncanaaytayaayccnwsnytnaar
wsnmgngtncanathwsngtngaycanwsnaaraaycarttywsnytnaarytnwsnwsngtnc
angcngcngaycangcngtntaytaytgygcnmgnggnggntaywsnwsnwsntggttytggtt
ygayccntggggncarggncanytngtncangtnwsnwsn

FIGURA 16J

U-V_H-51 : Secuencia de nucléotidos de la región variable de la cadena pesada **(SEQ ID NO:712)**

cargtncarytncargarwsnggnccnggnytngtnaarccnwsngarcanytnwsnytncant
gycangtnwsnggnggnwsnathwsnwsntaytaytggwsntggathmgncarccngcnggnaa
rggnytngartggathggnmgnathtaycanwsnggncancanaaytayaayccnwsnytnaar
wsnmgngtncanatgwsngtngaycanwsnaaraaycarttywsnytnaarytnwsnwsngtnc
angcngcngaycangcngtntaytaytgygcnmgngayggntaywsntayggncaytaytayta
ytayggnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_H-52 : Secuencia de nucléotidos de la región variable de la cadena pesada **(SEQ ID NO:713)**

cargtncarytncargarwsnggnccnggnytngtnaarccnwsngarcanytnwsnytncant
gycangtnwsnggnggnwsngtnwsnwsnggnggnwsntaytggwsntggathmgncarccncc
nggnaarggnytngartggathggntayathtaytaywsnggnwsncanaaytayaayccnwsn
ytnaarwsnmgngtncanathwsnathgtncanwsnmgnaaycarttywsnytnaarytnwsnw
sngtncangcngcngaycangcngtntaytaytgygcnmgnwsngcnytnmgntayttygaytg
gytnttywsngaygtnwsngayathtggggncarggncanatggtncangtnwsnwsn

U-V_H-53 : Secuencia de nucléotidos de la región variable de la cadena pesada **(SEQ ID NO:713)**

cargtncarytncargarwsnggnccnggnytngtnaarccnwsngarcanytnwsnytncant
gycangtnwsnggnggnwsngtnwsnwsnggnggnwsntaytggwsntggathmgncarccncc
nggnaarggnytngartggathggntayathtaytaywsnggnwsncanaaytayaayccnwsn
ytnaarwsnmgngtncanathwsnathgtncanwsnmgnaaycarttywsnytnaarytnwsnw
sngtncangcngcngaycangcngtntaytaytgygcnmgnwsngcnytnmgntayttygaytg
gytnttywsngaygtnwsngayathtggggncarggncanatggtncangtnwsnwsn

U-V_H-54 : Secuencia de nucléotidos de la región variable de la cadena pesada **(SEQ ID NO:714)**

gargtncarytngtncarwsnggngcngarytnaaraarccnggngarwsnytnaarathwsnt
gyaarggnwsnggntaymgnttycanwsntaytggathggntgggtnmgncaratgccnggnaa
rggnytngartggatgggnathathtayccngaygaywsngaycanmgntaywsnccnwsntty
carggncargtncanathwsngcngayaarwsnathwsncangcntayytncartggwsnwsny
tnaargcnwsngaycangcnatgtaytaytgygcnmgncaraarwsntayggntaywsntaytt
ygaytaytggggncarggncanytngtncangtnwsnwsn

U-V_H-55 : Secuencia de nucléotidos de la región variable de la cadena pesada **(SEQ ID NO:715)**

gargtncarytngtncarwsnggngcngargtnaaraarccnggngarwsnytnaarathwsnt
gyaarggnwsnggntaywsnttycanwsntaytggathggntgggtnmgncaratgccnggnaa
rggnytngartggatgggnathathtayccngaygaywsngaygcnmgntaywsnccnwsntty
carggncargtncanathwsngcngayaarwsnathaaycangcntayytncartggwsnwsny
tnaargcnwsngaycangcnatgtaytaytgygcnmgncarggntayggnwsnggntggggnta
yttygaytaytggggncarggncanytngtncangtnwsnwsn

FIGURA 16K

U-V_H-56 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:716)

gargtncarytngtncarwsnggngcngargtnaaraarccnggngarwsnytnaarathwsnt
gyaarggnwsnggntaywsnttycanwsntaytggathggntgggtnmgncaratgccnggnaa
rggnytngartggatgggnathathtayccnggngaywsngayathmgntaywsnccnwsntty
carggncargtncanathwsngcngayaarwsnathwsncangcntayytncartggwsnwsny
tnaargcnwsngaycangcnatgtaytaytgygcnmgncarggnytngcngtngcnggncanws
ntaytaytaytaytayggnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_H-57 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:717)

cargtncarytncarcarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncant
gygcnathwsnggngaywsngtnwsnwsntaywsngcngcntggaaytggathmgncarwsncc
nwsnmgnggnytngartggytnggnmgncantaytgymgnwsnaartggtayaaygaytaygcn
gtnwsngtnaarwsnmgnathcanathaayccngaycanwsnaaraaycarttywsnytncary
tnaaywsngtncanccngargaycangcngtntaytaytgygcnmgngaymgngcngtngcngg
ntaytaytayggnatggaygtntggggncarggncancangtncangtnwsnwsn

U-V_H-58 : Secuencia de nucléotidos de la región variable de la cadena pesada (SEQ ID NO:697)

gargtncarytngtngarwsnggnggnggnytngtncarccnggnggnwsnytnmgnytnwsnt
gygcngcnwsnggnttycanttywsngcntaywsnatgaaytgggtnmgncargcnccnggnaa
rggnytngartgggtnwsntayathwsnwsnwsnggnmgncanathtaytaygcngaywsngtn
aarggnmgnttycanathwsnmgngayaaygcnaaraaywsnytnttyytncaratgaaywsny
tnmgngaygargaycangcngtntaytaytgygcnytntgggcnccnttygaytaytggggnca
rggncanytngtncangtnwsnwsn

FIGURA 16L

SECUENCIA DE NUCLEÓTIDOS DE LA REGIÓN CONSTANTE DE LA CADENA LIGERA

CGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCTAGCGTTGT
GTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACT
CCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCA
GACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAA
CAGGGGAGAGTGTTAG (SEQ ID NO:718)

FIGURA 17A

SECUENCIA DE NUCLEÓTIDOS DE LA REGIÓN CONSTANTE DE LA CADENA PESADA

GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCTAGAAGCACCTCCGAGAGCACAGCGGCCCTGGG
CTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCTCTGACCAGCGGCGTGCACA
CCTTCCCAGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGC
ACCCAGACCTACACATGCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTG
TGTCGAGTGCCCACCGTGCCCAGCACCACCTGTGGCAGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACA
CCCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTC
AACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGCACGTTCCG
TGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
GCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCC
CCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGC
CGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCT
TCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:719)

FIGURA 17B

SECUENCIAS DE NUCLEÓTIDOS DE CDR DE LA CADENA LIGERA

NOMBRE	SECUENCIA	SEQ ID NO
CDRL1-1	mgnwsnwsncarwsnytngtntaywsngayggnaaycantayytnaay	720
CDRL1-2	mgnwsnwsncarwsnytngtntaywsngayggnaaycantayytnaay	720
CDRL1-3	mgnwsnwsncarwsnytngtntaywsngayggnaaycantayytnaay	720
CDRL1-4	mgnwsnwsncarwsnytngtntaywsngayggnaaycantayytnaay	720
CDRL1-5	aarwsnwsncarwsnytnytncaywsngayggnaarcantayytntay	721
CDRL1-6	aarwsnwsncarwsnytnytncaywsngayggnaarcantayytntay	721
CDRL1-7	aarwsnwsncarwsnytnytncaywsngayggnaarcantayytntay	721
CDRL1-8	aarwsnwsncarwsnytnytncaywsngayggnaarcantayytntay	721
CDRL1-9	aarwsnwsncarwsnytnytncaywsngayggnaarcantayytntay	721
CDRL1-11	mgngcnwsncarggnathgcnaaytayytngcn	722
CDRL1-12	mgngcnwsncarggnathwsnaaygayytngcn	723
CDRL1-13	mgnwsnwsncarwsnytngtncaywsngayggnaaycantayytnwsn	724
CDRL1-14	mgnwsnwsncarwsnytngtncaywsngayggnaaycantayytnwsn	724
CDRL1-15	mgnwsnwsncarwsnytngtncaywsngayggnaaycantayytnwsn	724
CDRL1-16	mgngcnwsncarcangtnathwsnwsntayytngcn	725
CDRL1-17	mgngcnwsncarwsngtnwsnmgnytngcn	726
CDRL1-18	mgngcnwsncarggnathmgnaaygayytnggn	727
CDRL1-19	aarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngtn	728
CDRL1-20	aarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngtn	728
CDRL1-21	aarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngcn	729
CDRL1-22	aarwsnwsncaraaygtnytntaywsnwsnaayaayaaraaytayytngcn	730
CDRL1-23	aarwsnwsncaraaygtnytntaywsnwsnaayaayaaraaytayytngcn	730
CDRL1-24	aarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngcn	729
CDRL1-25	aarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngcn	729
CDRL1-26	aarwsnwsncarwsngtnytntayaaywsnaayaayaaraaytayytngcn	731

FIGURA 18A

NOMBRE	SECUENCIA	SEQ ID NO
CDRL1-27	aarwsnwsncarwsngtnytntayaaywsnaayaayaaraaytayytngcn	731
CDRL1-28	aarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngcn	729
CDRL1-29	aarwsnwsncarwsngtnytntaywsnwsnaayaayaaraaytayytngcn	729
CDRL1-30	aarwsnwsncarwsngtnytngaywsnwsnaayaayaaraaytayytngcn	732
CDRL1-31	aarwsnwsncarwsngtnytngaywsnwsnaayaayaaraaytayytngcn	732
CDRL1-32	aarwsnwsncarwsnathytntaymgnwsnaayaayaaraaytayytngcn	733
CDRL1-33	aarwsnwsncarwsnathytntaymgnwsnaayaayaaraaytayytngcn	733
CDRL1-34	mgngcnwsncargayathwsncaytayytngcn	734
CDRL1-35	mgngcnwsncargayathwsnaaytayytngcn	735
CDRL1-36	mgngcnwsncarwsngtnwsnwsnaayytngcn	736
CDRL1-37	mgngcnwsncarwsngtnwsnwsnaayytngcn	736
CDRL1-38	mgngcnwsncargayathwsnmgntggytngcn	737
CDRL1-39	mgngcnwsncarwsnathwsncantayytnaay	738
CDRL1-40	mgngcnwsncarcanathwsnathtayytnaay	739
CDRL1-41	mgngcnwsncarwsnathmgnwsntayytnaay	740
CDRL1-42	mgngcnwsncarcanathwsnmgntayytnaay	741
CDRL1-43	mgngcnwsncarmgnathwsnwsntayytnaay	742
CDRL1-44	mgngcnwsncarwsnathwsnmgntayytnaay	743
CDRL1-45	mgngcnwsncarwsnathwsnwsntayytnaay	744
CDRL1-46	mgngcnwsncarwsnathwsnwsntayytnaay	744
CDRL1-47	mgngcnwsncarwsnathwsnwsntayytnaay	744
CDRL1-48	mgngcnwsncarwsnathwsnwsntayytnaay	744
CDRL1-49	mgngcnwsncarwsnathwsnwsntayytnaay	744
CDRL1-50	mgngcnwsncarwsnathwsnwsntayytnaay	744
CDRL1-51	mgngcnwsncarwsnathwsnwsntayytnaay	744
CDRL1-52	mgngcnwsncarwsnathwsnwsntayytnaay	744
CDRL1-53	mgngcnwsncarwsnathwsnwsntayytnaay	744
CDRL1-54	cargcnwsncargayathwsnaaytayytnaay	745
CDRL1-55	cargcnwsncargayathwsnaaytayytnaay	745
CDRL1-56	cargcnwsncargayathwsnaaywsnytnaay	746
CDRL1-57	cargcnwsncargayathwsngaytayytnaay	747

FIGURA 18B

NOMBRE	SECUENCIA	SEQ ID NO
CDRL1-58	cargcnwsncargayathwsnaaytayytnaay	745
CDRL1-59	cargcnwsncargayathwsnaaytayytnaay	745
CDRL1-60	cargcnwsncargayathwsnaaywsnytnaay	746
CDRL1-61	cargcnwsncargayathwsnaaywsnytnaay	746
CDRL1-62	cargcnwsncargayathcanaaytayytnaay	748
CDRL1-63	cargcnwsncargayathwsnaaytayytnaay	745
CDRL1-64	cargcnwsncargayathwsngaytayytnaay	747
CDRL1-65	cargcnwsncargayathwsnaaywsnytnaay	746
CDRL2-1	aargtnwsnaaytgggaywsn	749
CDRL2-2	aargtnwsnaaytgggaywsn	749
CDRL2-3	aargtnwsnaaytgggaywsn	749
CDRL2-4	aargtnwsnaaytgggaywsn	749
CDRL2-5	gargtnwsnaaymgnttywsn	750
CDRL2-6	gargtnwsnaaymgnttywsn	750
CDRL2-7	gargtnwsnaaymgnttywsn	750
CDRL2-8	gargtnwsnaaymgnttywsn	750
CDRL2-9	gargtnwsnaaymgnttywsn	750
CDRL2-11	gtngcnwsncanytncarwsn	751
CDRL2-12	gcngcnwsncanytncarwsn	752
CDRL2-13	aarathwsnaaymgnttywsn	753
CDRL2-14	aarathwsnaaymgnttywsn	753
CDRL2-15	aarathwsnaaymgnttywsn	753
CDRL2-16	ggngcnwsnwsnmgngcncan	754
CDRL2-17	ggngcnwsnmgnmgngcncan	755
CDRL2-18	gcngcnwsnwsnytncarwsn	756
CDRL2-19	tgggcnwsncanmgngarwsn	757
CDRL2-20	tgggcnwsncanmgngarwsn	757
CDRL2-21	tgggcnwsncanmgngarwsn	757
CDRL2-22	tgggcnwsncanmgngarwsn	757
CDRL2-23	tgggcnwsncanmgngarwsn	757
CDRL2-24	tgggcnwsncanmgngarwsn	757
CDRL2-25	tgggcnwsncanmgngarwsn	757
CDRL2-26	tgggcnwsncanmgngarwsn	757
CDRL2-27	tgggcnwsncanmgngarwsn	757
CDRL2-28	tgggcnwsncanmgnaarwsn	758
CDRL2-29	tgggcnwsncanmgnaarwsn	758

FIGURA 18C

NOMBRE	SECUENCIA	SEQ ID NO
CDRL2-30	tgggcnwsncanmgngarwsn	757
CDRL2-31	tgggcnwsncanmgngarwsn	757
CDRL2-32	tgggcnwsngcnmgngarwsn	759
CDRL2-33	tgggcnwsngcnmgngarwsn	759
CDRL2-34	gcngcnwsnwsnytncarwsn	756
CDRL2-35	gcngcnwsnwsnytncarwsn	756
CDRL2-36	ggngcnwsnmgnmgngcncan	755
CDRL2-37	ggngcnwsnmgnmgngcncan	755
CDRL2-38	gcngcnwsnwsnytncarwsn	756
CDRL2-39	gcngcnwsnwsnytncarwsn	756
CDRL2-40	gcngcnwsnwsnytncarwsn	756
CDRL2-41	gcngcnwsnwsnytncarwsn	756
CDRL2-42	gcngcnwsncanytncarwsn	752
CDRL2-43	gcngarwsnwsnytncarwsn	760
CDRL2-44	cangcnwsnwsnytncarwsn	761
CDRL2-45	cangcnwsnwsnytncarwsn	761
CDRL2-46	cangcnwsnwsnytncarwsn	761
CDRL2-47	cangcnwsnwsnytncarwsn	761
CDRL2-48	cangtnwsnwsnytncarwsn	762
CDRL2-49	cangtnwsnwsnytncarwsn	762
CDRL2-50	cangtnwsnwsnytncarwsn	762
CDRL2-51	cangcnwsnwsnytncarwsn	761
CDRL2-52	cangcnwsnwsnytncarwsn	761
CDRL2-53	cangcnwsnwsnytncarwsn	761
CDRL2-54	gaygcnwsnaayytngarcan	763
CDRL2-55	gaygcnwsnaayytngarcan	763
CDRL2-56	gaygcnwsnaayytngarcan	763
CDRL2-57	gaygcnwsnaayytngarcan	763
CDRL2-58	gaygcnwsnaayytngarcan	763
CDRL2-59	gaygcnwsnaayytngarcan	763
CDRL2-60	gaygcnwsnathytngarcan	764
CDRL2-61	gaygcnwsnaayytngarcan	763
CDRL2-62	gaygcnwsnaayytngarcan	763
CDRL2-63	gaygcnwsnaayytngarcan	763
CDRL2-64	gaygcnwsnaayytngarcan	763
CDRL2-65	gaygcnwsnaayytngarcan	763

FIGURA 18D

NOMBRE	SECUENCIA	SEQ ID NO
CDRL3-1	atgcarwsncancaytggccnathcan	765
CDRL3-2	athcarggncancaytggccncancan	766
CDRL3-3	atgcarggncancaytggccnathcan	767
CDRL3-4	atgcarggncancaytggccnathcan	767
CDRL3-5	atgcarggnathcarytnccntgywsn	768
CDRL3-6	atgcarwsnathcarytnccnytncan	769
CDRL3-7	atgcarwsnathcarytnccnytncan	769
CDRL3-8	atgcarwsnathcarytnccnathcan	770
CDRL3-9	atgcarwsnathcarytnccnathcan	770
CDRL3-11	caraaytayaaywsngcnccnttycan	771
CDRL3-12	caraartayaaywsngtnccnytncan	772
CDRL3-13	atgcargcncancarttyccncaycan	773
CDRL3-14	atgcargcncancarttyccncaycan	773
CDRL3-15	atgcargcncancarttyccncaycan	773
CDRL3-16	carcartayggnwsnwsnccnmgncan	774
CDRL3-17	carcartayggnwsnwsnccnmgnwsn	775
CDRL3-18	ytncarcayaaywsntayccnccncan	776
CDRL3-19	carcartaytaywsnttyccntggcan	777
CDRL3-20	carcartaytaywsnttyccntggcan	777
CDRL3-21	carcartaytaywsncancantggcan	778
CDRL3-22	carcartaytayggncanccnmgncan	779
CDRL3-23	carcartaytayggncanccnmgncan	779
CDRL3-24	carcartaytaywsnathwsnmgncan	780
CDRL3-25	carcartaytaywsnathwsnmgncan	780
CDRL3-26	carcartaytaywsncancantggcan	778
CDRL3-27	carcartaytaywsncancantggcan	778
CDRL3-28	carcartaytaywsncanatgttywsn	781
CDRL3-29	carcartaytaywsncanatgttywsn	781
CDRL3-30	caycartaytaywsncanccnytncan	782
CDRL3-31	caycartaytaywsncanccnytncan	782
CDRL3-32	carcartayttyathcanccnytncan	783
CDRL3-33	carcartayttyathcanccnytncan	783
CDRL3-34	carcartayaayaaytayccnttycan	784
CDRL3-35	carcartayaaycantayccnttycan	785
CDRL3-36	carcarcayaayaaytggccnccntggcan	786
CDRL3-37	carcarcayaayaaytggccnccntggcan	786

FIGURA **18E**

NOMBRE	SECUENCIA	SEQ ID NO
CDRL3-38	carcargcnaaywsnttyccnccncan	787
CDRL3-39	carcarwsncaywsngcnccnttycan	788
CDRL3-40	carcarwsntaywsncanytncan	789
CDRL3-41	carcarwsntaywsnathccnytncan	790
CDRL3-42	carcarathtaywsncanwsnathcan	791
CDRL3-43	carcarwsntayathcanccnathcan	792
CDRL3-44	carcarwsntayttycanccnathcan	793
CDRL3-45	carcarwsntayttywsnccnathcan	794
CDRL3-46	carcarwsnttytaycanccnathcan	795
CDRL3-47	carcarwsnttytaycanccnathcan	795
CDRL3-48	carcarwsntayttycanccnathcan	793
CDRL3-49	carcarwsntayttycanccnathcan	793
CDRL3-50	carcarwsntayttycanccnathcan	793
CDRL3-51	carcarwsnttytaygcnccnathcan	796
CDRL3-52	carcarwsnttytaygcnccnathcan	796
CDRL3-53	carcarwsntayttycanccnathcan	793
CDRL3-54	carcartaygaytayytnccnttycan	797
CDRL3-55	carcartaygaytayytnccnttycan	797
CDRL3-56	carcartgygaygayytnccnytncan	798
CDRL3-57	carcaytaygayaayytnccnytncan	799
CDRL3-58	carcartaygayaayytnccnytncan	800
CDRL3-59	carcartaygayaayytnccnytncan	800
CDRL3-60	carcartgygayathytnccnytnwsn	801
CDRL3-61	carcartaygayaayytnccnytngcn	802
CDRL3-62	carcartaygaywsnytnccnathcan	803
CDRL3-63	carcartaygayaayytnccnathcan	804
CDRL3-64	carcaytaygayaayytnccnathcan	805
CDRL3-65	carcaytaygayaayytnccnathcan	805

FIGURA 18F

SECUENCIAS DE NUCLEÓTIDOS DE CDR DE LA CADENA PESADA

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
CDRH1-1	CDRH1-10.1	ggntaycanttycanwsntayggnathwsn	806
CDRH1-2	CDRH1-10	ggntaycanttycanwsntayggnathwsn	806
CDRH1-3	CDRH1-42	ggntaycanttycanggncaytayatgcay	807
CDRH1-4	CDRH1-40	ggntaycanttycanggntaytayatgcay	808
CDRH1-5	CDRH1-30	ggntaycanytncangarytnwsnatgcay	809
CDRH1-6	CDRH1-31	ggntaycanytncangarytnwsnatgcay	809
CDRH1-7	CDRH1-29	ggnttywsnytnwsnaaygcnmgnatgggngtnwsn	810
CDRH1-8	CDRH1-20	ggnttywsnytnwsnaaygcnmgnatgggngtnwsn	810
CDRH1-9	CDRH1-65	ggnttywsnytnwsncanggnggngtnggngtnggn	811
CDRH1-10	CDRH1-56	ggnttywsnytnwsncanggnggngtnggngtnggn	811
CDRH1-11	CDRH1-62	ggnttywsnytnaaycanggnggngtnggngtnggn	812
CDRH1-12	CDRH1-2	ggnttywsnytnwsncanggnggngtnggngtnggn	811
CDRH1-13	CDRH1-59	ggnttywsnytnwsncanggnggngtnggngtnggn	811
CDRH1-14	CDRH1-57	ggnttywsnytnwsncanggnggngtnggngtnggn	811
CDRH1-15	CDRH1-64	ggnttywsnytnwsncanggnggngtnggngtnggn	811
CDRH1-16	CDRH1-41	ggnttyccnttywsnmgntaywsnatgaay	813
CDRH1-17	CDRH1-45	ggnttycanttywsnwsntaygcnatgaay	814
CDRH1-18	CDRH1-47	ggnttycanttywsnwsntaygcnatgwsn	815
CDRH1-19	CDRH1-51	ggnttycanttywsnwsntaygcnatgwsn	815
CDRH1-20	CDRH1-52	ggnttycanttywsnwsntaygcnatgwsn	815
CDRH1-21	CDRH1-13	ggnttycanttywsnwsntayggnatgcay	816
CDRH1-22	CDRH1-14	ggnttycanttywsnwsntayggnatgcay	816
CDRH1-23	CDRH1-1	ggnttycanttywsnwsntayggnatgcay	816
CDRH1-24	CDRH1-22	ggnttycanttywsnwsntaygayatgcay	817
CDRH1-25	CDRH1-23	ggnttycanttywsnwsntaygayatgcay	817
CDRH1-26	CDRH1-12	ggnttycanttywsnwsntayggnatgcay	816
CDRH1-27	CDRH1-5	ggnttycanttywsnwsntayggnatgcay	816
CDRH1-28	CDRH1-15	ggnttycanttywsnwsntayggnatgcay	816
CDRH1-29	CDRH1-7	ggnttycanttywsnwsntayggnatgcay	816
CDRH1-30	CDRH1-61	ggnttycanttymgnwsncayggnatgcay	818
CDRH1-31	CDRH1-39	ggnttycanttywsngcntaywsnatgaay	819
CDRH1-32	CDRH1-34	ggnttycanttywsnwsntaywsnatgaay	820
CDRH1-33	CDRH1-6	ggnttycanttywsnwsntaywsnatgaay	820
CDRH1-34	CDRH1-35	ggnttycanttywsnwsntaywsnatgaay	820
CDRH1-35	CDRH1-21	ggnggnwsngtnwsnwsnggnggntaytaytggwsn	821
CDRH1-36	CDRH1-8	ggnggnwsnathwsnmgnggnggntaytaytggwsn	822
CDRH1-37	CDRH1-9	ggnggnwsnathwsnmgnggnggntaytaytggwsn	822
CDRH1-38	CDRH1-18	ggnggnwsnathwsnwsnggnggntaytaytggwsn	823

FIGURA 19A

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
CDRH1-39	CDRH1-24	ggnggnwsnathwsnwsnggnggntaytaytggwsn	823
CDRH1-40	CDRH1-25	ggnggnwsnathwsnwsnggnggntaytaytggwsn	823
CDRH1-41	CDRH1-26	ggnggnwsnathwsnwsnggnggntaytaytggwsn	823
CDRH1-42	CDRH1-27	ggnggnwsnathwsnwsnggnggntaytaytggwsn	823
CDRH1-43	CDRH1-38	ggnggnwsnathwsnwsnggnggntaytaytggwsn	823
CDRH1-44	CDRH1-54	ggnggnwsnathwsnwsnggngaytaytaytggaay	824
CDRH1-45	CDRH1-55	ggnggnwsnathwsnwsnggngaytaytaytggaay	824
CDRH1-46	CDRH1-43	ggnggnwsnttywsnggntaytaytggwsn	825
CDRH1-47	CDRH1-44	ggnggnwsnttywsnggntaytaytggwsn	825
CDRH1-48	CDRH1-49	ggnggnwsnttywsnggntaytaytggwsn	825
CDRH1-49	CDRH1-50	ggnggnwsnttywsnggntaytaytggwsn	825
CDRH1-50	CDRH1-53	ggnggnwsnttywsnggntaytaytggwsn	825
CDRH1-51	CDRH1-33	ggnggnwsnathwsnwsntaytaytggwsn	826
CDRH1-52	CDRH1-3	ggnggnwsngtnwsnwsnggnggnwsntaytggwsn	827
CDRH1-53	CDRH1-4	ggnggnwsngtnwsnwsnggnggnwsntaytggwsn	827
CDRH1-54	CDRH1-16	ggntaymgnttycanwsntaytggathggn	828
CDRH1-55	CDRH1-17	ggntaywsnttycanwsntaytggathggn	829
CDRH1-56	CDRH1-11	ggntaywsnttycanwsntaytggathggn	829
CDRH1-57	CDRH1-37	ggngaywsngtnwsnwsntaywsngcngcntggaay	830
CDRH1-58	CDRH1-39.1	ggnttycanttywsngcntaywsnatgaay	819
CDRH2-1	CDRH2-10.1	tggathwsngcnwsnaayggnaaycanaaytaygcncaraar ytncargay	831
CDRH2-2	CDRH2-10	tggathwsngcnwsnaayggnaaycanaaytaygcncaraar ytncargay	831
CDRH2-3	CDRH2-42	tggathaayccnaaywsnggnggncanaaytgygcncaraar ttycarggn	832
CDRH2-4	CDRH2-40	tggathaayccnaaywsnggnggncanaaycaycancaraar ttycarggn	833
CDRH2-5	CDRH2-30	wsnttygayccngargayggngarcanathtaygcncaraar ttycarggn	834
CDRH2-6	CDRH2-31	wsnttygayccngargayggngarcanathtaygcncaraar ttycarggn	834
CDRH2-7	CDRH2-29	cayathttywsnaaygaygaraarwsntaywsncanwsnytn aarwsn	835
CDRH2-8	CDRH2-20	ytnathttywsnaaygaygaraarwsntaywsncanwsnytn aarwsn	836
CDRH2-9	CDRH2-65	ytnathtaytggaaygaygayaarmgntaywsnccnwsnytn aarwsn	837

FIGURA 19B

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
CDRH2-10	CDRH2-56	ytnathtaytggaaygaygayaarmgntaywsnccnwsnytn aarwsn	837
CDRH2-11	CDRH2-62	ytnathtaytggaaygaygayaarmgntaywsnccnwsnytn aarwsn	837
CDRH2-12	CDRH2-2	ytnathtaytggaaygaygayaarmgntaywsnccnwsnytn aarwsn	837
CDRH2-13	CDRH2-59	ytnathtaytggaaygtngaraarmgntaywsnccnwsnytn mgnwsn	838
CDRH2-14	CDRH2-57	ytnathtaytggaaygaygayaarmgntaywsnccnwsnytn aarwsn	837
CDRH2-15	CDRH2-64	ytnathtaytggaaygaygayaarmgntaywsnccnwsnytn aarwsn	837
CDRH2-16	CDRH2-41	gcnathwsnwsnwsnwsntayathtaytaygcngaywsn gtnaarggn	839
CDRH2-17	CDRH2-45	gcnathwsnggnwsnggnggnwsncantaytaygcngaywsn gtnaarggn	840
CDRH2-18	CDRH2-47	gcnathwsnggnwsnggnggnwsncantaytaygcngaywsn gtnaarggn	840
CDRH2-19	CDRH2-51	gcnathwsnggnwsnggnggnwsncantaytaygcngaywsn gtnaarggn	840
CDRH2-20	CDRH2-52	gcnathwsnggnwsnggnggnwsncantaytaygcngaywsn gtnaarggn	840
CDRH2-21	CDRH2-13	ttyathwsngaygayggnwsncanaartaytaygcngaywsn gtnaarggn	841
CDRH2-22	CDRH2-14	ttyathwsngaygayggnwsncanaartaytaygcngaywsn gtnaarggn	841
CDRH2-23	CDRH2-1	gtnathtggtaygayggnwsnaayaartaytaygcngaywsn gtnaarggn	842
CDRH2-24	CDRH2-22	gtnathtggtaygayggnwsnathaartaytaygcngaywsn gtnaarggn	843
CDRH2-25	CDRH2-23	gtnathtggtaygayggnwsnathaartaytaygcngaywsn gtnaarggn	843
CDRH2-26	CDRH2-12	gtnathtggtaygayggnwsnaayaartaytaygcngaywsn gtnaarggn	842
CDRH2-27	CDRH2-5	gtnathtggwsngayggnwsnaayaartaytaygcngaywsn gtnaarggn	844
CDRH2-28	CDRH2-15	gtnathtgggaygayggnwsnaaycartaytaycangaywsn gtnaarggn	845

FIGURA 19C

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
CDRH2-29	CDRH2-7	gtnathtggtaygayggnwsnaayaarmgntaygtngaywsn gtnaarggn	846
CDRH2-30	CDRH2-61	gtnathtggtaygayggnwsnaayaaraaytaygcngaywsn gtnmgnggn	847
CDRH2-31	CDRH2-39	tayathwsnwsnwsnggnmgncanathtaytaygcngaywsn gtnaarggn	848
CDRH2-32	CDRH2-34	cayathwsnwsnwsnwsnmgncanathtaytaygcngaywsn gtnaarggn	849
CDRH2-33	CDRH2-6	cayathwsnmgnwsnwsnmgncanathtaytaygcngaywsn gtnaarggn	850
CDRH2-34	CDRH2-35	cayathwsnmgnwsnwsnmgncanathtaytaygcngaywsn gtnaarggn	850
CDRH2-35	CDRH2-21	tayathcaywsnwsnggnwsncantaytayaayccnwsnytn aarwsn	851
CDRH2-36	CDRH2-8	tayathtaycaywsnggnwsncantaytayaayccnwsnytn aarwsn	852
CDRH2-37	CDRH2-9	tayathtaycaywsnggnwsncantaytayaayccnwsnytn aarwsn	852
CDRH2-38	CDRH2-18	tayathtaytaywsnggnwsncantaytayaayccnwsnytn aarwsn	853
CDRH2-39	CDRH2-24	tayathcaytaywsnggnwsncantaytayaayccnwsnytn aarwsn	854
CDRH2-40	CDRH2-25	tayathcaytaywsnggnwsncantaytayaayccnwsnytn aarwsn	854
CDRH2-41	CDRH2-26	tayathcaywsnwsnggnwsncantaytayaayccnwsnytn aarwsn	851
CDRH2-42	CDRH2-27	tayathcaywsnwsnggnwsncantaytayaayccnwsnytn aarwsn	851
CDRH2-43	CDRH2-38	tayathcaytaywsnggnwsncantaytayaayccnwsnytn aarwsn	854
CDRH2-44	CDRH2-54	tayathtaytaywsnggnggncantaytayaayccnwsnytn aarwsn	855
CDRH2-45	CDRH2-55	tayathtaytaywsnggnggncantaytayaayccnwsnytn aarwsn	855
CDRH2-46	CDRH2-43	garathaaycaywsnggnwsncanaaytayaayccnwsnytn aarwsn	856
CDRH2-47	CDRH2-44	garathaaycaywsnggnwsncanaaytayaayccnwsnytn aarwsn	856

FIGURA 19D

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
CDRH2-48	CDRH2-49	garathaaycaywsnggnwsncanaaytayaayccnwsnytn aarwsn	856
CDRH2-49	CDRH2-50	garathaaycaywsnggnwsncanaaytayaayccnwsnytn aarwsn	856
CDRH2-50	CDRH2-53	garathaaycaywsnggnwsncanaaytayaayccnwsnytn aarwsn	856
CDRH2-51	CDRH2-33	mgnathtaycanwsnggncancanaaytayaayccnwsnytn aarwsn	857
CDRH2-52	CDRH2-3	tayathtaytaywsnggnwsncanaaytayaayccnwsnytn aarwsn	858
CDRH2-53	CDRH2-4	tayathtaytaywsnggnwsncanaaytayaayccnwsnytn aarwsn	858
CDRH2-54	CDRH2-16	athathtayccngaygaywsngaycanmgntaywsnccnwsn ttycarggn	859
CDRH2-55	CDRH2-17	athathtayccngaygaywsngaygcnmgntaywsnccnwsn ttycarggn	860
CDRH2-56	CDRH2-11	athathtayccnggngaywsngayathmgntaywsnccnwsn ttycarggn	861
CDRH2-57	CDRH2-37	mgncantaytgymgnwsnaartggtayaaygaytaygcngtn wsngtnaarwsn	862
CDRH2-58	CDRH2-39.1	tayathwsnwsnwsnggnmgncanathtaytaygcngaywsn gtnaarggn	848
CDRH3-1	CDRH3-10.1	gargayaaytggaaytayggnttyttygaytay	863
CDRH3-2	CDRH3-10	gargayaaytggaaytayggnttyttygaytay	863
CDRH3-3	CDRH3-42	wsnathgcngtngcnytngaytay	864
CDRH3-4	CDRH3-40	wsnathgcngtngcnytngaytay	864
CDRH3-5	CDRH3-30	garggngayggnggntaytaytaytayggnatggaygtn	865
CDRH3-6	CDRH3-31	garggngayggnggntaytaytaytayggnatggaygtn	865
CDRH3-7	CDRH3-29	atgtaywsnwsnggntggtayggngtnttygaytay	866
CDRH3-8	CDRH3-20	gtntaywsnwsnggntggwsnttytayggnatggaygtn	867
CDRH3-9	CDRH3-65	mgnmgngarytnccnttygaytay	868
CDRH3-10	CDRH3-56	mgnaaytggcanccnttygaytay	869
CDRH3-11	CDRH3-62	mgnytngarytnccnttygaytay	870
CDRH3-12	CDRH3-2	mgnmgngargtnccnttygaytay	871
CDRH3-13	CDRH3-59	mgncaycanaayccnttygartay	872
CDRH3-14	CDRH3-57	mgnggngarytnccnttygaytay	873
CDRH3-15	CDRH3-64	mgnggngarytnccnttygaytay	873
CDRH3-16	CDRH3-41	gaymgngtnggngcncanccngaygcnttygayath	874

FIGURA 19E

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
CDRH3-17	CDRH3-45	garggnathgcngtngcnggncangcngartaytaytaytay taygcnatggaygtn	875
CDRH3-18	CDRH3-47	garggnathgcngcnmgngaywsntaytaytaytaygcnatg gaygtn	876
CDRH3-19	CDRH3-51	garggnathgcnggnmgngaywsntaytaytaytayggnatg gaygtn	877
CDRH3-20	CDRH3-52	garggnathgcnggnmgngaywsntaytaytaytayggnatg gaygtn	877
CDRH3-21	CDRH3-13	wsntaytaygaywsnwsnggntaytaytayggnttygaytay	878
CDRH3-22	CDRH3-14	wsntaytaygaywsnwsnggntaytaytayggnttygaytay	878
CDRH3-23	CDRH3-1	aaygtnathgaytay	879
CDRH3-24	CDRH3-22	ggnggngcncanggngcngartayttycarcay	880
CDRH3-25	CDRH3-23	ggnggngcncanggngcngartayttycarcay	880
CDRH3-26	CDRH3-12	ytntggttyggngarcanttygaytay	881
CDRH3-27	CDRH3-5	aayytnccnttygaytay	882
CDRH3-28	CDRH3-15	wsncaytayggnggngaytaygaytaytayggnatggaygtn	883
CDRH3-29	CDRH3-7	gayggntggcarcarcargcnccnttygaytay	884
CDRH3-30	CDRH3-61	tggggnathwsngcnccnttygaytgy	885
CDRH3-31	CDRH3-39	tgggcnccnttygaytay	886
CDRH3-32	CDRH3-34	gayggntayaaytggaayggnggnggnaaytaytayggnatg gaygtn	887
CDRH3-33	CDRH3-6	gayggntayaaytggaayaayggnggntaytaytayggnatg gaygtn	888
CDRH3-34	CDRH3-35	gayggntayaaytggaayaayggnggntaytaytayggnatg gaygtn	888
CDRH3-35	CDRH3-21	ggnccntaytayggnatggaygtn	889
CDRH3-36	CDRH3-8	gcnytnmgnggnathgtnytnatggtntaygtnytnggngcn ytngayath	890
CDRH3-37	CDRH3-9	gcnytnmgnggnathgtnytnatggtntaygtnytnggngcn ytngayath	890
CDRH3-38	CDRH3-18	gaygarcangtngtnmgnggnytnathmgntaytgytayggn atggaygtn	891
CDRH3-39	CDRH3-24	gaymgnggnggnggngaytayggnmgnatggaygtn	892
CDRH3-40	CDRH3-25	gaymgnggnggnggngaytayggnmgnatggaygtn	892
CDRH3-41	CDRH3-26	wsnaayaaytayggntgyttygcnytn	893
CDRH3-42	CDRH3-27	wsnaayaaytayggntgyttygcnytn	893
CDRH3-43	CDRH3-38	ggntayaaytayggnytntaytaytaygaywsnwsnggntay ccnwsntaytaytayggnatggaygtn	894
CDRH3-44	CDRH3-54	cantaytaygayathytncanggntayccnttytayttygay tay	895

FIGURA 19F

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
CDRH3-45	CDRH3-55	cantaytaygayathytncanggntayccnttytayttygay tay	895
CDRH3-46	CDRH3-43	ggnggntaywsnwsnwsntggtaytggttygayccn	896
CDRH3-47	CDRH3-44	ggnggntaywsnwsnwsntggttytggttygayccn	897
CDRH3-48	CDRH3-49	ggnggntaywsnwsnwsntggttytggttygayccn	897
CDRH3-49	CDRH3-50	ggnggntaywsnwsnwsntggttytggttygayccn	897
CDRH3-50	CDRH3-53	ggnggntaywsnwsnwsntggttytggttygayccn	897
CDRH3-51	CDRH3-33	gayggntaywsntayggncaytaytaytaytayggnatggay gtn	898
CDRH3-52	CDRH3-3	wsngcnytnmgntayttygaytggytnttywsngaygtnwsn gayath	899
CDRH3-53	CDRH3-4	wsngcnytnmgntayttygaytggytnttywsngaygtnwsn gayath	899
CDRH3-54	CDRH3-16	caraarwsntayggntaywsntayttygaytay	900
CDRH3-55	CDRH3-17	carggntayggnwsnggntggggntayttygaytay	901
CDRH3-56	CDRH3-11	carggnytngcngtngcnggncanwsntaytaytaytaytay ggnatggaygtn	902
CDRH3-57	CDRH3-37	gaymgngcngtngcnggntaytaytayggnatggaygtn	903
CDRH3-58	CDRH3-39.1	tgggcnccnttygaytay	886

FIGURA 19G

SECUENCIAS DE NUCLEÓTIDOS DE FR
DE LA CADENA LIGERA

NOMBRE	SECUENCIA	SEQ ID NO:
FRL1-1	gaygtngtnatgcancarwsnccnytnwsnytnccngtncanytnggn carccngcnwsnathwsntgy	919
FRL1-2	gaygtngtnatgcancarwsnccnytnwsnytnccngtncanytnggn carccngcnwsnathwsntgy	919
FRL1-3	gaygtngtnatgcancarwsnccnytnwsnytnccngtncanytnggn carccngcnwsnathwsntgy	920
FRL1-4	gaygtngtnatgcancarwsnccnytnwsnytnccngtncanytnggn carccngcnwsnathwsntgy	920
FRL1-5	gayathgtnatgcancarcanccnytnwsnytnwsngtncanccnggn carccngcnwsnathwsntgy	921
FRL1-6	gayathgtnatgcancarcanccnytnwsnytnwsngtncanccnggn carccngcnwsnathwsntgy	921
FRL1-7	gayathgtnatgcancarcanccnytnwsnytnwsngtncanccnggn carccngcnwsnathwsntgy	921
FRL1-8	gayathgtnatgcancarcanccnytnwsnytnwsngtncanccnggn carccngcnwsnathwsntgy	922
FRL1-9	gayathgtnatgcancarcanccnytnwsnytnwsngtncanccnggn carccngcnwsnathwsntgy	922
FRL1-11	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	923
FRL1-12	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathathtgy	923
FRL1-13	aayathgtnatgcancarcanccnytnwsnwsnccngtncanytnggn carccngcnwsnathwsntgy	924
FRL1-14	aayathgtnatgcancarcanccnytnwsnwsnccngtncanytnggn carccngcnwsnathwsntgy	924
FRL1-15	garathgtnatgcancarcanccnytnwsnwsnccngtncanytnggn carccngcnwsnathwsntgy	924
FRL1-16	garathgtnytncancarwsnccnggncanytnwsnytnwsnccnggn garmgngcncanytnwsntgy	925
FRL1-17	garathgtnytncancarwsnccnggncanytnwsnytnwsnccnggn garmgngcncanytnwsntgy	926
FRL1-18	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	927
FRL1-19	gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggn garmgngcncanathaaytgy	928

FIGURA 20A

NOMBRE	SECUENCIA	SEQ ID NO:
FRL1-20	gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggn garmgngcncanathaaytgy	928
FRL1-21	gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggn garmgngcncanathaaytgy	929
FRL1-22	gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggn garmgngcncanathaaytgy	929
FRL1-23	gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggn garmgngcncanathaaytgy	929
FRL1-24	gayathgtnatgcancarwsnccngaywsnytncangtnwsnytnggn garmgngcncanathaaytgy	929
FRL1-25	gayathgtnatgcancarwsnccngaywsnytncangtnwsnytnggn garmgngcncanathaaytgy	929
FRL1-26	gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggn garmgngcncanathaaytgy	929
FRL1-27	gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggn garmgngcncanathaaytgy	929
FRL1-28	gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggn garmgngcncanathaaytgy	930
FRL1-29	gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggn garmgngcncanathaaytgy	930
FRL1-30	gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggn garmgngcncanathaaytgy	929
FRL1-31	gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggn garmgngcncanathaaytgy	929
FRL1-32	gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggn garmgngcncanathaaytgy	929
FRL1-33	gayathgtnatgcancarwsnccngaywsnytngcngtnwsnytnggn garmgngcncanathaaytgy	929
FRL1-34	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	931
FRL1-35	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtngcnathcantgy	932
FRL1-36	garathgtnatgcancarwsnccngcncanytnwsngtnwsnccnggn garmgngcncanytnwsntgy	933
FRL1-37	garathgtnatgcancarwsnccngcncanytnwsngtnwsnccnggn garmgngcncanytnwsntgy	933
FRL1-38	gayathcaratgcancarwsnccnwsnwsngtnwsngcnwsngtnggn gaymgngtncanathcantgy	934

FIGURA 20B

NOMBRE	SECUENCIA	SEQ ID NO:
FRL1-39	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	935
FRL1-40	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsnytnggn gaymgngtncanathcantgy	934
FRL1-41	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	936
FRL1-42	gayathcaratgcancarwsnccnwsnwsnmgnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-43	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	937
FRL1-44	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-45	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-46	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-47	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-48	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-49	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-50	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-51	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-52	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-53	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-54	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-55	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-56	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	938
FRL1-57	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934

FIGURA 20C

NOMBRE	SECUENCIA	SEQ ID NO:
FRL1-58	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtngcnathcantgy	934
FRL1-59	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtngcnathcantgy	934
FRL1-60	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-61	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-62	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gayggngtncanathcantgy	934
FRL1-63	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	939
FRL1-64	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL1-65	gayathcaratgcancarwsnccnwsnwsnytnwsngcnwsngtnggn gaymgngtncanathcantgy	934
FRL2-1	tggttycarcarmgnccnggncarwsnccnmgnmgnytnathtay	939
FRL2-2	tggttycarcarmgnccnggncarwsnccnmgnmgnytnathtay	939
FRL2-3	tggytncarcarmgnccnggncarwsnccnmgnmgnytnathtay	940
FRL2-4	tggytncarcarmgnccnggncarwsnccnmgnmgnytnathtay	940
FRL2-5	tggtayytncaraarccnggncarccnccncarytnytnathtay	941
FRL2-6	tggtayytncaraarccnggncarccnccncarytnytnathtay	941
FRL2-7	tggtayytncaraarccnggncarccnccncarytnytnathtay	941
FRL2-8	tggttyytncaraarccnggncarccnccncarccnytnathtay	942
FRL2-9	tggttyytncaraarccnggncarccnccncarccnytnathtay	942
FRL2-11	tggtaycarcaraarccnggnaargtnccnaarytnytnathtay	943
FRL2-12	tggtaycarcaraarccnggnaargtnccnaarytnytnathtay	943
FRL2-13	tggytncarcarmgnccnggncarccnccnmgnytnytnathtay	944
FRL2-14	tggytncarcarmgnccnggncarccnccnmgnytnytnathtay	944
FRL2-15	tggytncarcarmgnccnggncarccnccnmgnytnytnathtay	944
FRL2-16	tggtaycarcaraarccnggncargcnccnmgnytnytnathwsn	945
FRL2-17	tggtaycarcaraarccnggncargcnccnmgnytnytnathtay	946
FRL2-18	tggtaycarcaraarccnggnaargcnccnaarmgnytnathtay	947
FRL2-19	tggtaycarcaraarccnggncarccnccnaarytnttyathtay	948
FRL2-20	tggtaycarcaraarccnggncarccnccnaarytnttyathtay	948
FRL2-21	tggtaycarcaraarccnggncarccnccnaarytnytnathtay	949
FRL2-22	tggtaycarcaraarccnggncarccnccnaarytnytnathtay	949
FRL2-23	tggtaycarcaraarccnggncarccnccnaarytnytnathtay	949

FIGURA 20D

NOMBRE	SECUENCIA	SEQ ID NO:
FRL2-24	tggtaycarcaraarccnggncarccnccnaarytnytnathtay	949
FRL2-25	tggtaycarcaraarccnggncarccnccnaarytnytnathtay	949
FRL2-26	tggtaycarcaraarccnggncarccnccnaarytnytnathtay	949
FRL2-27	tggtaycarcaraarccnggncarccnccnaarytnytnathtay	949
FRL2-28	tggtaycarcaraarccnggncarccnccnaargtnytnathtay	950
FRL2-29	tggtaycarcaraarccnggncarccnccnaargtnytnathtay	950
FRL2-30	tggtaycarcaraarccnggncarccnccnaarytnytnathtay	949
FRL2-31	tggtaycarcaraarccnggncarccnccnaarytnytnathtay	949
FRL2-32	tggtaycarcaraarccnggncarccnccnaarytnytnathtay	949
FRL2-33	tggtaycarcaraarccnggncarccnccnaarytnytnathtay	949
FRL2-34	tggttycarcaraarccnggnaargcnccnaarwsnytnathtay	951
FRL2-35	tggytncarcaraarccnggnaargcnccnaarwsnytnathtay	952
FRL2-36	tggtaycarcargayccnggncargcnccnmgnytnytnathtay	953
FRL2-37	tggtaycarcargayccnggncargcnccnmgnytnytnathtay	953
FRL2-38	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-39	tggtaycarcaraarccnggnaargcnccnaarttyytnathtay	955
FRL2-40	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-41	tggtaycarcarmgnccnggnaaygcnccnaarytnytnathtay	956
FRL2-42	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-43	tggtaycarcaraarccnggnaargcnccnaargtnytnathtay	957
FRL2-44	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-45	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-46	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-47	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-48	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-49	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-50	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-51	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-52	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-53	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-54	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-55	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-56	tggtaycarcaraarccnggnaargcnccngarytnytnathtay	958
FRL2-57	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-58	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-59	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954

FIGURA 20E

NOMBRE	SECUENCIA	SEQ ID NO:
FRL2-60	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-61	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-62	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-63	tggtaycarcaraarytnggnaargcnccnaarytnytnathcay	959
FRL2-64	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL2-65	tggtaycarcaraarccnggnaargcnccnaarytnytnathtay	954
FRL3-1	ggngtnccngaymgnttyaayggnwsnggnwsnggncangayttycan ytnaarathwsnmgngtngargcngargaygtnggngtntaytaytgy	960
FRL3-2	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytnaarathwsnmgngtngargcngargaygtnggngtntaytaytgy	961
FRL3-3	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytnaarathwsnmgngtngargcngargaygtnggngtntaytaytgy	961
FRL3-4	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytnaarathwsnmgngtngargcngargaygtnggngtntaytaytgy	961
FRL3-5	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytnaarathwsnmgngtngargcngargaygtnggngtntaytaytgy	961
FRL3-6	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytnaarathwsnmgngtngargcngargaygtnggngtntaytaytgy	961
FRL3-7	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytnaarathwsnmgngtngargcngargaygtnggngtntaytaytgy	961
FRL3-8	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytnaarathwsnmgngtngargcngargaygtnggngtntaytaytgy	961
FRL3-9	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytnaarathwsnmgngtngargcngargaygtnggngtntaytaytgy	961
FRL3-11	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargaygtngcncantaytaytgy	962
FRL3-12	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargaygtngcncantaytaytgy	962
FRL3-13	ggngtnccngaymgnttywsnggnwsnggngcnggncangayttycan ytnaarathwsnmgngtngargcngargaygtnggngtntaytaytgy	963
FRL3-14	ggngtnccngaymgnttywsnggnwsnggngcnggncangayttycan ytnaarathwsnmgngtngargcngargaygtnggngtntaytaytgy	963
FRL3-15	ggngtnccngaymgnttywsnggncanggngcnggncangayttycan ytnaarathwsnmgngtngargcngargaygtnggngtntaytaytgy	964
FRL3-16	ggnathccngaymgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnmgnytngarccngargayttygcngtntaytaytgy	965
FRL3-17	ggnathccngaymgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnmgnytngarccngargayttygcngtntaytaytgy	965

FIGURA 20F

NOMBRE	SECUENCIA	SEQ ID NO:
FRL3-18	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangarttycan ytncanathwsnwsnytncarccngargayttygcncantaytaytgy	966
FRL3-19	ggngtnccngaymgnttycanggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncargcngargaygtngcngtntaytaytgy	967
FRL3-20	ggngtnccngaymgnttycanggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncargcngargaygtngcngtntaytaytgy	967
FRL3-21	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncargcngargaygtngcngtntaytaytgy	968
FRL3-22	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncargcngargaygtngcngtntayttytgy	969
FRL3-23	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncargcngargaygtngcngtntayttytgy	969
FRL3-24	ggngtnccngaymgnttyggnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncargcngargaygtngcngtntaytaytgy	970
FRL3-25	ggngtnccngaymgnttyggnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncargcngargaygtngcngtntaytaytgy	970
FRL3-26	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncargcngaygaygtngcngtntaytaytgy	971
FRL3-27	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncargcngaygaygtngcngtntaytaytgy	971
FRL3-28	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnggnytncargcngargaygtngcnytntaytaytgy	972
FRL3-29	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnggnytncargcngargaygtngcnytntaytaytgy	972
FRL3-30	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncargcngargaygtngcngtnttytaytgy	973
FRL3-31	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncargcngargaygtngcngtnttytaytgy	973
FRL3-32	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncargcngargaygtngcngtntayttytgy	969
FRL3-33	ggngtnccngaymgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncargcngargaygtngcngtntayttytgy	969
FRL3-34	ggngtnccnwsnaarttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargayttygcncantaytaytgy	974
FRL3-35	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargayttygcncantaytaytgy	975
FRL3-36	ggnathccngcnmgnttywsnggnwsnggnwsnggncangarttycan ytncanathwsnwsnytncarwsngargayttygcngtntaytaytgy	976

FIGURA 20G

NOMBRE	SECUENCIA	SEQ ID NO:
FRL3-37	ggnathccngcnmgnttywsnggnwsnggnwsnggncangarttycan ytncanathwsnwsnytncarwsngargayttygcngtntaytaytgy	976
FRL3-38	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargayttygcncantaytaytgy	975
FRL3-39	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargayttygcngcntaytaytgy	977
FRL3-40	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargayttygcncantaytaytgy	975
FRL3-41	ggngtnccnwsnmgngtnwsnggnwsnggnwsnggncangayttycan ytncanathmgnwsnytncarccngargayttygcncantaytaytgy	978
FRL3-42	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanytnwsnwsnytncarccngargayttygcncantaytaytgy	979
FRL3-43	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargayttygcncantaytaytgy	975
FRL3-44	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngaraayttygcncantaytaytgy	980
FRL3-45	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanttywsnwsnytncarccngargayttygcncantaytaytgy	981
FRL3-46	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanytnwsnwsnytncarccngargayttygcnwsntaytaytgy	982
FRL3-47	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanytnwsnwsnytncarccngargayttygcnwsntaytaytgy	982
FRL3-48	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargayttygcncantaytaytgy	975
FRL3-49	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargayttygcncantaytaytgy	975
FRL3-50	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargayttygcncantaytaytgy	975
FRL3-51	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargayttygcnwsntaytaytgy	983
FRL3-52	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargayttygcnwsntaytaytgy	983
FRL3-53	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ytncanathwsnwsnytncarccngargayttygcncantaytaytgy	975
FRL3-54	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ttycanathwsnwsnytncarccngargayathgcncantaytaytgy	984
FRL3-55	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ttycanathwsnwsnytncarccngargayathgcncantaytaytgy	984

FIGURA 20H

NOMBRE	SECUENCIA	SEQ ID NO:
FRL3-56	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ttycanathwsnwsnytncarccngargayathgcncantaytaytgy	984
FRL3-57	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ttycanathwsnwsnytncarccngargayathgcncantaytaytgy	984
FRL3-58	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ttycanathwsnwsnytncarccngargayathgcncantaytaytgy	984
FRL3-59	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ttycanathwsnwsnytncarccngargayathgcncantaytaytgy	984
FRL3-60	ggngtnccnwsnmgnttywsnggnwsnggnwsngarcangayttycan ttycanathwsnwsnytncarccngargayathgcncantaytaytgy	985
FRL3-61	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ttycanathwsnwsnytncarccngargayathgcncantaytaytgy	984
FRL3-62	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ttycanathwsnwsnytncarccngargayathgcncantaytaytgy	984
FRL3-63	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ttycanathwsnwsnytncarccngargayathgcncantaytaytgy	984
FRL3-64	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ttycanathwsnwsnytncarccngargayathgcncantaytaytgy	984
FRL3-65	ggngtnccnwsnmgnttywsnggnwsnggnwsnggncangayttycan ttycanathwsnwsnytncarccngargayathgcncantaytaytgy	984
FRL4-1	ttyggncarggncanmgnytngarathaar	986
FRL4-2	ttyggncarggncanmgnytngarathaar	986
FRL4-3	ttyggncarggncanmgnytngarathaar	986
FRL4-4	ttyggncarggncanmgnytngarathaar	986
FRL4-5	ttyggncarggncanaarytngarathaar	988
FRL4-6	ttyggnggnggncanaargtngarathaar	989
FRL4-7	ttyggnggnggncanaargtngarathaar	989
FRL4-8	ttyggncayggncanmgnytngarathaar	990
FRL4-9	ttyggncayggncanmgnytngarathaar	990
FRL4-11	ttyggnccnggncanaargtngayathaar	991
FRL4-12	ttyggnggnggncanaargtngarathaar	989
FRL4-13	ttyggnccnggncanaargtngayathaar	991
FRL4-14	ttyggnccnggncanaargtngayathaar	991
FRL4-15	ttyggnggnggncanaargtngarathaar	989
FRL4-16	ttyggncarggncanaargtngarathaar	992
FRL4-17	ttyggncarggncanaarytngarathaar	988
FRL4-18	ttyggncarggncanaargtngarathaar	992
FRL4-19	ttyggncarggncanaargtngarathaar	992
FRL4-20	ttyggncarggncanaargtngarathaar	992

FIGURA 20I

NOMBRE	SECUENCIA	SEQ ID NO:
FRL4-21	ttyggncarggncanaargtngarathaar	992
FRL4-22	ttyggncarggncanaargtngarathaar	992
FRL4-23	ttyggncarggncanaargtngarathaar	992
FRL4-24	ttyggncarggncanaargtngarathaar	992
FRL4-25	ttyggncarggncanaargtngarathaar	992
FRL4-26	ttyggnccnggncanaargtngarathaar	993
FRL4-27	ttyggnccnggncanaargtngarathaar	993
FRL4-28	ttyggncarggncanaarytngarathaar	988
FRL4-29	ttyggncarggncanaarytngarathaar	988
FRL4-30	ttyggnggnggncanaargtngcnathaar	994
FRL4-31	ttyggnggnggncanaargtngcnathaar	994
FRL4-32	ttyggnggnggncanaargtngarathaar	989
FRL4-33	ttyggnggnggncanaargtngarathaar	989
FRL4-34	ttyggnccnggncanaargtngayathaar	991
FRL4-35	ttyggnccnggncanaaratggayathaar	995
FRL4-36	ttyggncarggncanaargtngarathaar	992
FRL4-37	ttyggncarggncanaargtngarathaar	992
FRL4-38	ttyggncarggncanaargtngarttyaar	996
FRL4-39	ttyggnccnggncanaargtngayathaar	991
FRL4-40	ttyggnggnggncanaargtngarathaar	989
FRL4-41	ttyggnggnggncanaargtngarathaar	989
FRL4-42	ttyggncarggncanmgnytngarathaar	986
FRL4-43	ttyggncarggncanmgnytngarathath	987
FRL4-44	ttyggncarggncanmgnytngarathaar	986
FRL4-45	ttyggncarggncanmgnytngarathaar	986
FRL4-46	ttyggncarggncanmgnytngarathaar	986
FRL4-47	ttyggncarggncanmgnytngarathaar	986
FRL4-48	ttyggncarggncanmgnytngarathaar	986
FRL4-49	ttyggncarggncanmgnytngarathaar	986
FRL4-50	ttyggncarggncanmgnytngarathaar	986
FRL4-51	ttyggncarggncanmgnytngarathaar	986
FRL4-52	ttyggncarggncanmgnytngarathaar	986
FRL4-53	ttyggncarggncanmgnytngarathaar	986
FRL4-54	ttyggnccnggncanaargtngayathaar	991
FRL4-55	ttyggnccnggncanaargtngayathaar	991
FRL4-56	ttyggnggnggncanaargtngarathaar	989

FIGURA 20J

NOMBRE	SECUENCIA	SEQ ID NO:
FRL4-57	ttyggnggnggncanaargtngarathaar	989
FRL4-58	ttyggnggnggncanaargtngarathaar	989
FRL4-59	ttyggnggnggncanaargtngarathaar	989
FRL4-60	ttyggnggnggncanaargtngarathaar	989
FRL4-61	ttyggnggnggncanaargtngarathmgn	997
FRL4-62	ttyggncarggncanmgnytngarathaar	986
FRL4-63	ttyggncarggncanmgnytngarathaar	986
FRL4-64	ttyggncarggncanmgnytngarathaar	986
FRL4-65	ttyggncarggncanmgnytngarathaar	986

FIGURA 20K

SECUENCIAS DE NUCLEÓTIDOS DE FR DE LA CADENA PESADA

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
FRH1-1	FRH1-1	cargtncarytngtncarwsnggngcngargtnaaraarccngg ngcnwsngtnaargtnwsntgyaargcnwsn	998
FRH1-2	FRH1-2	cargtncarytngtncarwsnggngcngargtnaaraarccngg ngcnwsngtnaargtnwsntgyaargcnwsn	998
FRH1-3	FRH1-3	cargtncayytngtncarwsnggngcngargtnaaraarccngg ngcnwsngtnaargtnwsntgyaargtnwsn	999
FRH1-4	FRH1-4	cargtncarytngtncarwsnggngcngargtnaaraarccngg ngcnwsngtnaargtnwsntgyaargcnwsn	998
FRH1-5	FRH1-5	cargtncarytngtncarwsnggngcngargtnmgnaarccngg ngcnwsngtnaargtnwsntgyaargtnwsn	1000
FRH1-6	FRH1-6	cargtncarytngtncarwsnggngcngargtnmgnaarccngg ngcnwsngtnaargtnwsntgyaargtnwsn	1000
FRH1-7	FRH1-7	cargtncanytnaargarwsnggnccngtnytngtnaarccnca ngarcanytncanytncantgycangtnwsn	1001
FRH1-8	FRH1-8	cargtncanytnaargarwsnggnccngtnytngtnaarccnca ngarcanytncanytncantgycangtnwsn	1001
FRH1-9	FRH1-9	carathcanytnaargarwsnggnccncanytngtnaarccnca ncarcanytncanytncantgycanttywsn	1002
FRH1-10	FRH1-10	carathcanytnaargarwsnggnccncanytngtnaarccnca ncarcanytncanytncantgycanttywsn	1002
FRH1-11	FRH1-11	carathcanytnaargarwsnggnccncanytngtnaarccnca ncarcanytncanytncantgycanttywsn	1002
FRH1-12	FRH1-12	carathcanytnaargarwsnggnccncanytngtnaarccnca ncarcanytncanytncantgycanttywsn	1002
FRH1-13	FRH1-13	carathcanytnaargarwsnggnccncanytngtnaarccnca ncarcanytncanytncantgycanttywsn	1002
FRH1-14	FRH1-14	carathcanytnaargarwsnggnccncanytngtnaarccnca ncarcanytncanytncantgycanttywsn	1002
FRH1-15	FRH1-15	carathcanytnaargarwsnggnccncanytngtnaarccnca ncarcanytncanytncantgycanttywsn	1002
FRH1-16	FRH1-16	gargtncarytngtngarwsnggnggnggnytngtnaarccngg nggnwsnytnmgnytnwsntgygcngcnwsn	1003
FRH1-17	FRH1-17	gargtncarytnytngarwsnggnggnggnytngtncarccngg nggnwsnytnmgnytnwsntgygcngcnwsn	1004
FRH1-18	FRH1-18	gargtncarytnytngarwsnggnggnggnytngtncarccngg nggnwsnytnmgnytnwsntgygcngcnwsn	1004

FIGURA 21A

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
FRH1-19	FRH1-19	gargtncarytnytngarwsnggnggnggnytngtncarccngg nggnwsnytnmgnytnwsntgycangcnwsn	1005
FRH1-20	FRH1-20	gargtncarytnytngarwsnggnggnggnytngtncarccngg nggnwsnytnmgnytnwsntgycangcnwsn	1005
FRH1-21	FRH1-21	cargtncarytngtngarwsnggnggnggngtngtncarccngg nmgnwsnytnmgnytnwsntgygcngcnwsn	1006
FRH1-22	FRH1-22	cargtncarytngtngarwsnggnggnggngtngtncarccngg nmgnwsnytnmgnytnwsntgygcngcnwsn	1006
FRH1-23	FRH1-23	cargtncarytngtngarwsnggnggnggngtngtncarccngg nmgnwsnytnmgnytnwsntgygcngcnwsn	1006
FRH1-24	FRH1-24	cargtncarytngtngarwsnggnggnggngtngtncarccngg nmgnwsnytnmgnytnwsntgygcngcnwsn	1006
FRH1-25	FRH1-25	cargtncarytngtngarwsnggnggnggngtngtncarccngg nmgnwsnytnmgnytnwsntgygcngcnwsn	1006
FRH1-26	FRH1-26	cargtncarytngtngarwsnggnggnggngtngtncarccngg nmgnwsnytnmgnytnwsntgygcngcnwsn	1006
FRH1-27	FRH1-27	cargtncarytngtngarwsnggnggnggngtngtncarccngg nmgnwsnytnmgnytnwsntgygcngcnwsn	1006
FRH1-28	FRH1-28	cargtncarytngtngarwsnggnggnggngtngtncarccngg nmgnwsnytnmgnytnwsntgygcngcnwsn	1006
FRH1-29	FRH1-29	cargtncarytngtngarwsnggnggnggngtngtncarccngg nmgnwsnytnmgnytnwsntgygcngcnwsn	1006
FRH1-30	FRH1-30	cargtncarytngtngarwsnggnggnggngtngtncarccngg nmgnwsnytnmgnytnwsntgygcngcnwsn	1006
FRH1-31	FRH1-31	gargtncarytngtngarwsnggnggnggnytngtncarccngg nggnwsnytnmgnytnwsntgygcngcnwsn	1007
FRH1-32	FRH1-32	gargtncarytngtngarwsnggnggnggnytngtncarccngg nggnwsnytnmgnytnwsntgygcngcnwsn	1007
FRH1-33	FRH1-33	gargtncarytngtngarwsnggnggnggnytngtncarccngg nggnwsnytnmgnytnwsntgygcngcnwsn	1007
FRH1-34	FRH1-34	gargtncarytngtngarwsnggnggnggnytngtncarccngg nggnwsnytnmgnytnwsntgygcngcnwsn	1007
FRH1-35	FRH1-35	cargtncarytncargarwsnggnccnggnytngtnaarccnws ncarcanytnwsnytncantgycangtnwsn	1008
FRH1-36	FRH1-36	cargtncarytncargarwsnggnccnggnytngtnaarccnws ncarcanytnwsnytncantgycangtnwsn	1008
FRH1-37	FRH1-37	cargtncarytncargarwsnggnccnggnytngtnaarccnws ncarcanytnwsnytncantgycangtnwsn	1008

FIGURA 21B

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
FRH1-38	FRH1-38	Cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncantgycangtnwsn	1008
FRH1-39	FRH1-39	cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytnaaytgycangtnwsn	1009
FRH1-40	FRH1-40	cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytnaaytgycangtnwsn	1009
FRH1-41	FRH1-41	cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncantgycangtnwsn	1008
FRH1-42	FRH1-42	cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncantgycangtnwsn	1008
FRH1-43	FRH1-43	cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncantgycangtnwsn	1008
FRH1-44	FRH1-44	cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncantgycangtnwsn	1008
FRH1-45	FRH1-45	cargtncarytncargarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncantgycangtnwsn	1008
FRH1-46	FRH1-46	cargtncarytncarcartggggngcnggnytnytnaarccnwsngarcanytnwsnytncantgygcngtntay	1010
FRH1-47	FRH1-47	cargtncarytncarcartggggngcnggnytnytnaarccnwsngarcanytnwsnytncantgygcngtntay	1010
FRH1-48	FRH1-48	gargtncarytncarcartggggngcnggnytnytnaarccnwsngarcanytnwsnytncantgygcngtntay	1010
FRH1-49	FRH1-49	cargtncarytncarcartggggngcnggnytnytnaarccnwsngarcanytnwsnytncantgygcngtntay	1010
FRH1-50	FRH1-50	cargtncarytncarcartggggngcnggnytnytnaarccnwsngarcanytnwsnytncantgygcngtntay	1010
FRH1-51	FRH1-51	cargtncarytncargarwsnggnccnggnytngtnaarccnwsngarcanytnwsnytncantgycangtnwsn	1011
FRH1-52	FRH1-52	cargtncarytncargarwsnggnccnggnytngtnaarccnwsngarcanytnwsnytncantgycangtnwsn	1011
FRH1-53	FRH1-53	cargtncarytncargarwsnggnccnggnytngtnaarccnwsngarcanytnwsnytncantgycangtnwsn	1011
FRH1-54	FRH1-54	gargtncarytngtncarwsnggngcngarytnaaraarccnggngarwsnytnaarathwsntgyaarggnwsn	1012
FRH1-55	FRH1-55	gargtncarytngtncarwsnggngcngargtnaaraarccnggngarwsnytnaarathwsntgyaarggnwsn	1013
FRH1-56	FRH1-56	gargtncarytngtncarwsnggngcngargtnaaraarccnggngarwsnytnaarathwsntgyaarggnwsn	1013
FRH1-57	FRH1-57	cargtncarytncarcarwsnggnccnggnytngtnaarccnwsncarcanytnwsnytncantgygcnathwsn	1014
FRH1-58	FRH1-58	gargtncarytngtngarwsnggnggnggnytngtncarccngg	1007

FIGURA 21C

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
FRH2-1	FRH2-1	tgggtnmgncargcnccnggncarggnytngartggatgggn	1015
FRH2-2	FRH2-2	tgggtnmgncargcnccnggncarggnytngartggatgggn	1015
FRH2-3	FRH2-3	tgggtnmgncargcnccnggncarggnytngartggatgggn	1015
FRH2-4	FRH2-4	tgggtnmgncargcnccnggncarggnytngartggatgggn	1015
FRH2-5	FRH2-5	tgggtnmgncargcnccnggnaarggnytngartggatgggn	1016
FRH2-6	FRH2-6	tgggtnmgncargcnccnggnaarggnytngartggatgggn	1016
FRH2-7	FRH2-7	tggathmgncarccnccnggnaargcnytngartggytngcn	1017
FRH2-8	FRH2-20	tggathmgncarccnccnggnaargcnytngartggytngtn	1018
FRH2-9	FRH2-65	tggathmgncarccnccnggnaargcnytngartggytngcn	1017
FRH2-10	FRH2-56	tggathmgncarccnccnggnaargcnytngartggytngcn	1017
FRH2-11	FRH2-62	tggathmgncarccnccnggnaargcnytngartggytngcn	1017
FRH2-12	FRH2-2	tggathmgncarccnccnggnaargcnytngartggytngcn	1017
FRH2-13	FRH2-59	tggathmgncarccnccnggnaargcnytngartggytngcn	1017
FRH2-14	FRH2-57	tggathmgncarccnccnggnaargcnytngartggytngcn	1017
FRH2-15	FRH2-64	tggathmgncarccnccnggnaargcnytngartggytngcn	1017
FRH2-16	FRH2-41	Tgggtnmgncargcnccnggnaarggnytngartgggtnwsn	1019
FRH2-17	FRH2-45	tgggtnmgncargcnccnggnaarggnytngartgggtnwsn	1019
FRH2-18	FRH2-47	tgggtnmgncargcnccnggnaarggnytngartgggtnwsn	1019
FRH2-19	FRH2-51	tgggtnmgncargcnccnggnaarggnytngartgggtnwsn	1019
FRH2-20	FRH2-52	tgggtnmgncargcnccnggnaarggnytngartgggtnwsn	1019
FRH2-21	FRH2-13	tgggtnmgncargcnccnggnaarggnytngartgggtngcn	1020
FRH2-22	FRH2-14	tgggtnmgncargcnccnggnaarggnytngartgggtngcn	1020
FRH2-23	FRH2-1	tgggtnmgncargcnccnggnaarggnytngartgggtngcn	1020
FRH2-24	FRH2-22	tgggtnmgncargcnccnggnaarggnytngartgggtngcn	1020
FRH2-25	FRH2-23	tgggtnmgncargcnccnggnaarggnytngartgggtngcn	1020
FRH2-26	FRH2-12	tgggtnmgncargcnccnggnaarggnytngartgggtngcn	1020
FRH2-27	FRH2-5	tgggtnmgncargcnccnggnaarggnytngartgggtngcn	1020
FRH2-28	FRH2-15	tgggtnmgncargcnccnggnaarggnytngartgggtngcn	1020
FRH2-29	FRH2-7	tgggtnmgncargcnccnggnaarggnytngartgggtngcn	1020
FRH2-30	FRH2-61	tgggtnmgncargcnccnggnaarggnytngartgggtngcn	1020
FRH2-31	FRH2-39	tgggtnmgncargcnccnggnaarggnytngartgggtnwsn	1019
FRH2-32	FRH2-34	tgggtnmgncargcnccnggnaarggnytngartgggtnwsn	1019
FRH2-33	FRH2-6	tgggtnmgncargcnccnggnaarggnytngartgggtnwsn	1019
FRH2-34	FRH2-35	tgggtnmgncargcnccnggnaarggnytngartgggtnwsn	1019
FRH2-35	FRH2-21	tggathmgncarcayccnggnaarggnytngartggathggn	1021
FRH2-36	FRH2-8	tggathmgncarcayccnggnaarggnytngartggathggn	1021
FRH2-37	FRH2-9	tggathmgncarcayccnggnaarggnytngartggathggn	1021
FRH2-38	FRH2-18	tggathmgncarcayccnggnaarggnytngartggathggn	1021
FRH2-39	FRH2-24	tggathmgncarcayccnggnaarggnytngartggathggn	1021

FIGURA 21D

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
FRH2-40	FRH2-25	tggathmgncarcayccnggnaarggnytngartggathggn	1021
FRH2-41	FRH2-26	tggathmgncarcayccnggnaarggnytngartggathggn	1021
FRH2-42	FRH2-27	tggathmgncarcayccnggnaarggnytngartggathggn	1021
FRH2-43	FRH2-38	tggathmgncarcayccnggnaarggnytngartggathggn	1021
FRH2-44	FRH2-54	tgggtnmgncarcayccnggnaarggnytngartggathggn	1022
FRH2-45	FRH2-55	tgggtnmgncarcayccnggnaarggnytngartggathggn	1022
FRH2-46	FRH2-43	tggathmgncarccnccnggnaarggnytngartggathggn	1023
FRH2-47	FRH2-44	tggathmgncarccnccnggnaarggnytngartggathggn	1023
FRH2-48	FRH2-49	tggathmgncarccnccnggnaarggnytngartggathggn	1023
FRH2-49	FRH2-50	tggathmgncarccnccnggnaarggnytngartggathggn	1023
FRH2-50	FRH2-53	tggathmgncarccnccnggnaarggnytngartggathggn	1023
FRH2-51	FRH2-33	tggathmgncarccngcnggnaarggnytngartggathggn	1024
FRH2-52	FRH2-3	tggathmgncarccnccnggnaarggnytngartggathggn	1023
FRH2-53	FRH2-4	tggathmgncarccnccnggnaarggnytngartggathggn	1023
FRH2-54	FRH2-16	tgggtnmgncaratgccnggnaarggnytngartggatgggn	1025
FRH2-55	FRH2-17	tgggtnmgncaratgccnggnaarggnytngartggatgggn	1025
FRH2-56	FRH2-11	tgggtnmgncaratgccnggnaarggnytngartggatgggn	1025
FRH2-57	FRH2-37	tggathmgncarwsnccnwsnmgnggnytngartggytnggn	1026
FRH2-58	FRH2-39.1	tgggtnmgncargcnccnggnaarggnytngartgggtnwsn	1019
FRH3-1	FRH3-10.1	mgngtncanatgcancangaycanwsncanwsncangcntayat ggarytnmgnwsnytnmgnwsngaygaycangcngtntaytayt gygcnmgn	1027
FRH3-2	FRH3-10	mgngtncanatgcancangaycanwsncanwsncangcntayat ggarytnmgnwsnytnmgnwsngaygaycangcngtntaytayt gygcnmgn	1027
FRH3-3	FRH3-42	mgngtncanatgcanmgngaycanwsnathwsncangcntayat ggarytnwsnmgnytnmgnwsngaygaycangcngtntaytayt gygcnmgn	1028
FRH3-4	FRH3-40	mgngtncanatgcanmgngaycanwsnathwsncangcntayat ggarytnwsnmgnytnmgnwsngaygaycangcngtntaytayt gygcnmgn	1028
FRH3-5	FRH3-30	mgngtncanatgytngargaycanwsncangaycangcntayat ggarytnwsnwsnytnmgnwsngargaycangcngtntaytayt gygcncan	1029

FIGURA 21E

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
FRH3-6	FRH3-31	mgngtncanatgytngargaycanwsncangaycangcntayat ggarytnwsnwsnytnmgnwsngargaycangcngtntaytayt gygcncan	1029
FRH3-7	FRH3-29	mgnytncanathwsnaargaycanwsnaarwsncargtngtnyt ncanatgcanaayatggayccngtngaycangcncantaytayt gygcnmgn	1030
FRH3-8	FRH3-20	mgnytncanathwsnaargaycanwsnaarwsncargtngtnyt ncanatgcanaayatggayccngtngaycangcncantaytayt gygcnmgn	1030
FRH3-9	FRH3-65	mgnytncanathcanaargaycanwsnaaraaycargtngtnyt ncanatgcanaayatggayccngtngaycangcncantaytayt gygcncay	1031
FRH3-10	FRH3-56	mgnytncanathcanaargaycanwsnaarcancargtngtnyt ncangtncangayatggayccngtngaycangcncantaytayt gygcncay	1032
FRH3-11	FRH3-62	mgnytncanathcanaargaycanwsnaaraaycargtngtnyt ncanatgcanaayatggayccngtngaycangcncantaytayt gygcncay	1031
FRH3-12	FRH3-2	mgnytncanathcanaargaycanwsnaaraaycargtngtnyt ncanatgcanaayytngayccngtngaycangcncantaytayt gygcncay	1033
FRH3-13	FRH3-59	mgnytncanathcanaargcncanwsnaaraaycargtngtnyt ncanatgcanaayatggayccngtngaycangcncantaytayt gygcncay	1034
FRH3-14	FRH3-57	mgnytncanathcanaargaycanwsnaaraaycargtngtnyt ncanatgcanaayatggayccngtngaycangcncantaytayt gygcncay	1031
FRH3-15	FRH3-64	mgnytncanathcanaargaycanwsnaaraaycargtngtnyt ncanatgcanaayatggayccngtngaycangcncantaytayt gygcncay	1031
FRH3-16	FRH3-41	mgnttycanathwsnmgngayaaygcnaaraaywsnytntayyt ncaratgaaywsnytnmgngcngargaycangcngtntaytayt gygcnmgn	1035
FRH3-17	FRH3-45	mgnttycanathwsnmgngayaaywsnaaraaycanytntayyt ncaratgaaywsnytnmgngcngargaycangcngtntaytayt gygcnaar	1036

FIGURA 21F

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
FRH3-18	FRH3-47	mgnttycanathwsnmgngayaaywsnaaraaycanytntayyt ncaratgaaywsnytnmgngcngargaycangcngtntaytayt gygcnaar	1036
FRH3-19	FRH3-51	mgnttycanathwsnmgngayaaywsnaaraaycanytntayyt ncaratgaaywsnytnmgngcngargaycangcngartaytayt gygcnaar	1037
FRH3-20	FRH3-52	mgnttycanathwsnmgngayaaywsnaaraaycanytntayyt ncaratgaaywsnytnmgngcngargaycangcngartaytayt gygcnaar	1037
FRH3-21	FRH3-13	mgnttycanathwsnmgngayaaywsnatgaaycanytntayyt ncaratgaaywsnytnmgngcngargaycangcngtntaytayt gygcnmgn	1038
FRH3-22	FRH3-14	mgnttycanathwsnmgngayaaywsnatgaaycanytntayyt ncaratgaaywsnytnmgngcngargaycangcngtntaytayt gygcnmgn	1038
FRH3-23	FRH3-1	mgnttycanathwsnmgngayaaywsnaaraaycanytntayyt ncaratgaaywsnytnmgngcngargaycangcngtntaytayt gygcnmgn	1039
FRH3-24	FRH3-22	mgnttycanathwsnmgngayaaywsnaaraaycanytntayyt ncaratgaaywsnytnmgngcngargaycangcngtntaytayt gygcnmgn	1039
FRH3-25	FRH3-23	mgnttycanathwsnmgngayaaywsnaaraaycanytntayyt ncaratgaaywsnytnmgngcngargaycangcngtntaytayt gygcnmgn	1039
FRH3-26	FRH3-12	mgnttycanathwsnmgngayaaywsnaaraaycanytntayyt ncaratgaaywsnytnmgngcngargaycangcngtntaytayt gygtnytn	1040
FRH3-27	FRH3-5	mgnttycanathwsnmgngayaaywsnaaraaycanytntayyt ncaratgaaywsnytnmgngcngargaycangcngtntaytayt gygcnmgn	1039
FRH3-28	FRH3-15	mgnttycangtnwsnmgngayaaywsnaaraaycanytnttyyt ncaratgaaywsnytnmgngcngargaycangcngtntaytayt gygcnmgn	1041
FRH3-29	FRH3-7	mgnttycanathwsnmgngayaaywsnaaraaycanytntayyt ncaratgaaywsnytnmgngcngargaycangcngtntaytayt gygcnmgn	1039

FIGURA 21G

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
FRH3-30	FRH3-61	mgnttycanathwsnmgngayaaywsnaaraaycanytngayyt ncaratgaaywsnytnmgngcngargaycangcngtntaytayt gygcnmgn	1041
FRH3-31	FRH3-39	mgnttycanathwsnmgngayaaygcnaaraaywsnytnttyyt ncaratgaaywsnytnmgngaygargaycangcngtntaytayt gygcnytn	1042
FRH3-32	FRH3-34	mgnttycanathwsnmgngayaaygcnaaraaywsngtntayyt ncaratgaaywsnytnmgngaygargaycangcngtntaytayt gygcnmgn	1043
FRH3-33	FRH3-6	mgnttycanathwsnmgngayaaygcnaaraaywsnytntayyt ncaratgaaywsnytnmgngaygargaycangcngtntaytayt gygcnmgn	1044
FRH3-34	FRH3-35	mgnttycanathwsnmgngayaaygcnaaraaywsnytntayyt ncaratgaaywsnytnmgngaygargaycangcngtntaytayt gygcnmgn	1044
FRH3-35	FRH3-21	mgngtncanathwsngtngaycanwsnaaraaycarttywsnyt naayytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1045
FRH3-36	FRH3-8	mgngtnaayatgwsngtngaycanwsnaaraaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1046
FRH3-37	FRH3-9	mgngtnaayatgwsngtngaycanwsnaaraaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1046
FRH3-38	FRH3-18	mgngtncanathwsngtngaycanwsnaaraaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1047
FRH3-39	FRH3-24	mgnathcanathwsngcngaycanwsnaaraaycarttywsnyt naarytnaaywsngtncangcngcngaycangcngtntaytayt gygcnmgn	1048
FRH3-40	FRH3-25	mgnathcanathwsngcngaycanwsnaaraaycarttywsnyt naarytnaaywsngtncangcngcngaycangcngtntaytayt gygcnmgn	1048
FRH3-41	FRH3-26	mgnathcanaarwsngtngaycanwsnaaraaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1049

FIGURA 21H

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
FRH3-42	FRH3-27	mgnathcanaarwsngtngaycanwsnaaraaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1049
FRH3-43	FRH3-38	mgngtncanathwsngtngaycanwsnaaraaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnwsn	1050
FRH3-44	FRH3-54	mgngtncanathwsngtngaycanwsnaaraaycarttywsnyt naarytnttywsngtncangcngcngaycangcngtntayttyt gygcnmgn	1051
FRH3-45	FRH3-55	mgngtncanathwsngtngaycanwsnaaraaycarttywsnyt naarytnttywsngtncangcngcngaycangcngtntayttyt gygcnmgn	1051
FRH3-46	FRH3-43	mgngtncanathwsngtngaycanwsnaaraaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1047
FRH3-47	FRH3-44	mgngtncanathwsngtngaycanwsnaaraaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1047
FRH3-48	FRH3-49	mgngtncanathwsngtngaycanwsnaaraaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1047
FRH3-49	FRH3-50	mgngtncanathwsngtngaycanwsnaaraaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1047
FRH3-50	FRH3-53	mgngtncanathwsngtngaycanwsnaaraaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1047
FRH3-51	FRH3-33	mgngtncanatgwsngtngaycanwsnaaraaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1052
FRH3-52	FRH3-3	mgngtncanathwsnathgtncanwsnmgnaaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1053
FRH3-53	FRH3-4	mgngtncanathwsnathgtncanwsnmgnaaycarttywsnyt naarytnwsnwsngtncangcngcngaycangcngtntaytayt gygcnmgn	1053

FIGURA 211

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
FRH3-54	FRH3-16	cargtncanathwsngcngayaarwsnathwsncangcntayyt ncartggwsnwsnytnaargcnwsngaycangcnatgtaytayt gygcnmgn	1054
FRH3-55	FRH3-17	cargtncanathwsngcngayaarwsnathaaycangcntayyt ncartggwsnwsnytnaargcnwsngaycangcnatgtaytayt gygcnmgn	1055
FRH3-56	FRH3-11	cargtncanathwsngcngayaarwsnathwsncangcntayyt ncartggwsnwsnytnaargcnwsngaycangcnatgtaytayt gygcnmgn	1054
FRH3-57	FRH3-37	mgnathcanathaayccngaycanwsnaaraaycarttywsnyt ncarytnaaywsngtncanccngargaycangcngtntaytayt gygcnmgn	1056
FRH3-58	FRH3-39.1	mgnttycanathwsnmgngayaaygcnaaraaywsnytnttyyt ncaratgaaywsnytnmgngaygargaycangcngtntaytayt gygcnytn	1042
FRH4-1	FRH4-10.1	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-2	FRH4-10	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-3	FRH4-42	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-4	FRH4-40	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-5	FRH4-30	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-6	FRH4-31	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-7	FRH4-29	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-8	FRH4-20	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-9	FRH4-65	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-10	FRH4-56	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-11	FRH4-62	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-12	FRH4-2	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-13	FRH4-59	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-14	FRH4-57	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-15	FRH4-64	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-16	FRH4-41	tggggncarggncanatggtncangtnwsnwsn	1059
FRH4-17	FRH4-45	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-18	FRH4-47	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-19	FRH4-51	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-20	FRH4-52	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-21	FRH4-13	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-22	FRH4-14	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-23	FRH4-1	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-24	FRH4-22	tggggncarggncanytngtncangtnwsnwsn	1057

FIGURA 21J

NOMBRE	NOMBRE	SECUENCIA	SEQ ID NO:
FRH4-25	FRH4-23	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-26	FRH4-12	tggggncarggnwsnytngtncangtnwsnccn	1060
FRH4-27	FRH4-5	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-28	FRH4-15	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-29	FRH4-7	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-30	FRH4-61	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-31	FRH4-39	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-32	FRH4-34	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-33	FRH4-6	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-34	FRH4-35	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-35	FRH4-21	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-36	FRH4-8	tggggncarggncanaargtncangtnwsnwsn	1061
FRH4-37	FRH4-9	tggggncarggncanaargtncangtnwsnwsn	1061
FRH4-38	FRH4-18	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-39	FRH4-24	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-40	FRH4-25	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-41	FRH4-26	tggggnmgnggncanytngtncangtnwsnwsn	1062
FRH4-42	FRH4-27	tggggnmgnggncanytngtncangtnwsnwsn	1062
FRH4-43	FRH4-38	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-44	FRH4-54	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-45	FRH4-55	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-46	FRH4-43	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-47	FRH4-44	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-48	FRH4-49	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-49	FRH4-50	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-50	FRH4-53	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-51	FRH4-33	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-52	FRH4-3	tggggncarggncanatggtncangtnwsnwsn	1059
FRH4-53	FRH4-4	tggggncarggncanatggtncangtnwsnwsn	1059
FRH4-54	FRH4-16	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-55	FRH4-17	tggggncarggncanytngtncangtnwsnwsn	1057
FRH4-56	FRH4-11	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-57	FRH4-37	tggggncarggncancangtncangtnwsnwsn	1058
FRH4-58	FRH4-39.1	tggggncarggncanytngtncangtnwsnwsn	1057

FIGURA 21K

1843

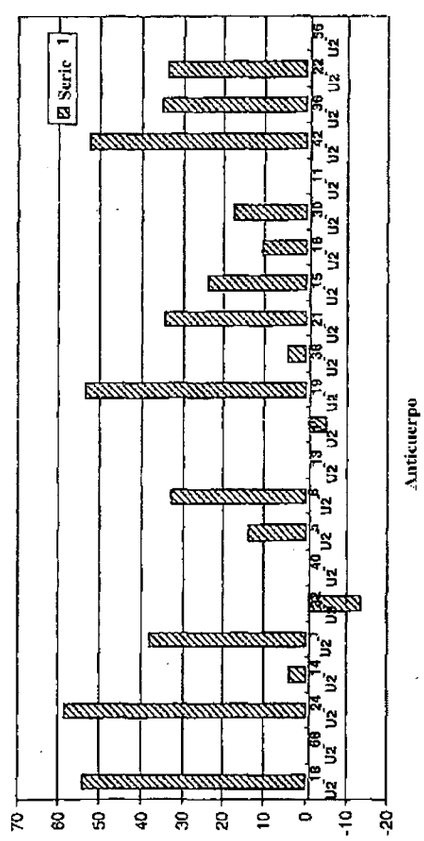


FIGURA 22A

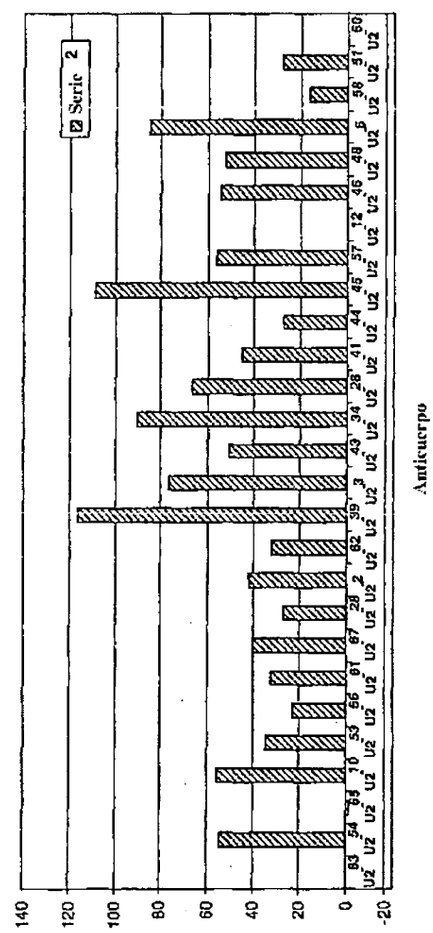


FIGURA 22B

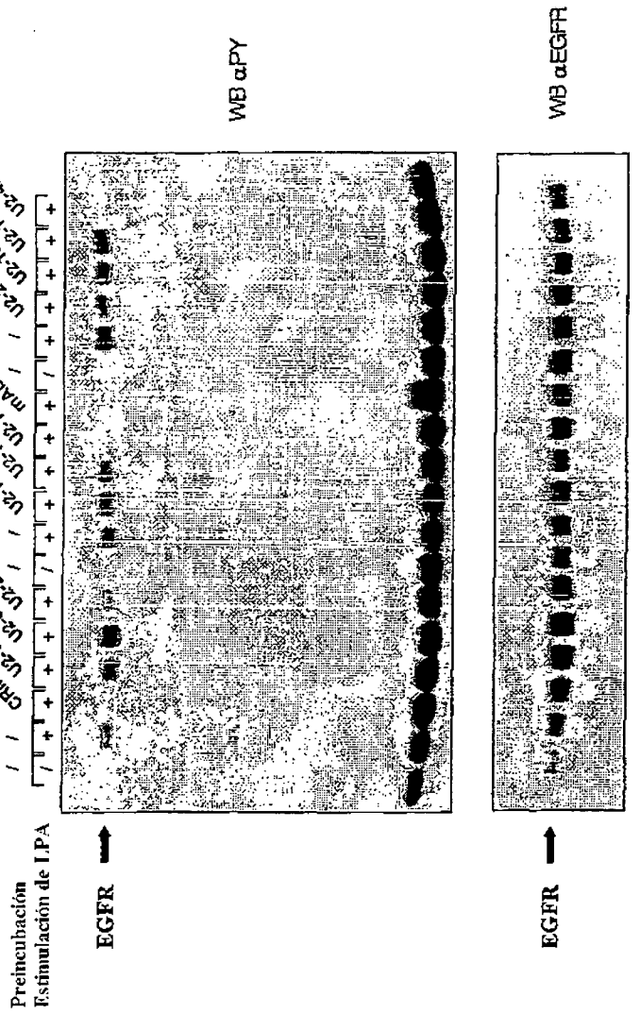
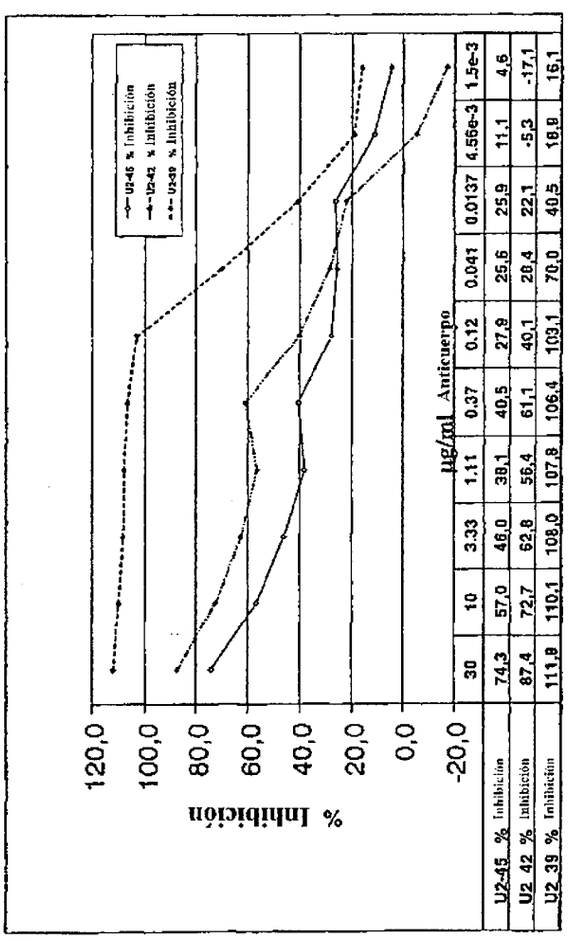

WB αPY
WB αEGFR
EGFR
EGFR
Preincubación
Estimulación de LPA
CRM 197
UC-18
UC-68
UC-24
UC-1
UC-17
UC-19
mAb 225
UC-21
UC-15
UC-11
UC-42

FIGURA 23



	30	10	3.33	1.11	0.37	0.12	0.041	0.0137	4.56e-3	1.5e-3
U2-45 % Inhibición	74,3	57,0	46,0	38,1	40,5	27,9	25,6	25,9	11,1	4,6
U2 42 % Inhibición	87,4	72,7	62,8	56,4	61,1	40,1	28,4	22,1	-5,3	-17,1
U2 39 % Inhibición	111,8	110,1	108,0	107,8	106,4	103,1	70,0	40,5	18,8	16,1

FIGURA 24

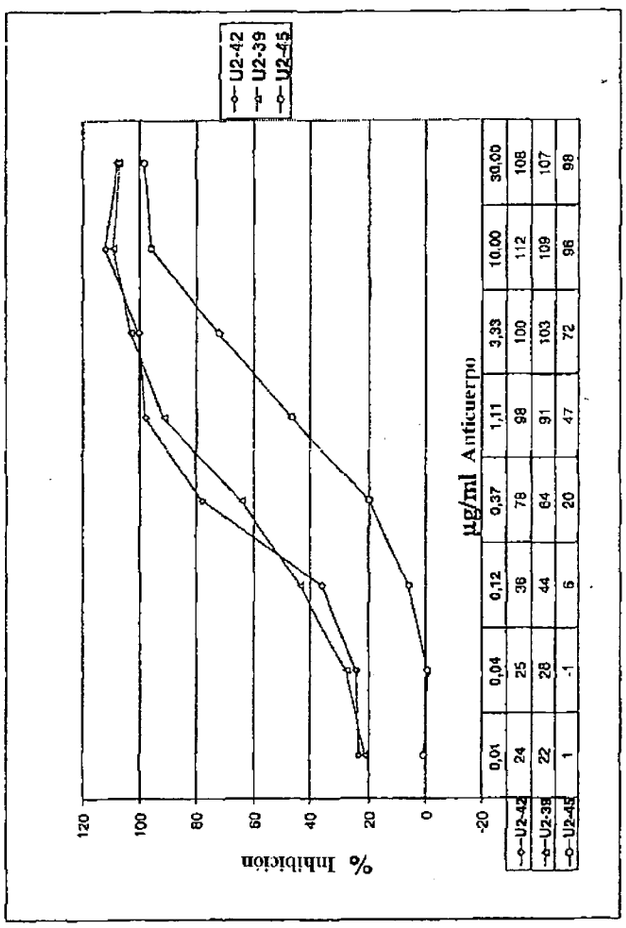

U2-42
U2-39
U2-45
% Inhibición
µg/ml Anticuerpo
120
100
80
60
40
20
0
-20
0,01 0,04 0,12 0,37 1,11 3,33 10,00 30,00
U2-42 24 25 36 78 98 100 112 108
U2-39 22 28 44 64 91 103 109 107
U2-45 1 -1 6 20 47 72 96 98

FIGURA 25

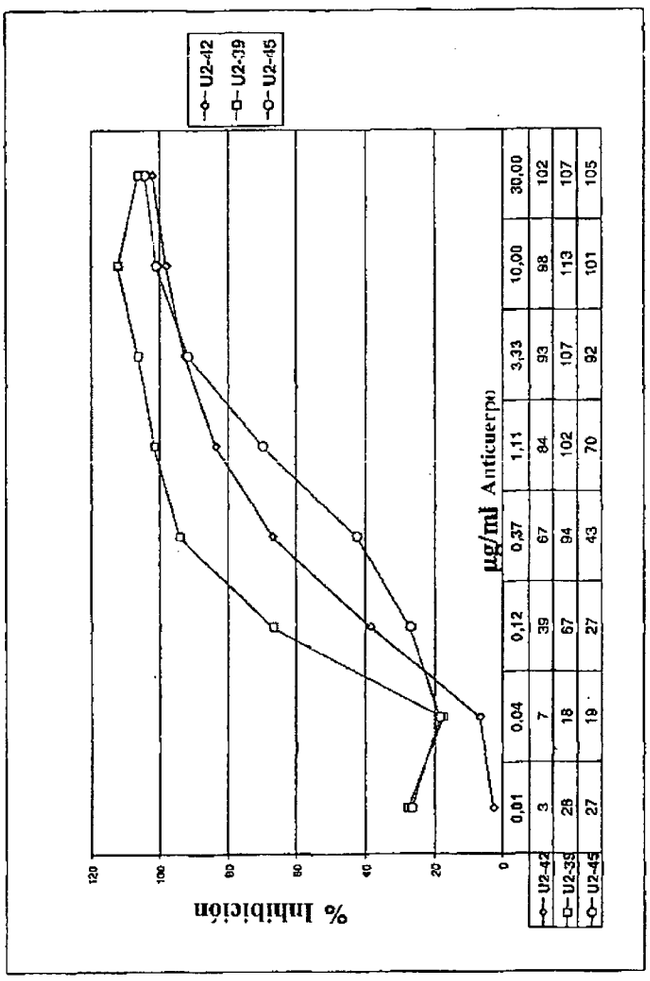

U2-42
U2-39
U2-45
% Inhibición
120
100
80
60
40
20
0
µg/ml Anticuerpo
0,01
0,04
0,12
0,37
1,11
3,33
10,00
30,00
U2-42 3 7 39 67 84 93 98 102
U2-39 28 18 67 84 102 107 113 107
U2-45 27 19 27 43 70 92 101 105

FIGURA 26

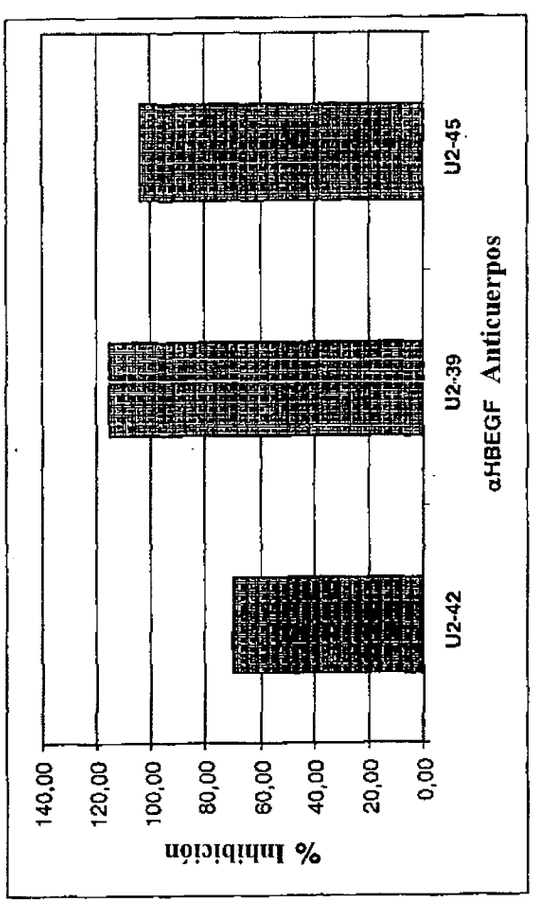

% Inhibición
140,00
120,00
100,00
80,00
60,00
40,00
20,00
0,00
U2-42
U2-39
U2-45
αHBEGF Anticuerpos

FIGURA 27

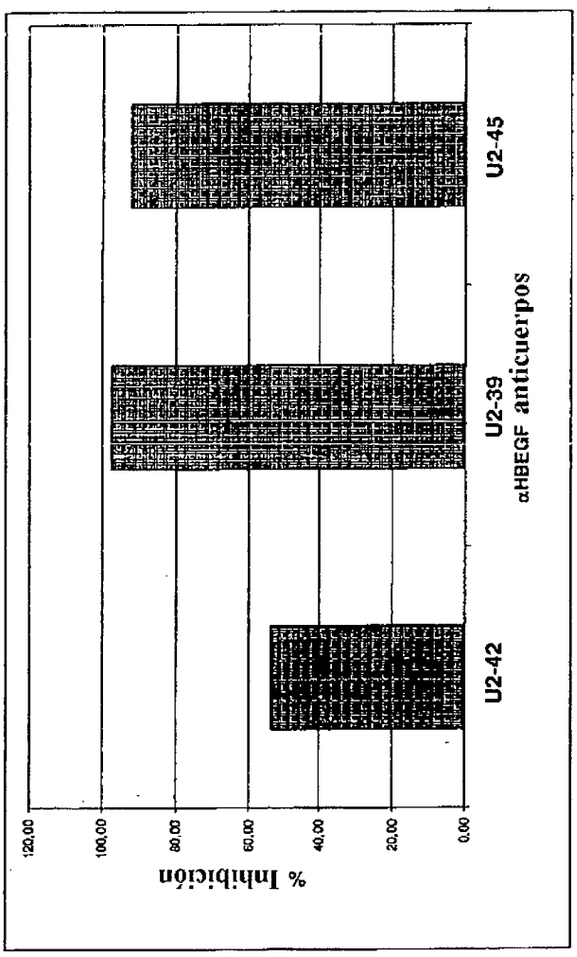

% Inhibición
120,00
100,00
80,00
60,00
40,00
20,00
0,00
U2-42
U2-39
U2-45
αHBEGF anticuerpos

FIGURA 28

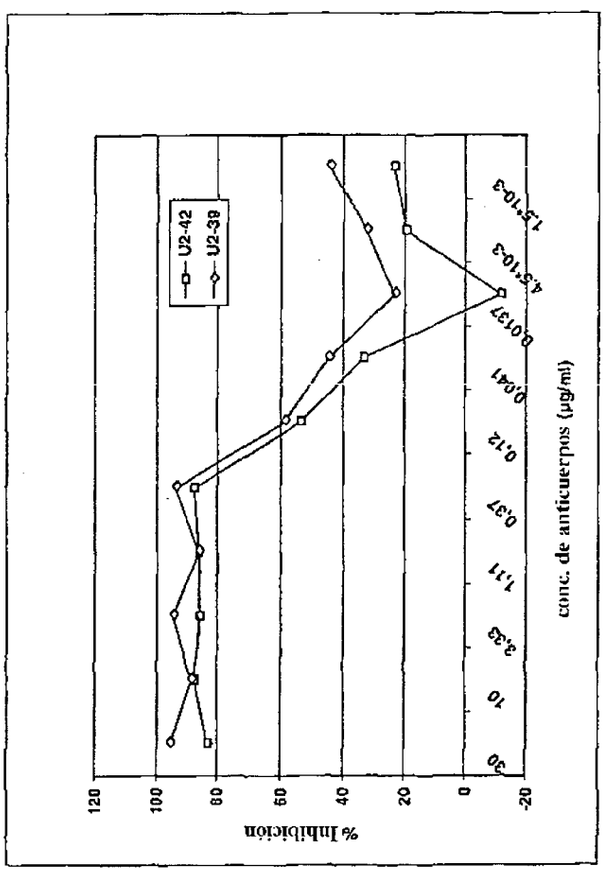
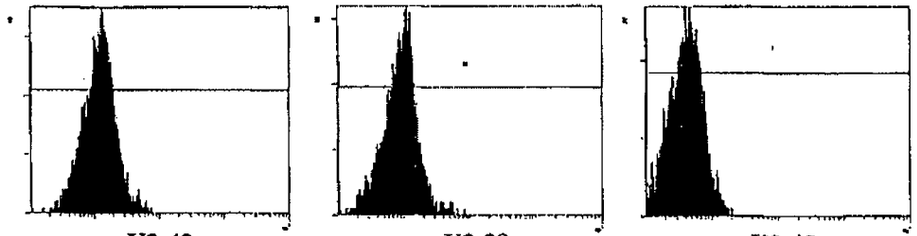

% Inhibición
120
100
80
60
40
20
0
-20
U2-42
U2-39
30
10
3,33
1,11
0,37
0,12
0,041
0,0137
4,5·10-3
1,5·10-3
conc. de anticuerpos (µg/ml)

FIGURA 29

Células HEK 293 transfectadas transitoriamente con pcDNA (vector vacío)



Células HEK 293 transfectadas transitoriamente con pcDNA-cino HBEGF

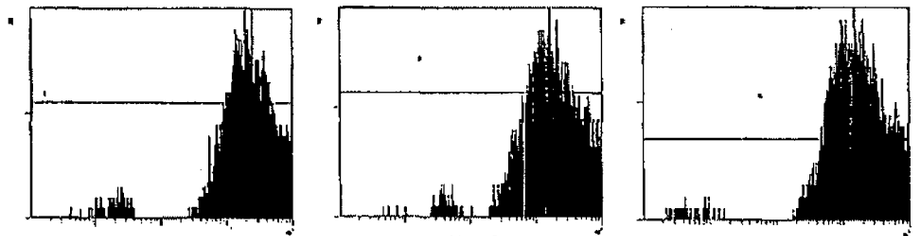


FIGURA 30 A

Células HEK 293 transfectadas transitoriamente con pcDNA-ratón HBEGF

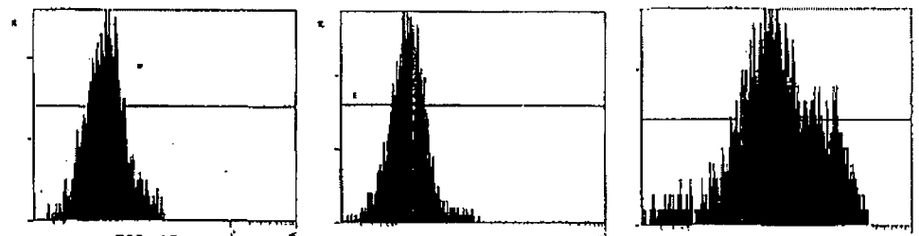
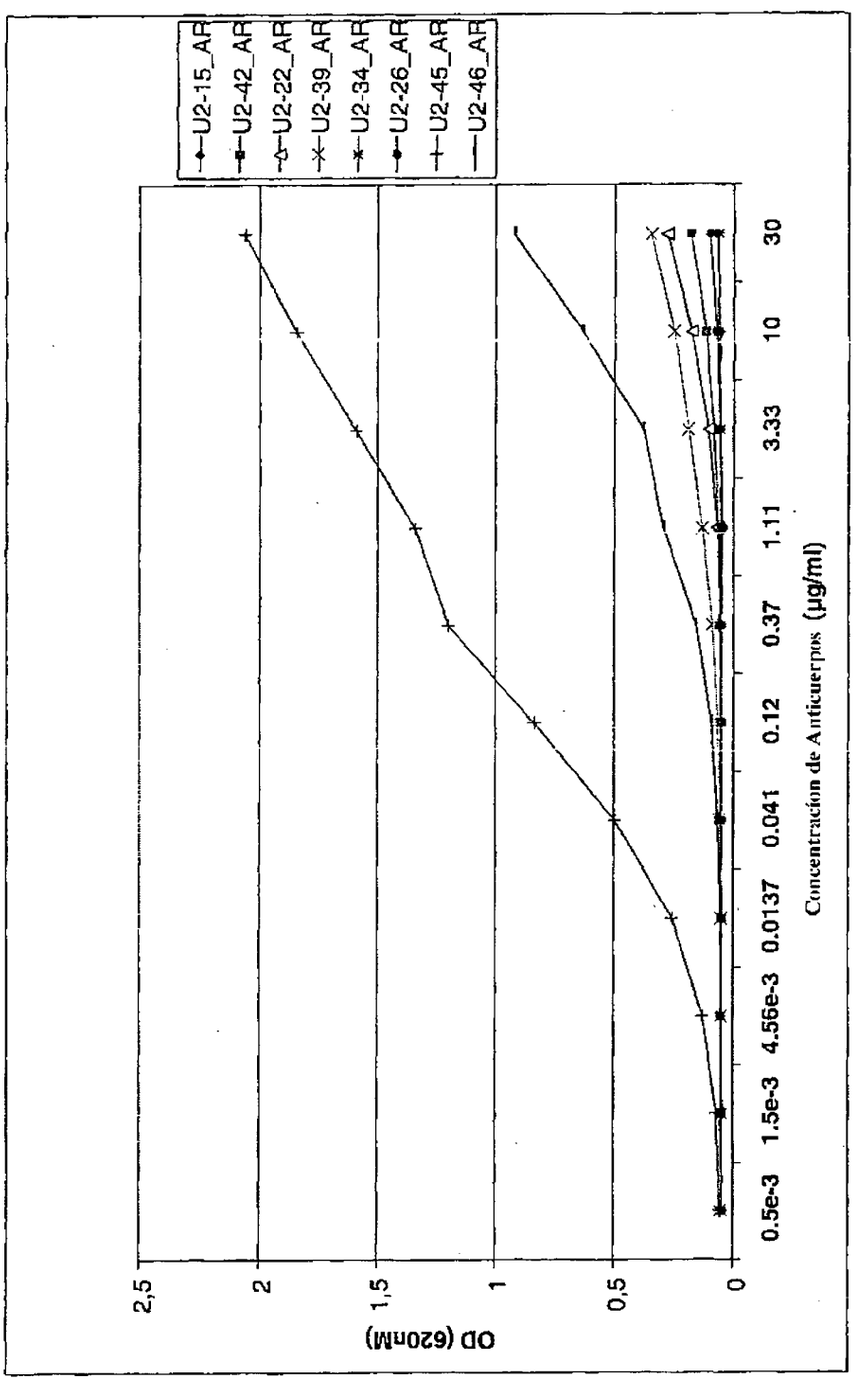


FIGURA 30 B

1852

FIGURA 30 C



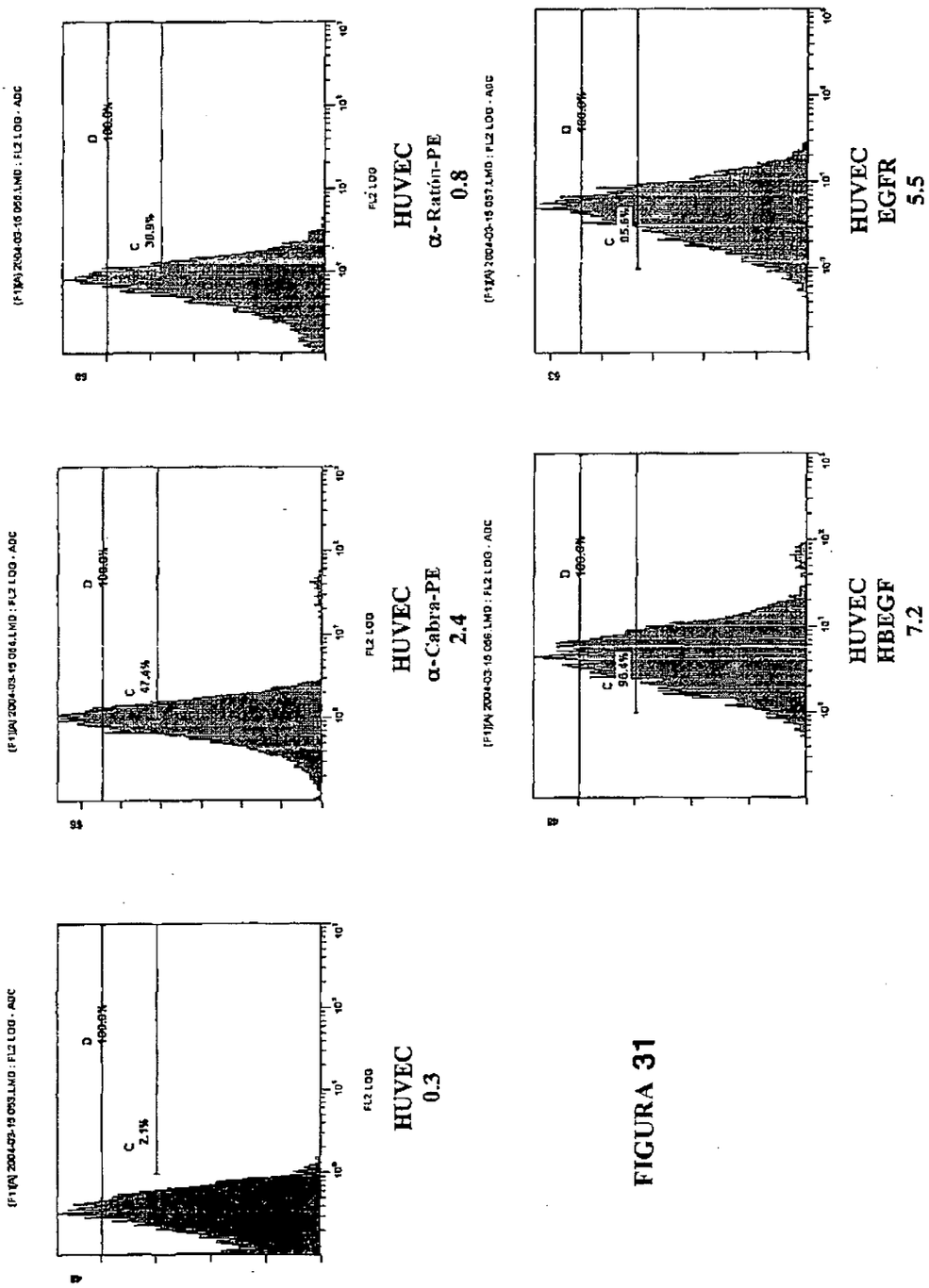

HUVEC
0.3
HUVEC
α-Cabra-PE
2.4
HUVEC
α-Ratón-PE
0.8
HUVEC
HBEGF
7.2
HUVEC
EGFR
5.5
FL2 LOG

FIGURA 31

FIGURA 32 B

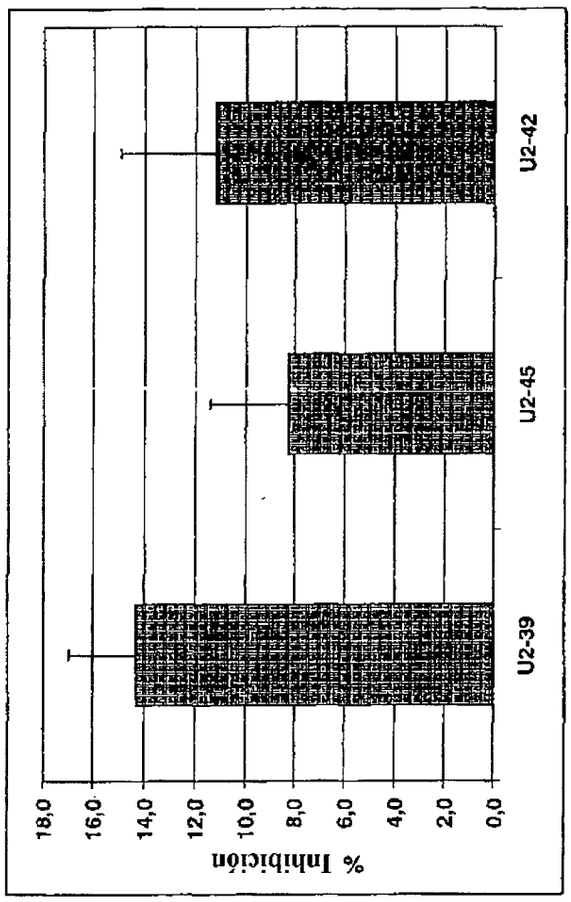
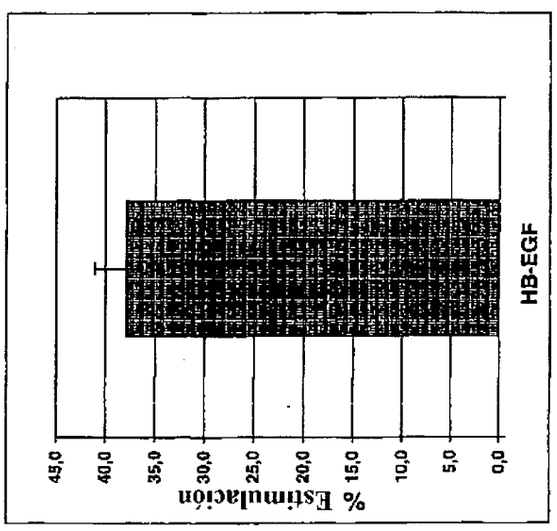


FIGURA 32 A



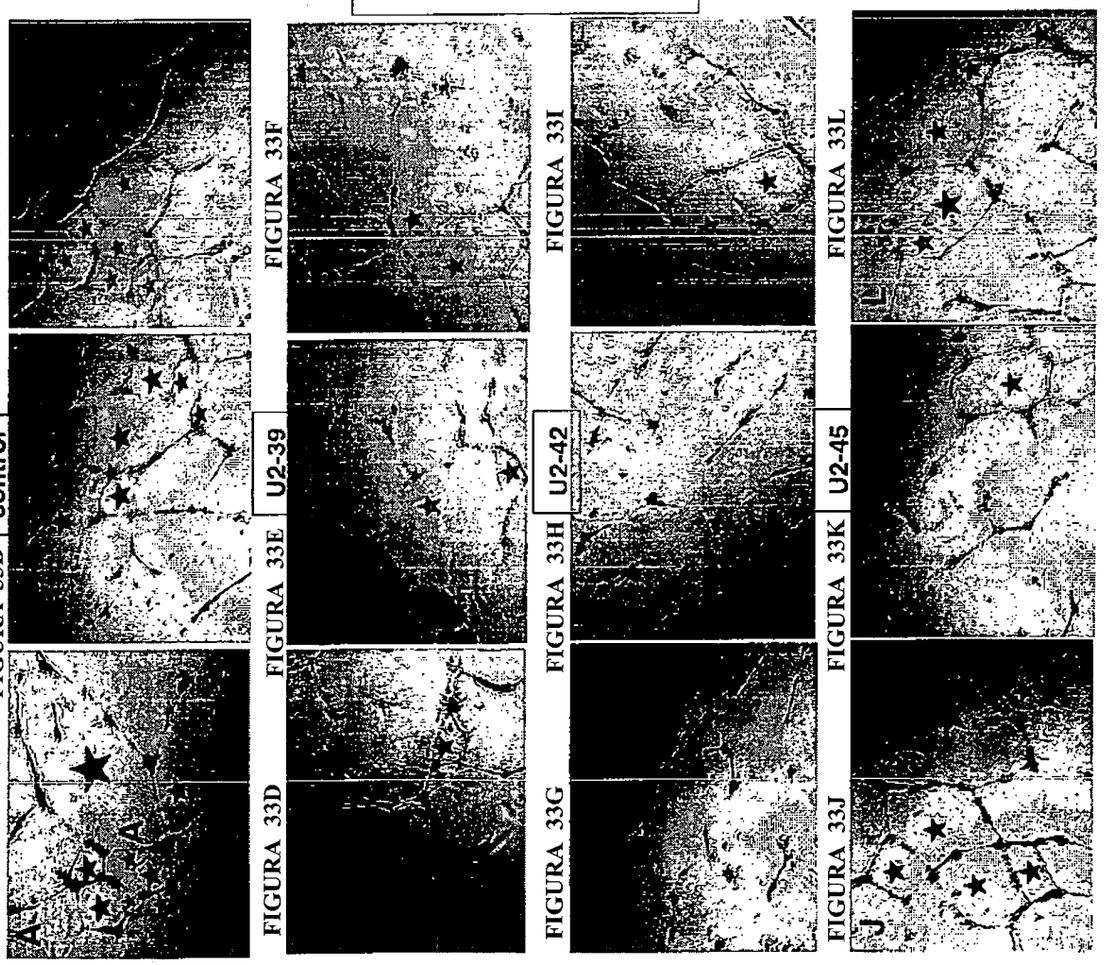


FIGURA 33A
FIGURA 33B
control
FIGURA 33C
FIGURA 33D
FIGURA 33E
U2-39
FIGURA 33F
FIGURA 33G
FIGURA 33H
U2-42
FIGURA 33I
FIGURA 33J
FIGURA 33K
U2-45
FIGURA 33L
A
J
Celdas centradas / campo
0
2
4
6
8
10
12
14
control
U2-39
U2-42
U2-45

FIGURA 33M

FIGURA 34 A

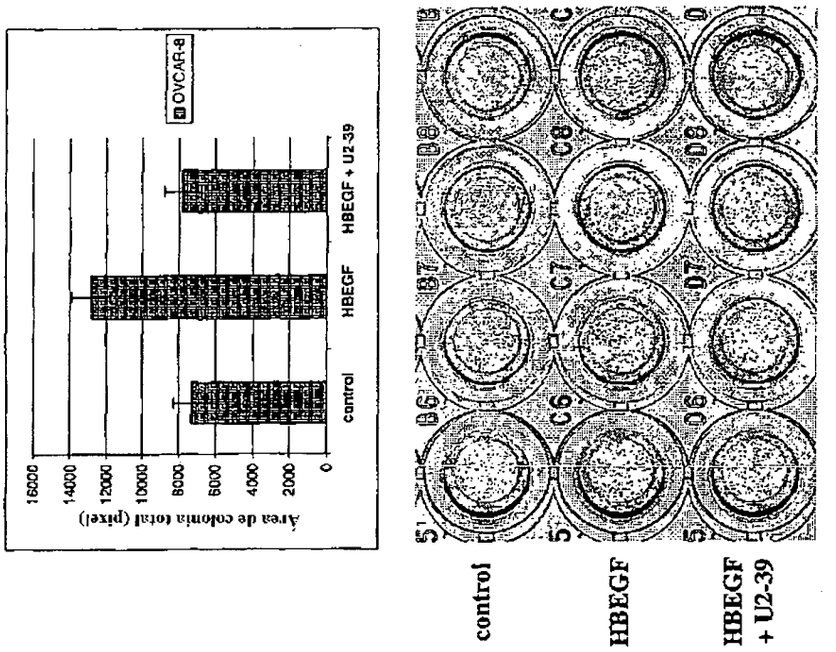


FIGURA 34 B

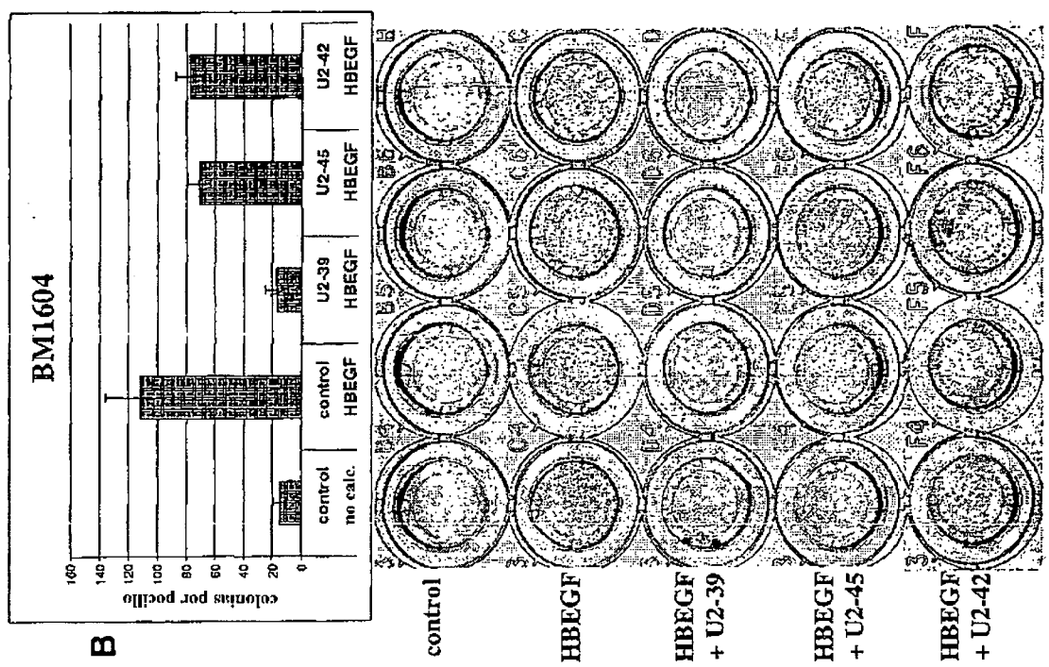
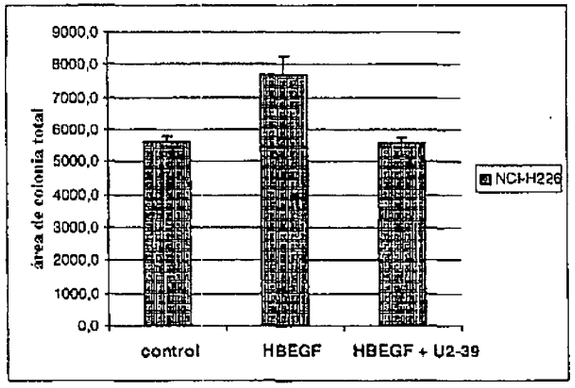


FIGURA 34 C

NCI-H226



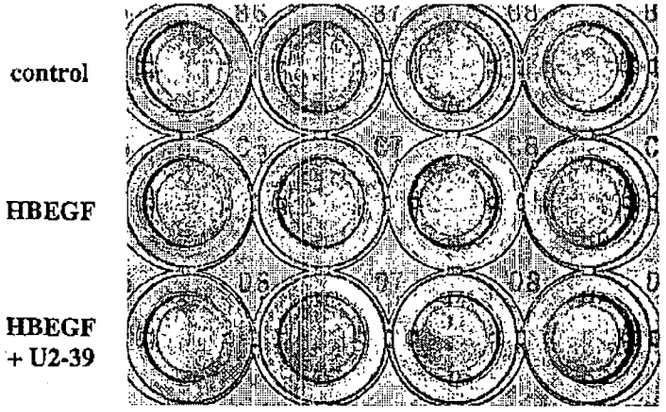
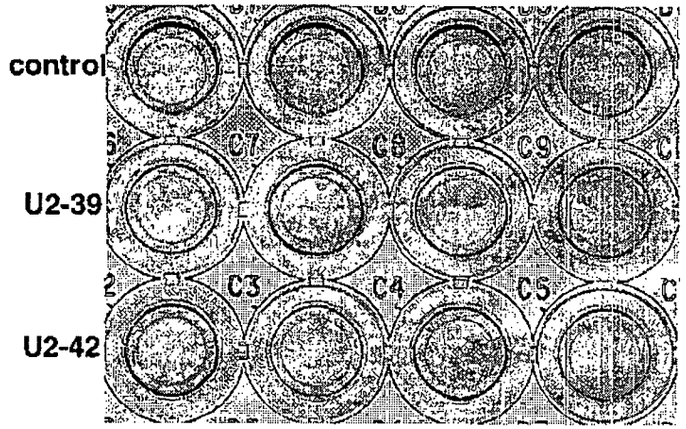


FIGURA 34 D



SkOV-3 clon 71

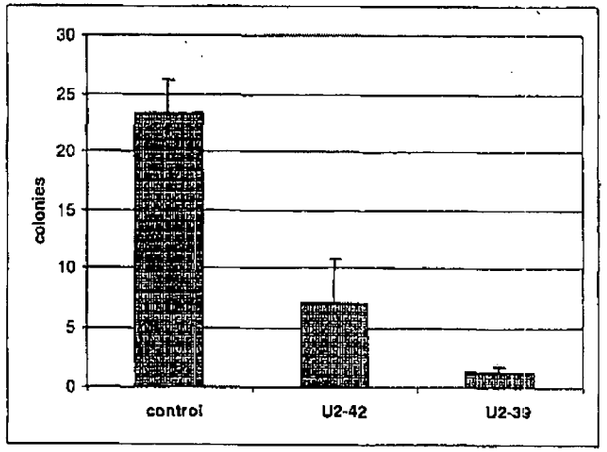
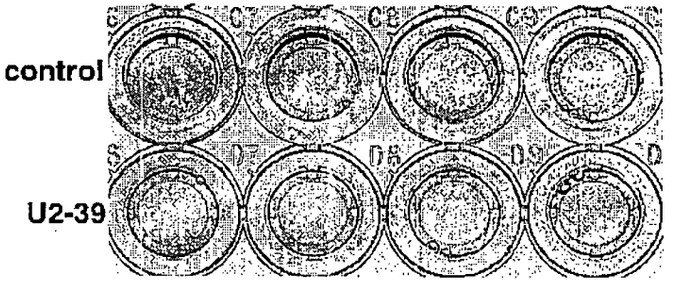


FIGURA 34 E



SkOV-3 clon 74

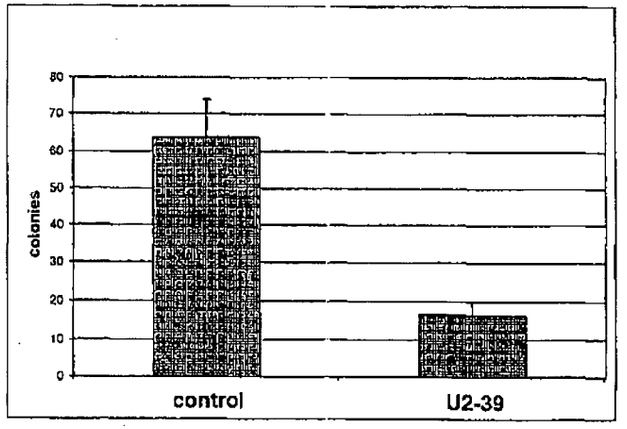
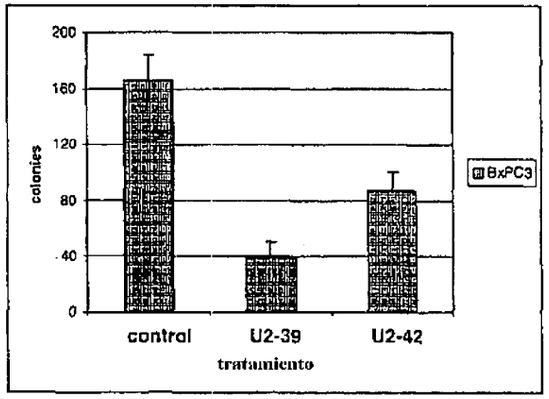
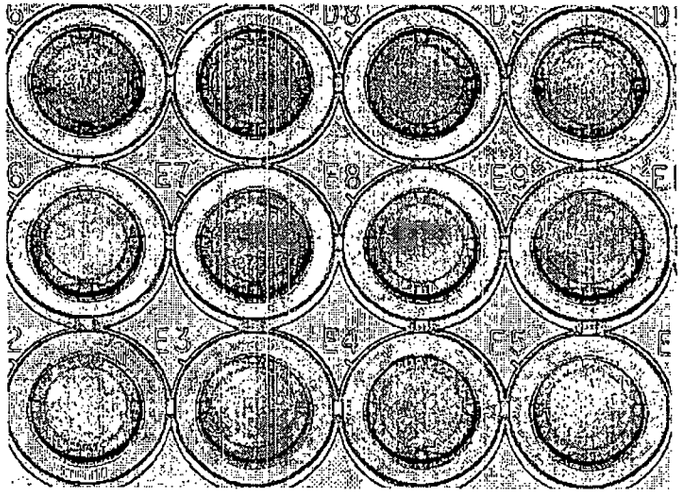


FIGURA 34 F





1859

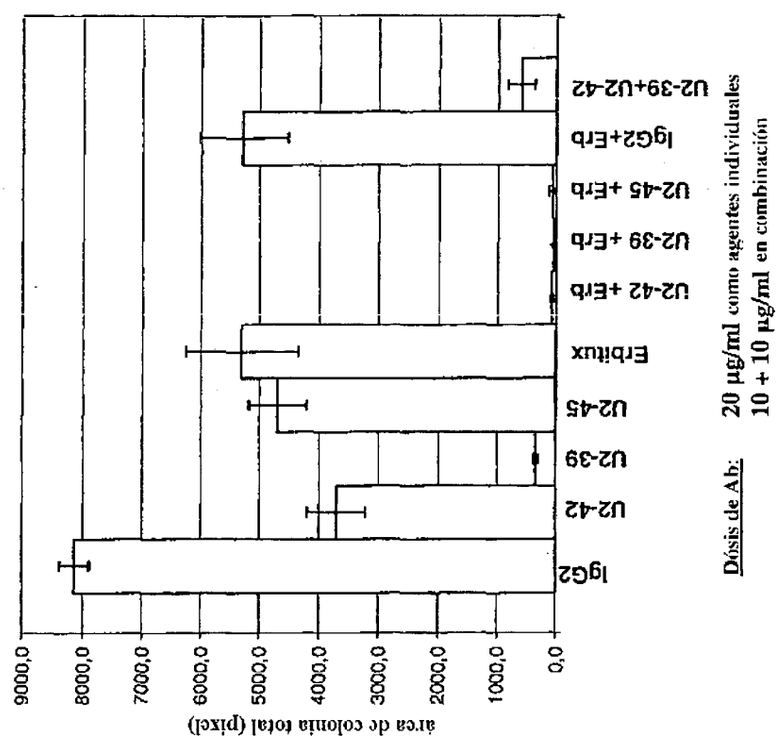
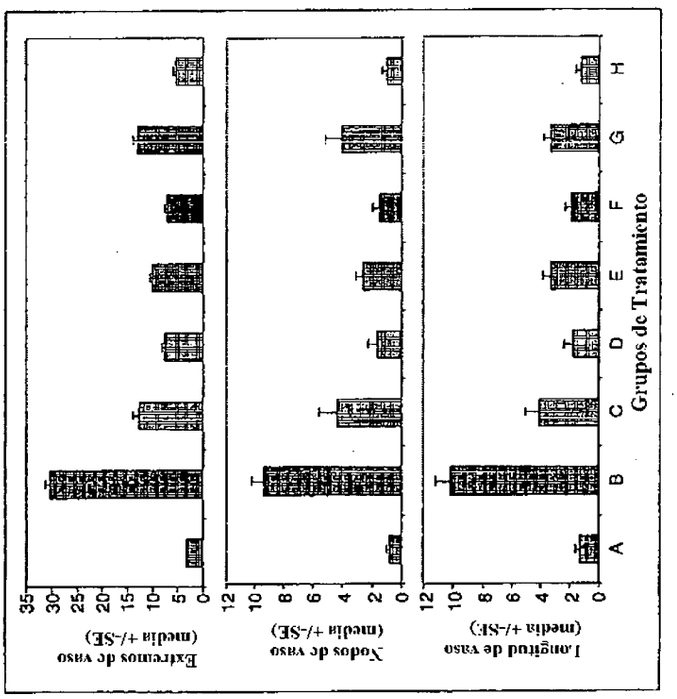

área de colonia total (pixel)
9000,0
8000,0
7000,0
6000,0
5000,0
4000,0
3000,0
2000,0
1000,0
0,0
IgG2
U2-42
U2-39
U2-45
Erbitux
U2-42 +Erb
U2-39 +Erb
U2-45 +Erb
IgG2+Erb
U2-39+U2-42
Dósis de Ab: 20 µg/ml como agentes individuales
10 + 10 µg/ml en combinación

FIGURA 35

1861

FIGURA 36



1862

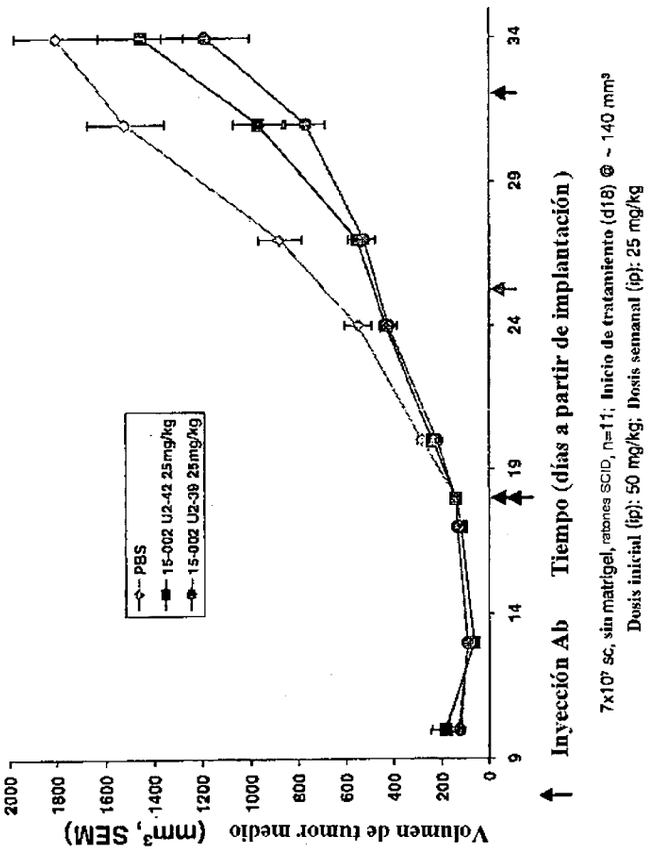
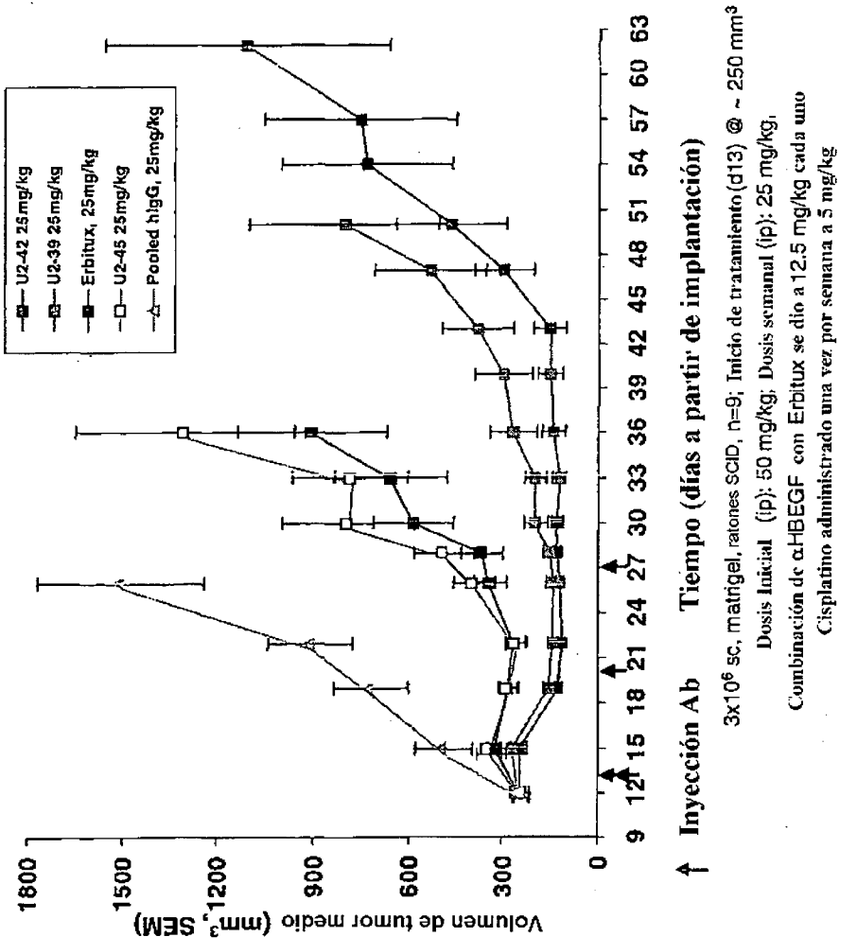


FIGURA 37

1863

FIGURA 38A



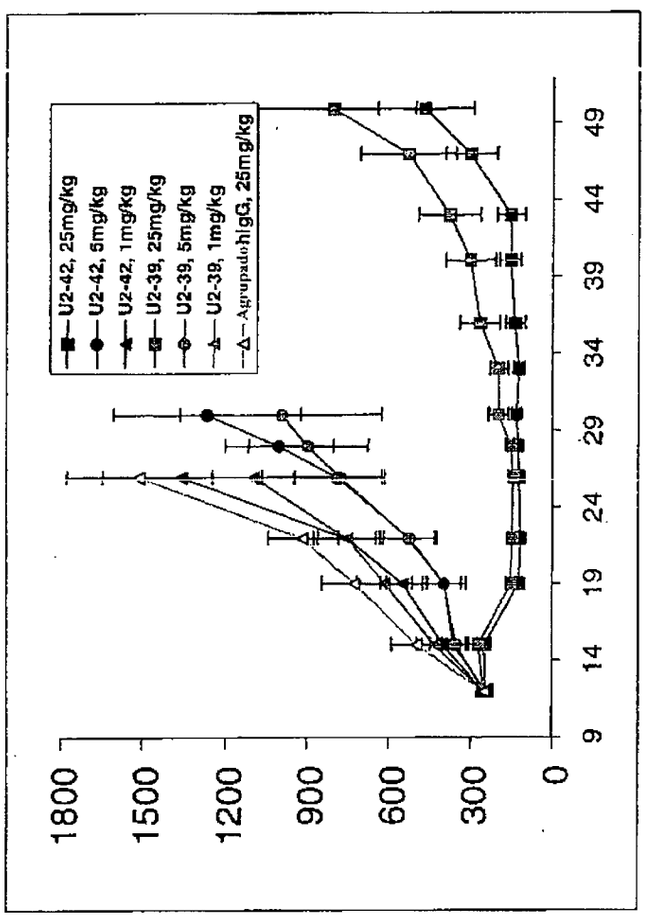

U2-42, 25mg/kg
U2-42, 5mg/kg
U2-42, 1mg/kg
U2-39, 25mg/kg
U2-39, 5mg/kg
U2-39, 1mg/kg
Agrupado hIgG, 25mg/kg
1800
1500
1200
900
600
300
0
9
14
19
24
29
34
39
44
49

FIGURA 38 B

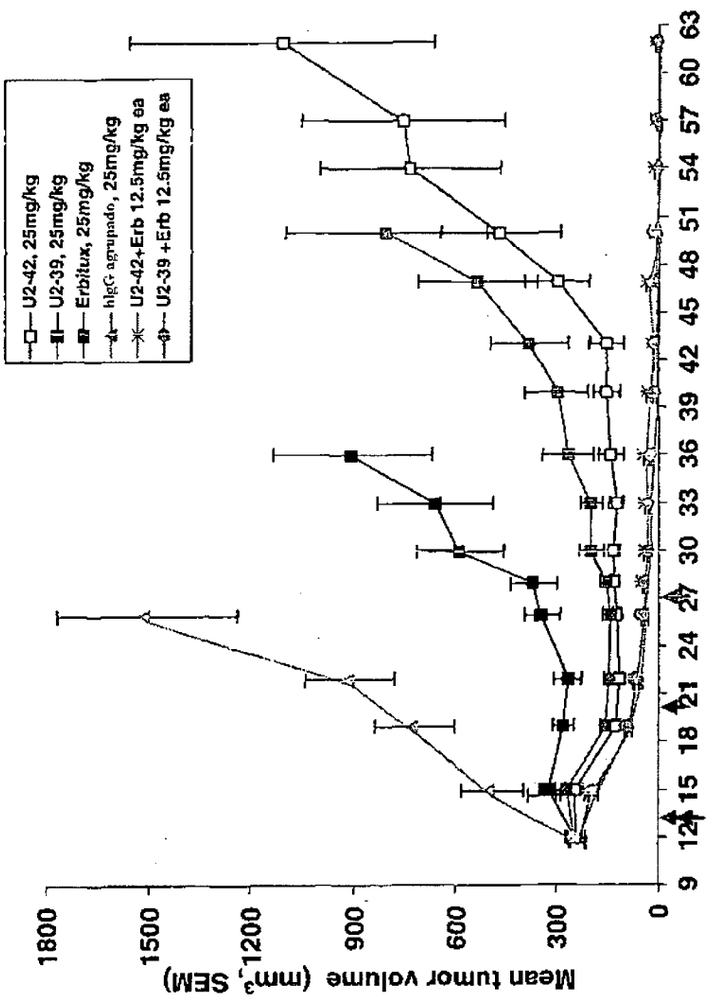
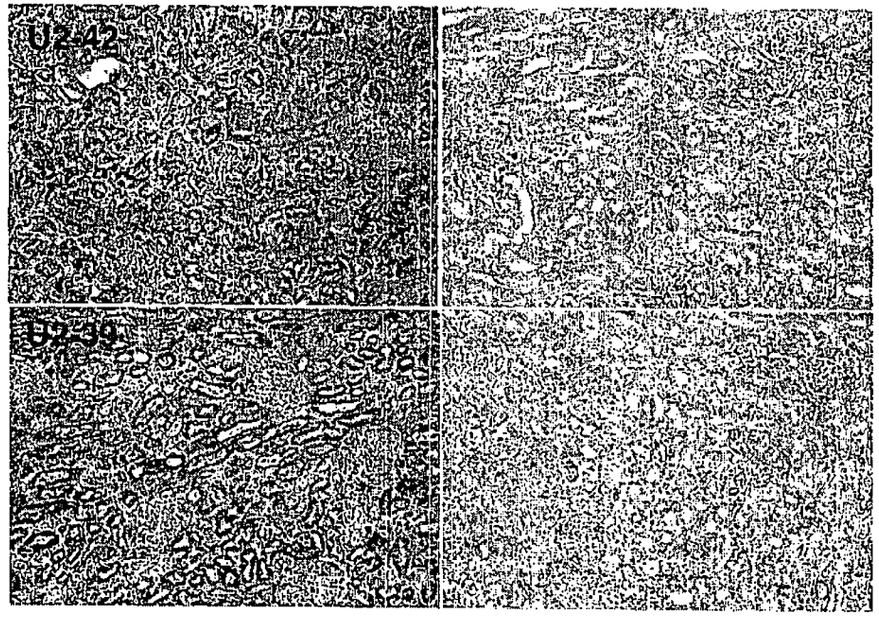

U2-42, 25mg/kg
U2-39, 25mg/kg
Erbitux, 25mg/kg
hIgG agrupado, 25mg/kg
U2-42+Erb 12.5mg/kg ea
U2-39 +Erb 12.5mg/kg ea
Mean tumor volume (mm³, SEM)
1800
1500
1200
900
600
300
0
9 12 15 18 21 24 27 30 33 36 39 42 45 48 51 54 57 60 63
Inyección Ab
Tiempo (días a partir de implantación)
3x10⁶ sc, matrigel, ratones SCID, n=9; Inicio de tratamiento (d13) @ ~ 250 mm³
Dosis Inicial (ip): 50 mg/kg; Dosis semanal (ip): 25 mg/kg,
Combinación de αHBEGF con Erbitux se dio a 12.5 mg/kg cada uno
Cisplatino administrado una vez por semana a 5 mg/kg

FIGURA 38C

Inmunohistoquimica de tejido humano con anticuerpos anti HB-EGF humanos

FIGURA 39 A



Tinción de membranas y citoplasma de células tubulares de riñón humano

Control de isotipo de IgG humana

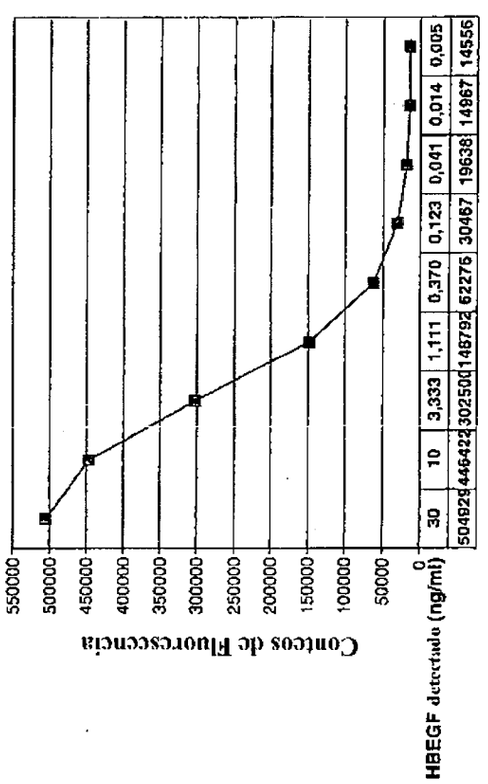
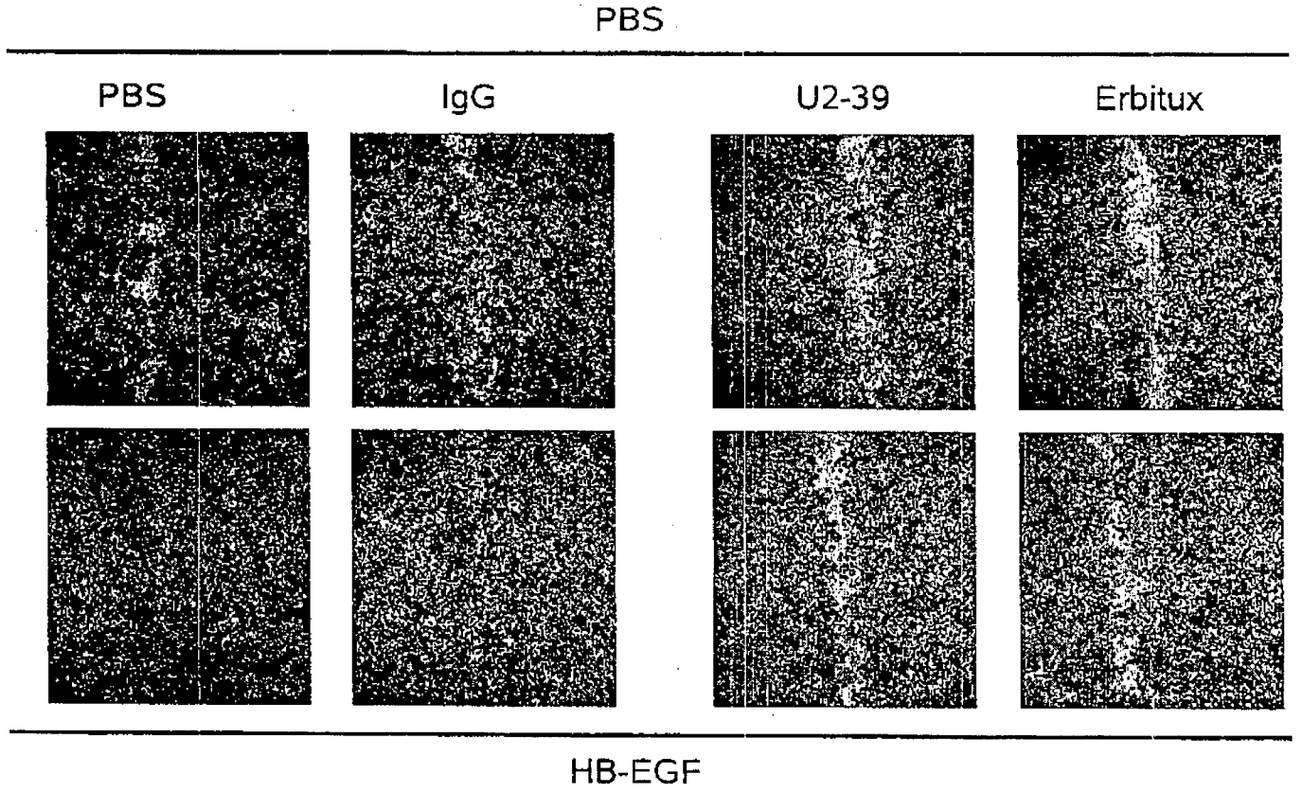

Contcos de Fluorescencia
550000
500000
450000
400000
350000
300000
250000
200000
150000
100000
50000
0
HBEGF detectado (ng/ml)
30
10
3,333
1,111
0,370
0,123
0,041
0,014
0,005
504929
446423
302500
148792
62276
30467
19638
14867
14556

FIGURA 39 B

FIGURA **40A**

Ensayo de rayado
- Inhibición de migración inducida por HB-EGF

Células de carcinoma escamoso epitelial CLS354 (boca)



1868

FIGURA **40B**

Ensayo de trasmigración
- Inhibición de migración inducida por HB-EGF

Células de carcinoma epitelial Detroit 562 (faringe)

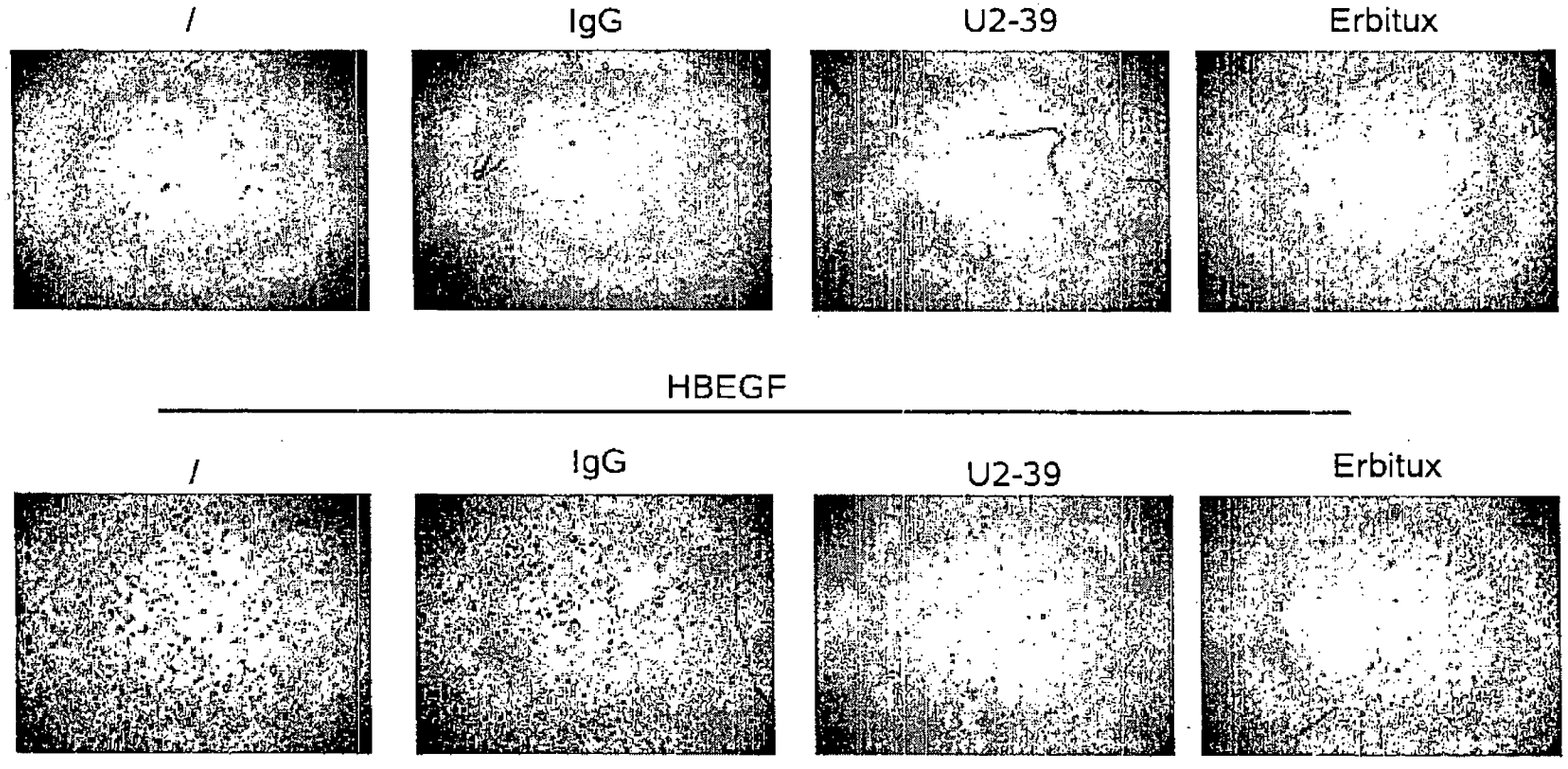


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FIGURA 41A

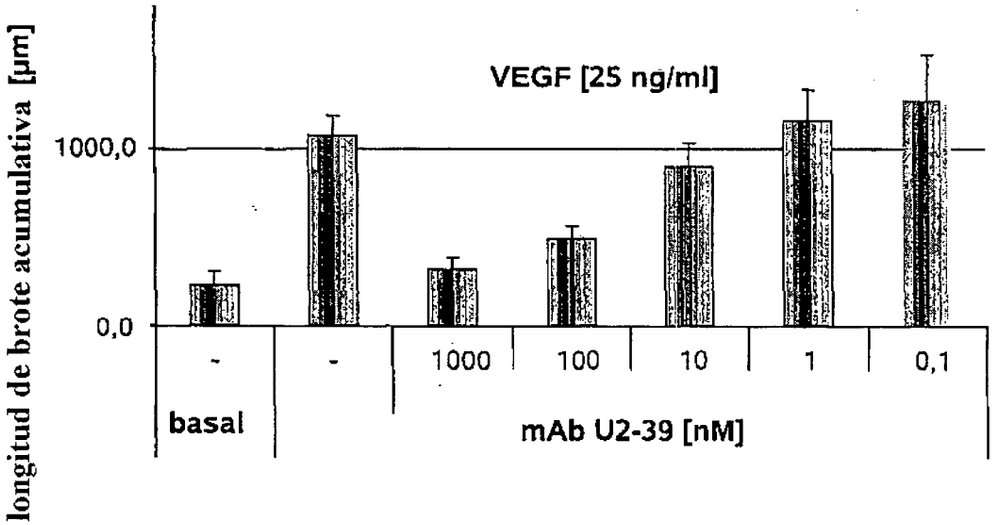


FIGURA 41B

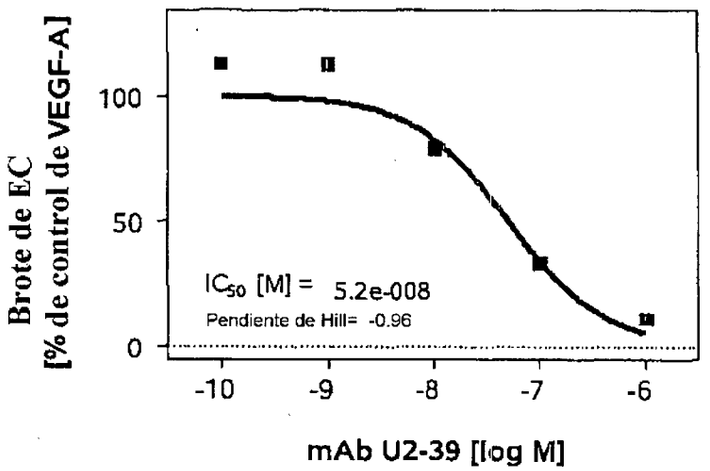


FIGURA 42

Análisis IHC de muestras de xenoinjerto de tumor-Inhibición de tinicón con CD31 de xenoinjertos de tumor humano *in vivo*

Xenoinjerto de tumor tratado con PBS

Xenoinjerto de tumor tratado con U2-39

Xenoinjerto de tumor tratado con Erbitux

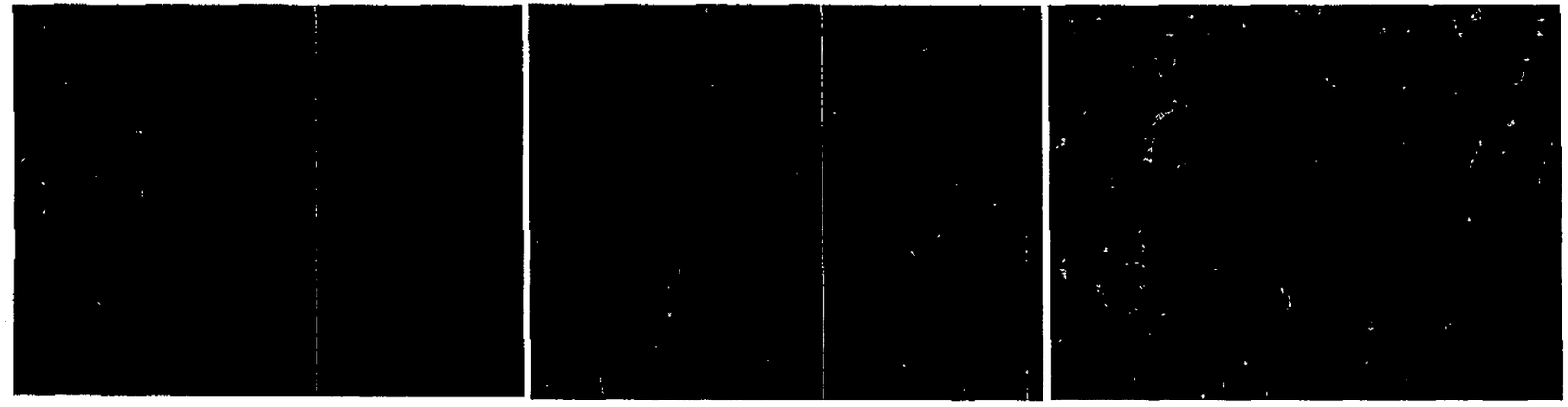
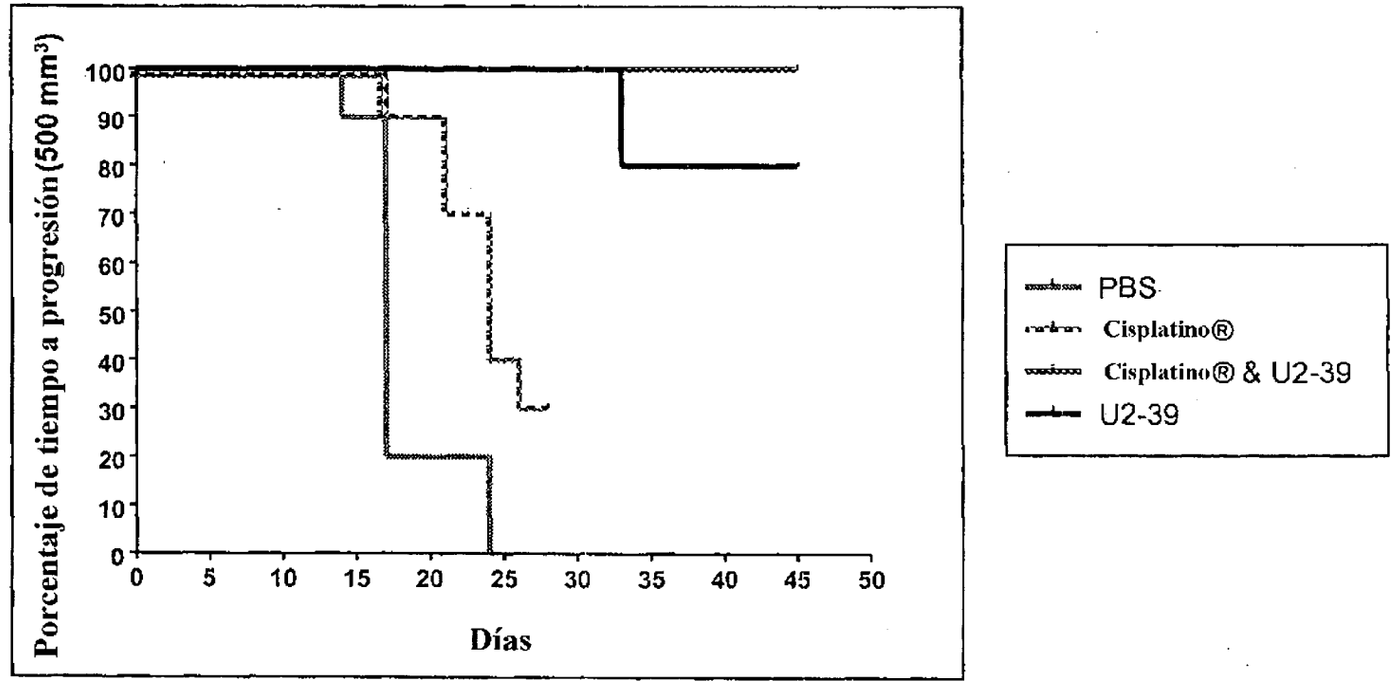


FIGURA **43A**


Porcentaje de tiempo a progresión (500 mm³)
100
90
80
70
60
50
40
30
20
10
0
0
5
10
15
20
25
30
35
40
45
50
Días
PBS
Cisplatino®
Cisplatino® & U2-39
U2-39

1873

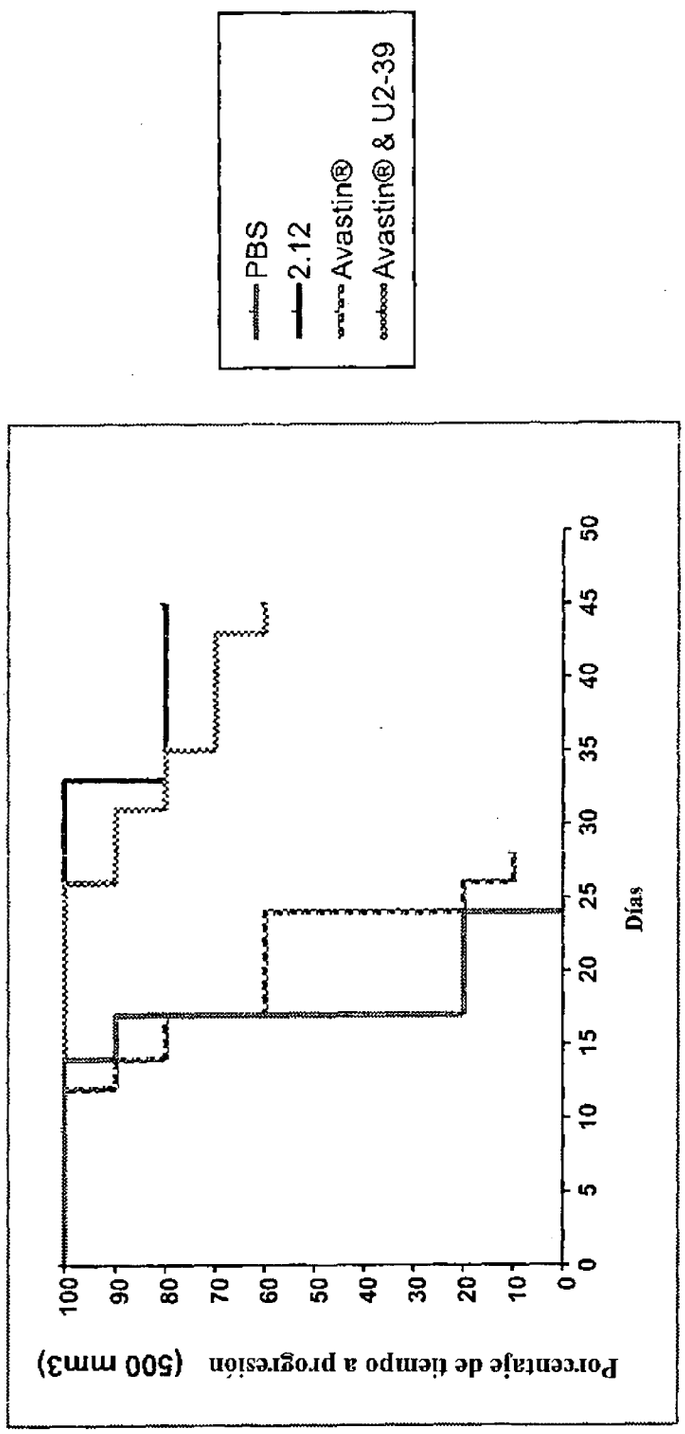


FIGURA 43B

LISTADO DE SECUENCIAS

<110> U3 Pharma AG/Amgen Inc.

<120> Proteínas de unión a antígeno de factor de crecimiento tipo factor de crecimiento epidérmico de unión a heparina

<130> 39562PWO

<141> 2008-09-26

<160> 1116

<170> PatentIn versión 3.3

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<213> Homo Sapiens

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Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
            20                  25                  30

Asp Gly Asn Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
        35                  40                  45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Asp Ser Gly Val Pro
    50                  55                  60

Asp Arg Phe Asn Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ser
                85                  90                  95

Thr His Trp Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105                 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
        115                 120                 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
    130                 135                 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145                 150                 155                 160
```

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 2
<211> 219
<212> PRT
<213> Homo Sapiens

<400> 2

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
20 25 30

Asp Gly Asn Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Asp Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ile Gln Gly
85 90 95

Thr His Trp Pro Thr Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

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<211> 219
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1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
20 25 30

Asp Gly Asn Thr Tyr Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Asp Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
85 90 95

Thr His Trp Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 4
<211> 219
<212> PRT
<213> Homo Sapiens

<400> 4

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1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Pro
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
85 90 95

Ile Gln Leu Pro Cys Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

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<211> 219
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<213> Homo Sapiens

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1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Pro
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ser
85 90 95

Ile Gln Leu Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 6
<211> 219
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<213> Homo Sapiens

<400> 6

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Tyr Trp Phe Leu Gln Lys Pro Gly Gln Pro
35 40 45

Pro Gln Pro Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ser
85 90 95

Ile Gln Leu Pro Ile Thr Phe Gly His Gly Thr Arg Leu Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

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1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ala Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
35 40 45

Tyr Val Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Asn Tyr Asn Ser Ala Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
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<210> 8
<211> 214
<212> PRT
<213> Homo Sapiens

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Ile Cys Arg Ala Ser Gln Gly Ile Ser Asn Asp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Val Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 9
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<213> Homo Sapiens

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Asn Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
        35                  40                  45

Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
    50                  55                  60

Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
                85                  90                  95

Thr Gln Phe Pro His Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
            100                 105                 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
        115                 120                 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
    130                 135                 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145                 150                 155                 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
                165                 170                 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
            180                 185                 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
        195                 200                 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215

<210>  10
<211>  219
<212>  PRT
<213>  Homo Sapiens

<400>  10

Glu Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
1               5                   10                  15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
            20                  25                  30

Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
        35                  40                  45
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Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Thr Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85 90 95

Thr Gln Phe Pro His Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
115 120 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 11
<211> 215
<212> PRT
<213> Homo Sapiens

<400> 11

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Thr Val Ile Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Ser Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 12
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Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Leu
20 25 30

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
35 40 45

Gly Ala Ser Arg Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
65 70 75 80

1885

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Arg Ser
85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 13
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<213> Homo Sapiens

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 14
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<212> PRT
<213> Homo Sapiens

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Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Phe Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

1887

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 15
<211> 220
<212> PRT
<213> Homo Sapiens

<400> 15

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Thr Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 16
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<213> Homo Sapiens

<400> 16

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Asn Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Phe Cys Gln Gln
85 90 95

Tyr Tyr Gly Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 17
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<213> Homo Sapiens

<400> 17

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Asn Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Phe Cys Gln Gln
85 90 95

Tyr Tyr Gly Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 18
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<213> Homo Sapiens

<400> 18

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Thr Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Gly Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Ile Ser Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 19
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<213> Homo Sapiens

<400> 19

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Asn
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Asp Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Thr Trp Thr Phe Gly Pro Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 20
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<212> PRT
<213> Homo Sapiens

<400> 20

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Asn
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Asp Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Thr Trp Thr Phe Gly Pro Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 21
<211> 220
<212> PRT
<213> Homo Sapiens

<400> 21

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Val Leu Ile Tyr Trp Ala Ser Thr Arg Lys Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Gly Leu Gln Ala Glu Asp Val Ala Leu Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Met Phe Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 22
<211> 220
<212> PRT
<213> Homo Sapiens

<400> 22

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Asp Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Phe Tyr Cys His Gln
85 90 95

Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Ala Ile
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 23
<211> 220
<212> PRT

<213> Homo Sapiens

<400> 23

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Ile Leu Tyr Arg
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ala Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Phe Cys Gln Gln
85 90 95

Tyr Phe Ile Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 24
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 24

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                  10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser His Tyr
            20                  25                  30

Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
        35                  40                  45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Lys Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Asn Tyr Pro Phe
                85                  90                  95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala
            100                 105                 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
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<210> 25
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<212> PRT
<213> Homo Sapiens

<400> 25

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                  10                  15
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Asp Arg Val Ala Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Ala Trp Leu Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Thr Tyr Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Met Asp Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 26
<211> 215
<212> PRT
<213> Homo Sapiens

<400> 26

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Asp Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Arg Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln His Asn Asn Trp Pro Pro
85 90 95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 27
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 27

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Arg Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

1899

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Phe Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 28
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 28

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Thr Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Phe Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Ala Tyr Tyr Cys Gln Gln Ser His Ser Ala Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 29
<211> 213
<212> PRT
<213> Homo Sapiens

<400> 29

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Ser Ile Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
115 120 125

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 30
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 30

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Asn Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Val Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Arg Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ile Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 31
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 31

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Arg Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Ser Arg Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Leu Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ile Tyr Ser Thr Ser Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 32
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 32

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Arg Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
35 40 45

Tyr Ala Glu Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ile Thr Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Ile Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 33
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 33

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Arg Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asn Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Phe Thr Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 34
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 34

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Phe Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Phe Ser Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 35
<211> 433
<212> PRT
<213> Homo Sapiens

<400> 35

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Leu Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Ser Phe Tyr Thr Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Ala Ser Thr Lys Gly
100 105 110

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
115 120 125

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
130 135 140

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
145 150 155 160

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
165 170 175

1907

Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val
180 185 190

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys
195 200 205

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
210 215 220

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
225 230 235 240

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
245 250 255

Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
260 265 270

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val
275 280 285

Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu
290 295 300

Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys
305 310 315 320

Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
325 330 335

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
340 345 350

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
355 360 365

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu
370 375 380

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
385 390 395 400

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
405 410 415

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
420 425 430

Lys

<210> 36
<211> 214
<212> PRT

<213> Homo Sapiens

<400> 36

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Thr Val Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Phe Thr Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 37
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 37

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Ser Phe Tyr Ala Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 38
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 38

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

1910

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Phe Thr Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 39
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 39

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Tyr Leu Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 40
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 40

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Ser
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Cys Asp Asp Leu Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 41
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 41

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asp Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln His Tyr Asp Asn Leu Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 42
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 42

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Ala Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 43
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 43

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Ser
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Ile Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Glu Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Cys Asp Ile Leu Pro Leu
85 90 95

Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 44
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 44

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Ser
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Leu
85 90 95

Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Arg Arg Thr Val Ala Ala
100 105 110

1916

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 45
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 45

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Gly Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Thr Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Ser Leu Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 46
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 46

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Leu Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

His Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 47
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 47

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asp Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln His Tyr Asp Asn Leu Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 48
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 48

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Ser
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln His Tyr Asp Asn Leu Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 49
<211> 446
<212> PRT
<213> Homo Sapiens

<400> 49

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Ser Ala Ser Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu
50 55 60

Gln Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Asp Asn Trp Asn Tyr Gly Phe Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val
210 215 220

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val
290 295 300

Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
325 330 335

Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 50
<211> 443
<212> PRT
<213> Homo Sapiens

<400> 50

Gln Val His Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Gly His
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Cys Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Ile Ala Val Ala Leu Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
115 120 125

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn
180 185 190

Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
195 200 205

Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro
210 215 220

Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro
225 230 235 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
245 250 255

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn
260 265 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
275 280 285

Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val
290 295 300

Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305 310 315 320

Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
325 330 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
340 345 350

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
355 360 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
370 375 380

Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe
385 390 395 400

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
405 410 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 51
<211> 443
<212> PRT
<213> Homo Sapiens

<400> 51

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn His Thr Gln Lys Phe
50 55 60

1924

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Ile Ala Val Ala Leu Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
115 120 125

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn
180 185 190

Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
195 200 205

Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro
210 215 220

Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro
225 230 235 240

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
245 250 255

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn
260 265 270

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
275 280 285

Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val
290 295 300

Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
305 310 315 320

Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
325 330 335

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
340 345 350

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
355 360 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
370 375 380

Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe
385 390 395 400

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
405 410 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 52
<211> 448
<212> PRT
<213> Homo Sapiens

<400> 52

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Arg Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Glu Leu
20 25 30

Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ser Phe Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Leu Glu Asp Thr Ser Thr Asp Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Thr Glu Gly Asp Gly Gly Tyr Tyr Tyr Tyr Gly Met Asp Val Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
130 135 140

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Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145                 150                 155                 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                165                 170                 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180                 185                 190

Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp
        195                 200                 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys
    210                 215                 220

Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr
                325                 330                 335

Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp
385                 390                 395                 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430
```

1927

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 53
<211> 448
<212> PRT
<213> Homo Sapiens

<400> 53

Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Ser Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Met Tyr Ser Ser Gly Trp Tyr Gly Val Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
130 135 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190

Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp
195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys
210 215 220

```
Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr
                325                 330                 335

Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp
385                 390                 395                 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445

<210>  54
<211>  449
<212>  PRT
<213>  Homo Sapiens

<400>  54

Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
1               5                   10                  15
```

```
Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asn Ala
            20                  25                  30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45

Trp Leu Val Leu Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
    50                  55                  60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Ser Gln Val
65                  70                  75                  80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala Arg Val Tyr Ser Ser Gly Trp Ser Phe Tyr Gly Met Asp Val
            100                 105                 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val
        195                 200                 205

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys
    210                 215                 220

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val
    290                 295                 300
```

Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys
325 330 335

Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 55
<211> 444
<212> PRT
<213> Homo Sapiens

<400> 55

Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Gly
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

```
Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala His Arg Arg Glu Leu Pro Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365
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1932

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
370 375 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser
385 390 395 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 56
<211> 444
<212> PRT
<213> Homo Sapiens

<400> 56

Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Gly
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Thr Gln Val
65 70 75 80

Val Leu Thr Val Thr Asp Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala His Arg Asn Trp Thr Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

```
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser
385                 390                 395                 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
                405                 410                 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            420                 425                 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440
```

1954

<210> 57
<211> 444
<212> PRT
<213> Homo Sapiens

<400> 57

Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Asn Thr Gly
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala His Arg Leu Glu Leu Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
210 215 220

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe
225 230 235 240

1925

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
245 250 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe
260 265 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
275 280 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr
290 295 300

Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305 310 315 320

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
325 330 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
340 345 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
355 360 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
370 375 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser
385 390 395 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 58
<211> 444
<212> PRT
<213> Homo Sapiens

<400> 58

Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Gly
20 25 30

```
Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35                  40                  45

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
    50                  55                  60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80

Val Leu Thr Met Thr Asn Leu Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala His Arg Arg Glu Val Pro Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320
```

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
325 330 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
340 345 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
355 360 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
370 375 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser
385 390 395 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 59
<211> 444
<212> PRT
<213> Homo Sapiens

<400> 59

Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Gly
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asn Val Glu Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Arg Ser Arg Leu Thr Ile Thr Lys Ala Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala His Arg His Thr Asn Pro Phe Glu Tyr Trp Gly Gln Gly Thr
100 105 110

```
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser
385                 390                 395                 400
```

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 60
<211> 444
<212> PRT
<213> Homo Sapiens

<400> 60

Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Gly
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala His Arg Gly Glu Leu Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

```
Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
        195                 200                 205

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser
385                 390                 395                 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
                405                 410                 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            420                 425                 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440
```

<210> 61
<211> 447
<212> PRT
<213> Homo Sapiens

<400> 61

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser Arg Tyr
20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Val Gly Ala Thr Pro Asp Ala Phe Asp Ile Trp Gly
100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys
210 215 220

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
290 295 300

Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
325 330 335

Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 62
<211> 454
<212> PRT
<213> Homo Sapiens

<400> 62

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Glu Gly Ile Ala Val Ala Gly Thr Ala Glu Tyr Tyr Tyr Tyr
            100                 105                 110

Tyr Ala Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
    130                 135                 140

Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
145                 150                 155                 160

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
                165                 170                 175

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
            180                 185                 190

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
        195                 200                 205

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
    210                 215                 220

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
225                 230                 235                 240

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
                245                 250                 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
            260                 265                 270

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
        275                 280                 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
    290                 295                 300

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
305                 310                 315                 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
                325                 330                 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
            340                 345                 350
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Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
385 390 395 400

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
435 440 445

Ser Leu Ser Pro Gly Lys
450

<210> 63
<211> 451
<212> PRT
<213> Homo Sapiens

<400> 63

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Gly Ile Ala Ala Arg Asp Ser Tyr Tyr Tyr Tyr Ala Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser
130 135 140

Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
180 185 190

Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys
195 200 205

Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu
210 215 220

Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
290 295 300

Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 64
<211> 451
<212> PRT
<213> Homo Sapiens

<400> 64

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Glu Tyr Tyr Cys
85 90 95

Ala Lys Glu Gly Ile Ala Gly Arg Asp Ser Tyr Tyr Tyr Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser
130 135 140

Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
180 185 190

Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys
195 200 205

Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu
210 215 220

Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
290 295 300

Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 65
<211> 449

<212> PRT
<213> Homo Sapiens

<400> 65

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Phe Ile Ser Asp Asp Gly Ser Thr Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Met Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Tyr Tyr Asp Ser Ser Gly Tyr Tyr Tyr Gly Phe Asp Tyr
            100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
    130                 135                 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val
        195                 200                 205

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys
    210                 215                 220

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255
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Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val
290 295 300

Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys
325 330 335

Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 66
<211> 440
<212> PRT
<213> Homo Sapiens

<400> 66

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asn Val Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
            100                 105                 110

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys
        115                 120                 125

Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys
    130                 135                 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
145                 150                 155                 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
                165                 170                 175

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr
            180                 185                 190

Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val
        195                 200                 205

Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro
    210                 215                 220

Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
225                 230                 235                 240

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
                245                 250                 255

Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
            260                 265                 270

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
        275                 280                 285

Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln
    290                 295                 300

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
305                 310                 315                 320
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Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro
325 330 335

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
340 345 350

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
355 360 365

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
370 375 380

Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
385 390 395 400

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
405 410 415

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
420 425 430

Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 67
<211> 446
<212> PRT
<213> Homo Sapiens

<400> 67

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Asp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Ile Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Ala Thr Gly Ala Glu Tyr Phe Gln His Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val
210 215 220

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val
290 295 300

Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
325 330 335

Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 68
<211> 444
<212> PRT
<213> Homo Sapiens

<400> 68

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Leu Leu Trp Phe Gly Glu Thr Phe Asp Tyr Trp Gly Gln Gly Ser
100 105 110

Leu Val Thr Val Ser Pro Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
210 215 220

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe
225 230 235 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
245 250 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe
260 265 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
275 280 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr
290 295 300

Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305 310 315 320

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
325 330 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
340 345 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
355 360 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
370 375 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser
385 390 395 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 69
<211> 441
<212> PRT
<213> Homo Sapiens

<400> 69

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Val Ile Trp Ser Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asn Leu Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
        115                 120                 125

Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val
    130                 135                 140

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145                 150                 155                 160

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
                165                 170                 175

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly
            180                 185                 190

Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys
        195                 200                 205

Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys
    210                 215                 220

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
225                 230                 235                 240

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
                245                 250                 255

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
            260                 265                 270
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Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
275 280 285

Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His
290 295 300

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
305 310 315 320

Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
325 330 335

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
340 345 350

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
355 360 365

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
370 375 380

Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
385 390 395 400

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
405 410 415

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
420 425 430

Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 70
<211> 449
<212> PRT
<213> Homo Sapiens

<400> 70

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Asp Asp Gly Ser Asn Gln Tyr Tyr Thr Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser His Tyr Gly Gly Asp Tyr Asp Tyr Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
180 185 190

Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val
195 200 205

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys
210 215 220

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val
290 295 300

Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys
325 330 335

Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
340 345 350

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu
385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<210> 71
<211> 446
<212> PRT
<213> Homo Sapiens

<400> 71

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Arg Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Trp Gln Gln Gln Ala Pro Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

1960

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val
210 215 220

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val
290 295 300

Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
325 330 335

Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 72
<211> 444
<212> PRT
<213> Homo Sapiens

<400> 72

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser His
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val
50 55 60

Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Trp Gly Ile Ser Ala Pro Phe Asp Cys Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

1962

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Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser
385                 390                 395                 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
                405                 410                 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            420                 425                 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440

<210>  73
<211>  441
<212>  PRT
<213>  Homo Sapiens

<400>  73
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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
            20                  25                  30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Tyr Ile Ser Ser Ser Gly Arg Thr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Phe
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Leu Trp Ala Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
            100                 105                 110

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
        115                 120                 125

Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val
    130                 135                 140

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145                 150                 155                 160

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
                165                 170                 175

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly
            180                 185                 190

Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys
        195                 200                 205

Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys
    210                 215                 220

Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
225                 230                 235                 240

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
                245                 250                 255

Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
            260                 265                 270

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
        275                 280                 285
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1964

Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His
290 295 300

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
305 310 315 320

Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln
325 330 335

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met
340 345 350

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
355 360 365

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
370 375 380

Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu
385 390 395 400

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
405 410 415

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
420 425 430

Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 74
<211> 451
<212> PRT
<213> Homo Sapiens

<400> 74

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser His Ile Ser Ser Ser Ser Arg Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Val Tyr
65 70 75 80

```
Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Gly Tyr Asn Trp Asn Gly Gly Gly Asn Tyr Tyr Gly Met
            100                 105                 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
        115                 120                 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser
    130                 135                 140

Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
145                 150                 155                 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
                165                 170                 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
            180                 185                 190

Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys
        195                 200                 205

Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu
    210                 215                 220

Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365
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Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 75
<211> 451
<212> PRT
<213> Homo Sapiens

<400> 75

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser His Ile Ser Arg Ser Ser Arg Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Asn Trp Asn Asn Gly Gly Tyr Tyr Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser
130 135 140

```
Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
145                 150                 155                 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
                165                 170                 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
            180                 185                 190

Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys
        195                 200                 205

Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu
    210                 215                 220

Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile
                325                 330                 335

Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
        355                 360                 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430
```

196 r

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 76
<211> 444
<212> PRT
<213> Homo Sapiens

<400> 76

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile His Ser Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Asn Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Gly Pro Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr
100 105 110

Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
210 215 220

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe
225 230 235 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
245 250 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe
260 265 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
275 280 285

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr
290 295 300

Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305 310 315 320

Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
325 330 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
340 345 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
355 360 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
370 375 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser
385 390 395 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440

<210> 77
<211> 453
<212> PRT
<213> Homo Sapiens

1970

<400> 77

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                  10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Arg Gly
            20                  25                  30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr His Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Asn Met Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Ala Leu Arg Gly Ile Val Leu Met Val Tyr Val Leu Gly
            100                 105                 110

Ala Leu Asp Ile Trp Gly Gln Gly Thr Lys Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser
    130                 135                 140

Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr
        195                 200                 205

Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr
    210                 215                 220

Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro
225                 230                 235                 240

Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270
```

Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
275 280 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
290 295 300

Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu
305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala
325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro
340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385 390 395 400

Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly Lys
450

<210> 78
<211> 453
<212> PRT
<213> Homo Sapiens

<400> 78

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

```
Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Asp Glu Thr Val Val Arg Gly Leu Ile Arg Tyr Cys Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
        115                 120                 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser
    130                 135                 140

Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145                 150                 155                 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
                165                 170                 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
            180                 185                 190

Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr
        195                 200                 205

Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr
    210                 215                 220

Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro
225                 230                 235                 240

Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
    290                 295                 300

Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu
305                 310                 315                 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala
                325                 330                 335
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1973

Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro
340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385 390 395 400

Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly Lys
450

<210> 79
<211> 448
<212> PRT
<213> Homo Sapiens

<400> 79

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Asn Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile His Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Ile Thr Ile Ser Ala Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Asp Arg Gly Gly Gly Asp Tyr Gly Arg Met Asp Val Trp
100 105 110

```
Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
        115                 120                 125

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
    130                 135                 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145                 150                 155                 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
                165                 170                 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
            180                 185                 190

Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp
        195                 200                 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys
    210                 215                 220

Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr
                325                 330                 335

Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp
385                 390                 395                 400
```

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
405 410 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
420 425 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 80
<211> 448
<212> PRT
<213> Homo Sapiens

<400> 80

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Asn Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile His Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Ile Thr Ile Ser Ala Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Asp Arg Gly Gly Gly Asp Tyr Gly Arg Met Asp Val Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
130 135 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190

1976

```
Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp
        195                 200                 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys
    210                 215                 220

Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser
225                 230                 235                 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
                245                 250                 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
            260                 265                 270

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
        275                 280                 285

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val
    290                 295                 300

Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305                 310                 315                 320

Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr
                325                 330                 335

Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
            340                 345                 350

Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
        355                 360                 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
    370                 375                 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp
385                 390                 395                 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
                405                 410                 415

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
            420                 425                 430

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        435                 440                 445

<210>  81
<211>  445
<212>  PRT
<213>  Homo Sapiens
```

<400> 81

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile His Ser Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Ile Thr Lys Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Ser Asn Asn Tyr Gly Cys Phe Ala Leu Trp Gly Arg Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu
210 215 220

Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln
260 265 270

1978

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu
290 295 300

Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
325 330 335

Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
340 345 350

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 82
<211> 445
<212> PRT
<213> Homo Sapiens

<400> 82

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile His Ser Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

1979

Leu Lys Ser Arg Ile Thr Lys Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Ser Asn Asn Tyr Gly Cys Phe Ala Leu Trp Gly Arg Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu
210 215 220

Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln
260 265 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu
290 295 300

Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
325 330 335

Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
340 345 350

1980

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 83
<211> 459
<212> PRT
<213> Homo Sapiens

<400> 83

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile His Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Ser Gly Tyr Asn Tyr Gly Leu Tyr Tyr Tyr Asp Ser Ser Gly
100 105 110

Tyr Pro Ser Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
115 120 125

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
130 135 140

1981

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
145 150 155 160

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
165 170 175

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
180 185 190

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn
195 200 205

Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
210 215 220

Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro
225 230 235 240

Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro
245 250 255

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
260 265 270

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn
275 280 285

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
290 295 300

Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val
305 310 315 320

Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
325 330 335

Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
340 345 350

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
355 360 365

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
370 375 380

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
385 390 395 400

Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe
405 410 415

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
420 425 430

1982

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
435 440 445

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455

<210> 84
<211> 451
<212> PRT
<213> Homo Sapiens

<400> 84

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Asp Tyr Tyr Trp Asn Trp Val Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Gly Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Phe Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe
85 90 95

Cys Ala Arg Thr Tyr Tyr Asp Ile Leu Thr Gly Tyr Pro Phe Tyr Phe
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser
130 135 140

Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
180 185 190

Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys
195 200 205

1983

Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu
210 215 220

Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
290 295 300

Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 85
<211> 451
<212> PRT
<213> Homo Sapiens

1984

<400> 85

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Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1               5                  10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
            20                  25                  30

Asp Tyr Tyr Trp Asn Trp Val Arg Gln His Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Gly Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Phe Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe
                85                  90                  95

Cys Ala Arg Thr Tyr Tyr Asp Ile Leu Thr Gly Tyr Pro Phe Tyr Phe
            100                 105                 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
        115                 120                 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser
    130                 135                 140

Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
145                 150                 155                 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
                165                 170                 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
            180                 185                 190

Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys
        195                 200                 205

Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu
    210                 215                 220

Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270
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1985

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
290 295 300

Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 86
<211> 446
<212> PRT
<213> Homo Sapiens

<400> 86

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

1986

Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gly Gly Tyr Ser Ser Ser Trp Tyr Trp Phe Asp Pro Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val
210 215 220

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val
290 295 300

Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
325 330 335

Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 87
<211> 446
<212> PRT
<213> Homo Sapiens

<400> 87

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gly Gly Tyr Ser Ser Ser Trp Phe Trp Phe Asp Pro Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

1988

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Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val
    210                 215                 220

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
225                 230                 235                 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            260                 265                 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val
    290                 295                 300

Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320

Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
                325                 330                 335

Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            340                 345                 350

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        355                 360                 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    370                 375                 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp
385                 390                 395                 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415
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Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 88
<211> 449
<212> PRT
<213> Homo Sapiens

<400> 88

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Arg Ile Tyr Thr Ser Gly Thr Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Gly Tyr Ser Tyr Gly His Tyr Tyr Tyr Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
180 185 190

Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val
195 200 205

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Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys
    210                 215                 220

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu
385                 390                 395                 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445

Lys
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<210> 89
<211> 452
<212> PRT
<213> Homo Sapiens

1991

<400> 89

```
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                  10                  15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Ser Gly
            20                  25                  30

Gly Ser Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser
    50                  55                  60

Leu Lys Ser Arg Val Thr Ile Ser Ile Val Thr Ser Arg Asn Gln Phe
65                  70                  75                  80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

Cys Ala Arg Ser Ala Leu Arg Tyr Phe Asp Trp Leu Phe Ser Asp Val
            100                 105                 110

Ser Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser
        115                 120                 125

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr
    130                 135                 140

Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
145                 150                 155                 160

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
                165                 170                 175

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
            180                 185                 190

Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr
        195                 200                 205

Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val
    210                 215                 220

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
225                 230                 235                 240

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                245                 250                 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            260                 265                 270
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His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
275 280 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
290 295 300

Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn
305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro
325 330 335

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln
340 345 350

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
355 360 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385 390 395 400

Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
405 410 415

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
435 440 445

Ser Pro Gly Lys
450

<210> 90
<211> 446
<212> PRT
<213> Homo Sapiens

<400> 90

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Leu Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Arg Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

```
Gly Ile Ile Tyr Pro Asp Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
    50                  55                  60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

Ala Arg Gln Lys Ser Tyr Gly Tyr Ser Tyr Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        115                 120                 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
    130                 135                 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145                 150                 155                 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                165                 170                 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            180                 185                 190

Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys
        195                 200                 205

Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val
    210                 215                 220

Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe
225                 230                 235                 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            260                 265                 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val
    290                 295                 300

Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320

Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
                325                 330                 335
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1994

Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 91
<211> 447
<212> PRT
<213> Homo Sapiens

<400> 91

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Asp Asp Ser Asp Ala Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Tyr Gly Ser Gly Trp Gly Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys
210 215 220

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
290 295 300

Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
325 330 335

Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
405 410 415

1996

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 92
<211> 453
<212> PRT
<213> Homo Sapiens

<400> 92

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Ile Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Leu Ala Val Ala Gly Thr Ser Tyr Tyr Tyr Tyr Tyr
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
115 120 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser
130 135 140

Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145 150 155 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
165 170 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
180 185 190

Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr
195 200 205

1997

Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr
210 215 220

Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro
225 230 235 240

Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
245 250 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
260 265 270

Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
275 280 285

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
290 295 300

Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu
305 310 315 320

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala
325 330 335

Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro
340 345 350

Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln
355 360 365

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
370 375 380

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385 390 395 400

Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
405 410 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
420 425 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
435 440 445

Leu Ser Pro Gly Lys
450

<210> 93
<211> 451
<212> PRT
<213> Homo Sapiens

1998

<400> 93

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Tyr
20 25 30

Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
35 40 45

Trp Leu Gly Arg Thr Tyr Cys Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Ala Arg Asp Arg Ala Val Ala Gly Tyr Tyr Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser
130 135 140

Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
180 185 190

Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys
195 200 205

Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu
210 215 220

Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

1999

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe
290 295 300

Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys
450

<210> 94
<211> 112
<212> PRT
<213> Homo Sapiens

<400> 94

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
20 25 30

Asp Gly Asn Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

2000

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Asp Ser Gly Val Pro
50 55 60

Asp Arg Phe Asn Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ser
85 90 95

Thr His Trp Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105 110

<210> 95
<211> 112
<212> PRT
<213> Homo Sapiens

<400> 95

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
20 25 30

Asp Gly Asn Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Asp Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ile Gln Gly
85 90 95

Thr His Trp Pro Thr Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105 110

<210> 96
<211> 112
<212> PRT
<213> Homo Sapiens

<400> 96

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val Tyr Ser
20 25 30

Asp Gly Asn Thr Tyr Leu Asn Trp Leu Gln Gln Arg Pro Gly Gln Ser
35 40 45

Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Trp Asp Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
85 90 95

Thr His Trp Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105 110

<210> 97
<211> 112
<212> PRT
<213> Homo Sapiens

<400> 97

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Pro
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
85 90 95

Ile Gln Leu Pro Cys Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 98
<211> 112
<212> PRT
<213> Homo Sapiens

<400> 98

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Pro
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ser
85 90 95

Ile Gln Leu Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 99
<211> 112
<212> PRT
<213> Homo Sapiens

<400> 99

Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asp Gly Lys Thr Tyr Leu Tyr Trp Phe Leu Gln Lys Pro Gly Gln Pro
35 40 45

Pro Gln Pro Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ser
85 90 95

Ile Gln Leu Pro Ile Thr Phe Gly His Gly Thr Arg Leu Glu Ile Lys
100 105 110

<210> 100
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 100

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ala Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
35 40 45

Tyr Val Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Asn Tyr Asn Ser Ala Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 101
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 101

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Ile Cys Arg Ala Ser Gln Gly Ile Ser Asn Asp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Val Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 102
<211> 112
<212> PRT
<213> Homo Sapiens

<400> 102

Asn Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
35 40 45

Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85 90 95

Thr Gln Phe Pro His Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105 110

<210> 103
<211> 112
<212> PRT
<213> Homo Sapiens

<400> 103

Glu Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Asp Gly Asn Thr Tyr Leu Ser Trp Leu Gln Gln Arg Pro Gly Gln Pro
35 40 45

Pro Arg Leu Leu Ile Tyr Lys Ile Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Thr Gly Ala Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85 90 95

Thr Gln Phe Pro His Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 104
<211> 108

<212> PRT
<213> Homo Sapiens

<400> 104

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Thr Val Ile Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Ser Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 105
<211> 106
<212> PRT
<213> Homo Sapiens

<400> 105

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Arg Leu
20 25 30

Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
35 40 45

Gly Ala Ser Arg Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu
65 70 75 80

Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro Arg Ser
85 90 95

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 106
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 106

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
20 25 30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Tyr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 107
<211> 113
<212> PRT
<213> Homo Sapiens

<400> 107

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Val Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Phe Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Phe Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 108
<211> 113
<212> PRT
<213> Homo Sapiens

<400> 108

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Thr Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 109
<211> 113
<212> PRT
<213> Homo Sapiens

<400> 109

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Asn Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Phe Cys Gln Gln
85 90 95

Tyr Tyr Gly Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 110
<211> 113
<212> PRT
<213> Homo Sapiens

<400> 110

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Asn Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Phe Cys Gln Gln
85 90 95

Tyr Tyr Gly Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 111
<211> 113
<212> PRT
<213> Homo Sapiens

<400> 111

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Thr Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Gly Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Ile Ser Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 112
<211> 113
<212> PRT
<213> Homo Sapiens

<400> 112

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Asn
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Asp Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Thr Trp Thr Phe Gly Pro Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 113
<211> 113
<212> PRT
<213> Homo Sapiens

<400> 113

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Asn
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Asp Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Thr Trp Thr Phe Gly Pro Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 114
<211> 113
<212> PRT
<213> Homo Sapiens

<400> 114

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Val Leu Ile Tyr Trp Ala Ser Thr Arg Lys Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Gly Leu Gln Ala Glu Asp Val Ala Leu Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Met Phe Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile
100 105 110

Lys

<210> 115
<211> 113
<212> PRT
<213> Homo Sapiens

<400> 115

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Asp Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Phe Tyr Cys His Gln
85 90 95

Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Ala Ile
100 105 110

Lys

<210> 116
<211> 113
<212> PRT
<213> Homo Sapiens

<400> 116

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Ile Leu Tyr Arg
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ala Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Phe Cys Gln Gln
85 90 95

Tyr Phe Ile Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 117
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 117

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser His Tyr
20 25 30

Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Lys Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Asn Tyr Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 118
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 118

2013

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                  10                  15

Asp Arg Val Ala Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
            20                  25                  30

Leu Ala Trp Leu Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
        35                  40                  45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Thr Tyr Pro Phe
                85                  90                  95

Thr Phe Gly Pro Gly Thr Lys Met Asp Ile Lys
            100                 105
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<210> 119
<211> 108
<212> PRT
<213> Homo Sapiens

<400> 119

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Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1               5                  10                  15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Asp Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45

Tyr Gly Ala Ser Arg Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65                  70                  75                  80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln His Asn Asn Trp Pro Pro
                85                  90                  95

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105
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<210> 120
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 120

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Arg Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Phe Lys
100 105

<210> 121
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 121

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Thr Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Phe Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Ala Tyr Tyr Cys Gln Gln Ser His Ser Ala Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 122
<211> 106

<212> PRT
<213> Homo Sapiens

<400> 122

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Ser Ile Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Thr
85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 123
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 123

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Arg Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Arg Pro Gly Asn Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Val Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Arg Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ile Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 124
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 124

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Arg Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Ser Arg Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Leu Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ile Tyr Ser Thr Ser Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 125
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 125

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Arg Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
35 40 45

Tyr Ala Glu Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ile Thr Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Ile
100 105

<210> 126
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 126

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Arg Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asn Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Phe Thr Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 127
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 127

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Phe Ser Ser Leu Gln Pro
65 70 75 80

2018

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Phe Ser Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 128
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 128

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Leu Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Ser Phe Tyr Thr Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 129
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 129

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Thr Val Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Phe Thr Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 130
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 130

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Ser Phe Tyr Ala Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 131
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 131

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

1020

Tyr Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Phe Thr Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 132
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 132

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Tyr Leu Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 133
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 133

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Ser
20 25 30

2021

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Cys Asp Asp Leu Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 134
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 134

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asp Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln His Tyr Asp Asn Leu Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 135
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 135

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Ala Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 136
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 136

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Ser
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Ile Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Glu Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Cys Asp Ile Leu Pro Leu
85 90 95

Ser Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 137
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 137

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Ser
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Leu
85 90 95

Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Arg
100 105

<210> 138
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 138

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Gly Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Thr Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Ser Leu Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 139
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 139

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Leu Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

His Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 140
<211> 107
<212> PRT
<213> Homo Sapiens

<400> 140

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asp Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln His Tyr Asp Asn Leu Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 141
<211> 107

<212> PRT
<213> Homo Sapiens

<400> 141

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Ser
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln His Tyr Asp Asn Leu Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105

<210> 142
<211> 120
<212> PRT
<213> Homo Sapiens

<400> 142

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Ser Ala Ser Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu
50 55 60

Gln Asp Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Asp Asn Trp Asn Tyr Gly Phe Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 143
<211> 117
<212> PRT
<213> Homo Sapiens

<400> 143

Gln Val His Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Phe Thr Gly His
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Cys Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Ile Ala Val Ala Leu Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 144
<211> 117
<212> PRT
<213> Homo Sapiens

<400> 144

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn His Thr Gln Lys Phe
50 55 60

1027

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Ile Ala Val Ala Leu Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser
115

<210> 145
<211> 122
<212> PRT
<213> Homo Sapiens

<400> 145

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Arg Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Glu Leu
20 25 30

Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ser Phe Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Leu Glu Asp Thr Ser Thr Asp Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Thr Glu Gly Asp Gly Gly Tyr Tyr Tyr Tyr Gly Met Asp Val Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 146
<211> 122
<212> PRT
<213> Homo Sapiens

<400> 146

Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
1 5 10 15

1028

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Ser Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Met Tyr Ser Ser Gly Trp Tyr Gly Val Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 147
<211> 123
<212> PRT
<213> Homo Sapiens

<400> 147

Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asn Ala
20 25 30

Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Val Leu Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Ser Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Val Tyr Ser Ser Gly Trp Ser Phe Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 148

2019

<211> 118
<212> PRT
<213> Homo Sapiens

<400> 148

Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Gly
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala His Arg Arg Glu Leu Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 149
<211> 118
<212> PRT
<213> Homo Sapiens

<400> 149

Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Gly
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Thr Gln Val
65 70 75 80

2030

Val Leu Thr Val Thr Asp Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala His Arg Asn Trp Thr Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 150
<211> 118
<212> PRT
<213> Homo Sapiens

<400> 150

Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Asn Thr Gly
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala His Arg Leu Glu Leu Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 151
<211> 118
<212> PRT
<213> Homo Sapiens

<400> 151

Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Gly
20 25 30

2031

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Leu Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala His Arg Arg Glu Val Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 152
<211> 118
<212> PRT
<213> Homo Sapiens

<400> 152

Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Gly
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asn Val Glu Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Arg Ser Arg Leu Thr Ile Thr Lys Ala Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala His Arg His Thr Asn Pro Phe Glu Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 153
<211> 118
<212> PRT
<213> Homo Sapiens

2032

<400> 153

Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Gly
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala His Arg Gly Glu Leu Pro Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 154
<211> 121
<212> PRT
<213> Homo Sapiens

<400> 154

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Ser Arg Tyr
20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Ser Ser Ser Ser Ser Tyr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Val Gly Ala Thr Pro Asp Ala Phe Asp Ile Trp Gly
100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 155
<211> 128
<212> PRT
<213> Homo Sapiens

<400> 155

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Gly Ile Ala Val Ala Gly Thr Ala Glu Tyr Tyr Tyr Tyr
100 105 110

Tyr Ala Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 156
<211> 125
<212> PRT
<213> Homo Sapiens

<400> 156

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Gly Ile Ala Ala Arg Asp Ser Tyr Tyr Tyr Tyr Ala Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 157
<211> 125
<212> PRT
<213> Homo Sapiens

<400> 157

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Glu Tyr Tyr Cys
85 90 95

Ala Lys Glu Gly Ile Ala Gly Arg Asp Ser Tyr Tyr Tyr Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 158
<211> 123
<212> PRT
<213> Homo Sapiens

<400> 158

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Phe Ile Ser Asp Asp Gly Ser Thr Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Met Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Tyr Tyr Asp Ser Ser Gly Tyr Tyr Tyr Gly Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 159
<211> 114
<212> PRT
<213> Homo Sapiens

<400> 159

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asn Val Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ser

<210> 160

<211> 120
<212> PRT
<213> Homo Sapiens

<400> 160

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Asp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Ile Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Ala Thr Gly Ala Glu Tyr Phe Gln His Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 161
<211> 118
<212> PRT
<213> Homo Sapiens

<400> 161

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Leu Leu Trp Phe Gly Glu Thr Phe Asp Tyr Trp Gly Gln Gly Ser
100 105 110

Leu Val Thr Val Ser Pro
115

<210> 162
<211> 115
<212> PRT
<213> Homo Sapiens

<400> 162

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Ser Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asn Leu Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 163
<211> 123
<212> PRT
<213> Homo Sapiens

<400> 163

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Asp Asp Gly Ser Asn Gln Tyr Tyr Thr Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser His Tyr Gly Gly Asp Tyr Asp Tyr Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 164
<211> 120
<212> PRT
<213> Homo Sapiens

<400> 164

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Arg Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Trp Gln Gln Gln Ala Pro Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 165
<211> 118
<212> PRT
<213> Homo Sapiens

<400> 165

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser His
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Val Ile Trp Tyr Asp Gly Ser Asn Lys Asn Tyr Ala Asp Ser Val
50 55 60

Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Asp
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Trp Gly Ile Ser Ala Pro Phe Asp Cys Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 166
<211> 115
<212> PRT
<213> Homo Sapiens

<400> 166

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Tyr Ile Ser Ser Ser Gly Arg Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Phe
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Leu Trp Ala Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser
115

<210> 167
<211> 125
<212> PRT
<213> Homo Sapiens

<400> 167

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser His Ile Ser Ser Ser Ser Arg Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Val Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Asn Trp Asn Gly Gly Gly Asn Tyr Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 168
<211> 125
<212> PRT
<213> Homo Sapiens

<400> 168

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ser Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser His Ile Ser Arg Ser Ser Arg Thr Ile Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Asn Trp Asn Asn Gly Gly Tyr Tyr Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 169
<211> 118
<212> PRT
<213> Homo Sapiens

<400> 169

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile His Ser Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Asn Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Gly Pro Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr
100 105 110

Thr Val Thr Val Ser Ser
115

<210> 170
<211> 127
<212> PRT
<213> Homo Sapiens

<400> 170

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

2042

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Arg Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr His Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Asn Met Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Ala Leu Arg Gly Ile Val Leu Met Val Tyr Val Leu Gly
100 105 110

Ala Leu Asp Ile Trp Gly Gln Gly Thr Lys Val Thr Val Ser Ser
115 120 125

<210> 171
<211> 127
<212> PRT
<213> Homo Sapiens

<400> 171

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Asp Glu Thr Val Val Arg Gly Leu Ile Arg Tyr Cys Tyr
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 172

2043

<211> 122
<212> PRT
<213> Homo Sapiens

<400> 172

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Asn Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile His Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Ile Thr Ile Ser Ala Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Asp Arg Gly Gly Gly Asp Tyr Gly Arg Met Asp Val Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 173
<211> 122
<212> PRT
<213> Homo Sapiens

<400> 173

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Asn Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile His Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Ile Thr Ile Ser Ala Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Asp Arg Gly Gly Gly Asp Tyr Gly Arg Met Asp Val Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 174
<211> 119
<212> PRT
<213> Homo Sapiens

<400> 174

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile His Ser Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Ile Thr Lys Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Ser Asn Asn Tyr Gly Cys Phe Ala Leu Trp Gly Arg Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 175
<211> 119
<212> PRT
<213> Homo Sapiens

<400> 175

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

1045

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile His Ser Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Ile Thr Lys Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Ser Asn Asn Tyr Gly Cys Phe Ala Leu Trp Gly Arg Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 176
<211> 133
<212> PRT
<213> Homo Sapiens

<400> 176

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile His Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Ser Gly Tyr Asn Tyr Gly Leu Tyr Tyr Tyr Asp Ser Ser Gly
100 105 110

Tyr Pro Ser Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
115 120 125

Val Thr Val Ser Ser
130

<210> 177

<211> 125
<212> PRT
<213> Homo Sapiens

<400> 177

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Asp Tyr Tyr Trp Asn Trp Val Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Gly Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Phe Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe
85 90 95

Cys Ala Arg Thr Tyr Tyr Asp Ile Leu Thr Gly Tyr Pro Phe Tyr Phe
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 178
<211> 125
<212> PRT
<213> Homo Sapiens

<400> 178

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Asp Tyr Tyr Trp Asn Trp Val Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Gly Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Phe Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe
85 90 95

Cys Ala Arg Thr Tyr Tyr Asp Ile Leu Thr Gly Tyr Pro Phe Tyr Phe
100 105 110

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 179
<211> 120
<212> PRT
<213> Homo Sapiens

<400> 179

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gly Gly Tyr Ser Ser Ser Trp Tyr Trp Phe Asp Pro Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 180
<211> 120
<212> PRT
<213> Homo Sapiens

<400> 180

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
20 25 30

1048

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Gly Gly Tyr Ser Ser Ser Trp Phe Trp Phe Asp Pro Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 181
<211> 123
<212> PRT
<213> Homo Sapiens

<400> 181

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Arg Ile Tyr Thr Ser Gly Thr Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Gly Tyr Ser Tyr Gly His Tyr Tyr Tyr Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 182
<211> 126
<212> PRT
<213> Homo Sapiens

<400> 182

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Val Ser Ser Gly
20 25 30

Gly Ser Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Ile Val Thr Ser Arg Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Ser Ala Leu Arg Tyr Phe Asp Trp Leu Phe Ser Asp Val
100 105 110

Ser Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120 125

<210> 183
<211> 120
<212> PRT
<213> Homo Sapiens

<400> 183

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Leu Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Arg Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Asp Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Gln Lys Ser Tyr Gly Tyr Ser Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 184
<211> 121
<212> PRT
<213> Homo Sapiens

<400> 184

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Asp Asp Ser Asp Ala Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Tyr Gly Ser Gly Trp Gly Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 185
<211> 127
<212> PRT
<213> Homo Sapiens

<400> 185

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Ile Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Gln Gly Leu Ala Val Ala Gly Thr Ser Tyr Tyr Tyr Tyr Tyr
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 186
<211> 125
<212> PRT
<213> Homo Sapiens

<400> 186

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Tyr
20 25 30

Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
35 40 45

Trp Leu Gly Arg Thr Tyr Cys Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Ala Arg Asp Arg Ala Val Ala Gly Tyr Tyr Tyr Gly Met
100 105 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

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Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
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Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
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Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

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Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
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Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
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Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr
65 70 75 80

Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro
100 105 110

Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
115 120 125

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
130 135 140

1053

Val Ser His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
145 150 155 160

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
165 170 175

Ser Thr Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp
180 185 190

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
195 200 205

Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu
210 215 220

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
225 230 235 240

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
245 250 255

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
260 265 270

Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
275 280 285

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
290 295 300

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
305 310 315 320

Ser Leu Ser Pro Gly Lys
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Arg Ser Ser Gln Ser Leu Val Tyr Ser Asp Gly Asn Thr Tyr Leu Asn
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Lys Ser Ser Gln Ser Leu Leu His Ser Asp Gly Lys Thr Tyr Leu Tyr
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Arg Ala Ser Gln Gly Ile Ala Asn Tyr Leu Ala
1 5 10

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Arg Ala Ser Gln Gly Ile Ser Asn Asp Leu Ala
1 5 10

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Arg Ala Ser Gln Ser Val Ser Arg Leu Ala
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Val

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Ala

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Ala

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Ala

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Ala

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Arg Ala Ser Gln Asp Ile Ser His Tyr Leu Ala
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Arg Ala Ser Gln Asp Ile Ser Asn Tyr Leu Ala
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Arg Ala Ser Gln Ser Val Ser Ser Asn Leu Ala
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Arg Ala Ser Gln Asp Ile Ser Arg Trp Leu Ala
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Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
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Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
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Gln Ala Ser Gln Asp Ile Ser Asn Ser Leu Asn
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Gln Ala Ser Gln Asp Ile Ser Asp Tyr Leu Asn
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Gln Ala Ser Gln Asp Ile Thr Asn Tyr Leu Asn
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Lys Val Ser Asn Trp Asp Ser
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Glu Val Ser Asn Arg Phe Ser
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1060

Val Ala Ser Thr Leu Gln Ser
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Ala Ala Ser Thr Leu Gln Ser
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Lys Ile Ser Asn Arg Phe Ser
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Gly Ala Ser Ser Arg Ala Thr
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Gly Ala Ser Arg Arg Ala Thr
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Ala Ala Ser Ser Leu Gln Ser
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Trp Ala Ser Thr Arg Glu Ser
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Trp Ala Ser Thr Arg Lys Ser
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Trp Ala Ser Ala Arg Glu Ser
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Ala Glu Ser Ser Leu Gln Ser
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Thr Ala Ser Ser Leu Gln Ser
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Thr Val Ser Ser Leu Gln Ser
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Asp Ala Ser Asn Leu Glu Thr
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Asp Ala Ser Ile Leu Glu Thr
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Met Gln Ser Thr His Trp Pro Ile Thr
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Ile Gln Gly Thr His Trp Pro Thr Thr
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Met Gln Gly Thr His Trp Pro Ile Thr
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Met Gln Gly Ile Gln Leu Pro Cys Ser
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Met Gln Ser Ile Gln Leu Pro Leu Thr
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Met Gln Ser Ile Gln Leu Pro Ile Thr
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Gln Asn Tyr Asn Ser Ala Pro Phe Thr
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Gln Lys Tyr Asn Ser Val Pro Leu Thr
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Met Gln Ala Thr Gln Phe Pro His Thr
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Gln Gln Tyr Gly Ser Ser Pro Arg Thr
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Gln Gln Tyr Gly Ser Ser Pro Arg Ser
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Leu Gln His Asn Ser Tyr Pro Pro Thr
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Gln Gln Tyr Tyr Ser Phe Pro Trp Thr
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Gln Gln Tyr Tyr Ser Thr Thr Trp Thr
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Gln Gln Tyr Tyr Ser Ile Ser Arg Thr
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His Gln Tyr Tyr Ser Thr Pro Leu Thr
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Gln Gln Tyr Phe Ile Thr Pro Leu Thr
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Gln Gln Tyr Asn Asn Tyr Pro Phe Thr
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Gly Phe Thr Phe Ser Ser Tyr Ser Met Asn
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Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
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Gly

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Gly

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Gly

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His Ile Ser Arg Ser Ser Arg Thr Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

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Tyr Ile His Ser Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys Ser
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Tyr Ile His Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys Ser
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Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys Ser
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Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys Ser
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Gly

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Gly

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Lys Ser

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Glu Asp Asn Trp Asn Tyr Gly Phe Phe Asp Tyr
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Ser Ile Ala Val Ala Leu Asp Tyr
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Met Tyr Ser Ser Gly Trp Tyr Gly Val Phe Asp Tyr
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Arg Asn Trp Thr Pro Phe Asp Tyr
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Trp Ala Pro Phe Asp Tyr
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Asp Gly Tyr Asn Trp Asn Gly Gly Gly Asn Tyr Tyr Gly Met Asp Val
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Gly Pro Tyr Tyr Gly Met Asp Val
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Ala Leu Arg Gly Ile Val Leu Met Val Tyr Val Leu Gly Ala Leu Asp
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Val

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Asp Arg Gly Gly Gly Asp Tyr Gly Arg Met Asp Val
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Ser Asn Asn Tyr Gly Cys Phe Ala Leu
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Gly Tyr Asn Tyr Gly Leu Tyr Tyr Tyr Asp Ser Ser Gly Tyr Pro Ser
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Thr Tyr Tyr Asp Ile Leu Thr Gly Tyr Pro Phe Tyr Phe Asp Tyr
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Gly Gly Tyr Ser Ser Ser Trp Tyr Trp Phe Asp Pro
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Gly Gly Tyr Ser Ser Ser Trp Phe Trp Phe Asp Pro
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Ser Ala Leu Arg Tyr Phe Asp Trp Leu Phe Ser Asp Val Ser Asp Ile
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Gln Lys Ser Tyr Gly Tyr Ser Tyr Phe Asp Tyr
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Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
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Gln Pro Ala Ser Ile Ser Cys
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Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
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Gln Pro Ala Ser Ile Ser Cys
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Gln Pro Ala Ser Ile Ser Cys
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Trp Tyr Gln Gln Asp Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
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Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile Tyr
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1 5 10 15

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys
20 25 30

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Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys
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1 5 10 15

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys
20 25 30

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1 5 10 15

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys
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Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
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Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
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Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Phe Cys
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Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
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2102

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Leu Thr Ile Ser Ser Leu Gln Ala Asp Asp Val Ala Val Tyr Tyr Cys
20 25 30

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1 5 10 15

Leu Thr Ile Ser Gly Leu Gln Ala Glu Asp Val Ala Leu Tyr Tyr Cys
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Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Phe Tyr Cys
20 25 30

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Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
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Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
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1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys
20 25 30

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20 25 30

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1 5 10 15

Leu Thr Ile Arg Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
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2104

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1 5 10 15

Leu Thr Leu Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
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Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

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20 25 30

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<400> 435

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Phe Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
20 25 30

<210> 436
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 436

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Leu Ser Ser Leu Gln Pro Glu Asp Phe Ala Ser Tyr Tyr Cys
20 25 30

<210> 437
<211> 32
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<213> Homo Sapiens

<400> 437

2103

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Ser Tyr Tyr Cys
20 25 30

<210> 438
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<213> Homo Sapiens

<400> 438

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys
20 25 30

<210> 439
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<213> Homo Sapiens

<400> 439

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Glu Thr Asp Phe Thr
1 5 10 15

Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys
20 25 30

<210> 440
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<213> Homo Sapiens

<400> 440

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
1 5 10

<210> 441
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<400> 441

Phe Gly Gln Gly Thr Arg Leu Glu Ile Ile
1 5 10

<210> 442

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<400> 442

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
1 5 10

<210> 443
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<400> 443

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 444
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<400> 444

Phe Gly His Gly Thr Arg Leu Glu Ile Lys
1 5 10

<210> 445
<211> 10
<212> PRT
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<400> 445

Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
1 5 10

<210> 446
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<400> 446

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 447
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<212> PRT
<213> Homo Sapiens

2107

<400> 447

Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 448
<211> 10
<212> PRT
<213> Homo Sapiens

<400> 448

Phe Gly Gly Gly Thr Lys Val Ala Ile Lys
1 5 10

<210> 449
<211> 10
<212> PRT
<213> Homo Sapiens

<400> 449

Phe Gly Pro Gly Thr Lys Met Asp Ile Lys
1 5 10

<210> 450
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<213> Homo Sapiens

<400> 450

Phe Gly Gln Gly Thr Lys Val Glu Phe Lys
1 5 10

<210> 451
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<212> PRT
<213> Homo Sapiens

<400> 451

Phe Gly Gly Gly Thr Lys Val Glu Ile Arg
1 5 10

<210> 452
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 452

2108

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> 453
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 453

Gln Val His Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Val Ser
20 25

<210> 454
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 454

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Arg Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Val Ser
20 25

<210> 455
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 455

Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Val Ser
20 25

<210> 456
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 456

2109

Gln Ile Thr Leu Lys Glu Ser Gly Pro Thr Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser
20 25

<210> 457
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 457

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 458
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 458

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 459
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 459

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser
20 25

<210> 460
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 460

2110

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 461
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 461

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 462
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 462

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser
20 25

<210> 463
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 463

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Asn Cys Thr Val Ser
20 25

<210> 464
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 464

2111

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Tyr
20 25

<210> 465
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 465

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser
20 25

<210> 466
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 466

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Leu Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser
20 25

<210> 467
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 467

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser
20 25

<210> 468
<211> 25
<212> PRT
<213> Homo Sapiens

<400> 468

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Ile Ser
20 25

<210> 469
<211> 14
<212> PRT
<213> Homo Sapiens

<400> 469

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
1 5 10

<210> 470
<211> 14
<212> PRT
<213> Homo Sapiens

<400> 470

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met Gly
1 5 10

<210> 471
<211> 14
<212> PRT
<213> Homo Sapiens

<400> 471

Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu Ala
1 5 10

<210> 472
<211> 14
<212> PRT
<213> Homo Sapiens

<400> 472

Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu Val
1 5 10

<210> 473
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<212> PRT
<213> Homo Sapiens

<400> 473

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
1 5 10

<210> 474
<211> 14
<212> PRT
<213> Homo Sapiens

<400> 474

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
1 5 10

<210> 475
<211> 14
<212> PRT
<213> Homo Sapiens

<400> 475

Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu Trp Ile Gly
1 5 10

<210> 476
<211> 14
<212> PRT
<213> Homo Sapiens

<400> 476

Trp Val Arg Gln His Pro Gly Lys Gly Leu Glu Trp Ile Gly
1 5 10

<210> 477
<211> 14
<212> PRT
<213> Homo Sapiens

<400> 477

Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
1 5 10

<210> 478
<211> 14
<212> PRT
<213> Homo Sapiens

<400> 478

Trp Ile Arg Gln Pro Ala Gly Lys Gly Leu Glu Trp Ile Gly
1 5 10

<210> 479
<211> 14
<212> PRT
<213> Homo Sapiens

<400> 479

Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly
1 5 10

<210> 480
<211> 14
<212> PRT
<213> Homo Sapiens

<400> 480

Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu Trp Leu Gly
1 5 10

<210> 481
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 481

Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 482
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 482

Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Arg Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 483
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 483

Arg Val Thr Met Leu Glu Asp Thr Ser Thr Asp Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Thr
20 25 30

<210> 484
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 484

Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Ser Gln Val Val Leu Thr
1 5 10 15

Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala Arg
20 25 30

<210> 485
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 485

Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val Val Leu Thr
1 5 10 15

Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala His
20 25 30

<210> 486
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 486

Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Thr Gln Val Val Leu Thr
1 5 10 15

Val Thr Asp Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala His
20 25 30

<210> 487
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 487

Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val Val Leu Thr
1 5 10 15

Met Thr Asn Leu Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala His
20 25 30

<210> 488
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 488

Arg Leu Thr Ile Thr Lys Ala Thr Ser Lys Asn Gln Val Val Leu Thr
1 5 10 15

Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala His
20 25 30

<210> 489
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 489

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 490
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 490

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys
20 25 30

<210> 491
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 491

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Glu Tyr Tyr Cys Ala Lys
20 25 30

<210> 492
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 492

Arg Phe Thr Ile Ser Arg Asp Asn Ser Met Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 493
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 493

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 494
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 494

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Val Leu
20 25 30

<210> 495
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 495

2118

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Asp Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 496
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 496

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Phe Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys Ala Leu
20 25 30

<210> 497
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 497

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Val Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 498
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 498

Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 499
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 499

Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Asn
1 5 10 15

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 500
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 500

Arg Val Asn Met Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys
1 5 10 15

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 501
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 501

Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys
1 5 10 15

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 502
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 502

Arg Ile Thr Ile Ser Ala Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys
1 5 10 15

Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 503
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 503

Arg Ile Thr Lys Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys
1 5 10 15

2120

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 504
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 504

Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys
1 5 10 15

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Ser
20 25 30

<210> 505
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 505

Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys
1 5 10 15

Leu Phe Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala Arg
20 25 30

<210> 506
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 506

Arg Val Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys
1 5 10 15

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 507
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 507

Arg Val Thr Ile Ser Ile Val Thr Ser Arg Asn Gln Phe Ser Leu Lys
1 5 10 15

2121

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 508
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 508

Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr Leu Gln
1 5 10 15

Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg
20 25 30

<210> 509
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 509

Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr Ala Tyr Leu Gln
1 5 10 15

Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg
20 25 30

<210> 510
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 510

Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn Gln Phe Ser Leu Gln
1 5 10 15

Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 511
<211> 11
<212> PRT
<213> Homo Sapiens

<400> 511

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 512

<211> 11
<212> PRT
<213> Homo Sapiens

<400> 512

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> 513
<211> 11
<212> PRT
<213> Homo Sapiens

<400> 513

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
1 5 10

<210> 514
<211> 11
<212> PRT
<213> Homo Sapiens

<400> 514

Trp Gly Gln Gly Ser Leu Val Thr Val Ser Pro
1 5 10

<210> 515
<211> 11
<212> PRT
<213> Homo Sapiens

<400> 515

Trp Gly Gln Gly Thr Lys Val Thr Val Ser Ser
1 5 10

<210> 516
<211> 11
<212> PRT
<213> Homo Sapiens

<400> 516

Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 517
<211> 657
<212> PRT
<213> Homo Sapiens

2123

<400> 517

Gly Ala Tyr Gly Thr Asn Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Met Thr Asn Trp Ser Asn Met Thr
20 25 30

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Met Thr Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr Met Gly Asn Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Met Thr Asn Gly Thr Asn Thr Ala Tyr Trp Ser Asn
85 90 95

Gly Ala Tyr Gly Gly Asn Ala Ala Tyr Ala Cys Asn Thr Ala Tyr Met
100 105 110

Thr Asn Ala Ala Tyr Thr Gly Gly Thr Thr Tyr Cys Ala Arg Cys Ala
115 120 125

Arg Met Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala Arg Trp Ser Asn
130 135 140

Cys Cys Asn Met Gly Asn Met Gly Asn Met Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Thr Gly
165 170 175

Gly Gly Ala Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
180 185 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Ala Ala Tyr Gly Gly Asn Trp
195 200 205

Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly Ala
210 215 220

Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Ala Arg Ala Thr His
225 230 235 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
245 250 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
260 265 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Trp Ser Asn
275 280 285

Ala Cys Asn Cys Ala Tyr Thr Gly Gly Cys Cys Asn Ala Thr His Ala
290 295 300

Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys
305 310 315 320

Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
325 330 335

Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn Cys
340 345 350

Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr Thr
355 360 365

Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala Arg
370 375 380

Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn Ala
385 390 395 400

Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr Gly
405 410 415

Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr Tyr
420 425 430

Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn Ala
435 440 445

Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly Thr
450 455 460

Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala Arg
465 470 475 480

Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg Gly
485 490 495

Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys Ala
500 505 510

Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser Asn
515 520 525

Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp
530 535 540

Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp Ser
545 550 555 560

Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala Arg
565 570 575

Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr Gly
580 585 590

Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys Ala
595 600 605

Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
610 615 620

Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn Thr
625 630 635 640

Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr Gly
645 650 655

Tyr

<210> 518
<211> 657
<212> PRT
<213> Homo Sapiens

<400> 518

Gly Ala Tyr Gly Thr Asn Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Met Thr Asn Trp Ser Asn Met Thr
20 25 30

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Met Thr Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr Met Gly Asn Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Met Thr Asn Gly Thr Asn Thr Ala Tyr Trp Ser Asn
85 90 95

Gly Ala Tyr Gly Gly Asn Ala Ala Tyr Ala Cys Asn Thr Ala Tyr Met
100 105 110

Thr Asn Ala Ala Tyr Thr Gly Gly Thr Thr Tyr Cys Ala Arg Cys Ala
115 120 125

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Arg Met Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala Arg Trp Ser Asn
    130                 135                 140

Cys Cys Asn Met Gly Asn Met Gly Asn Met Thr Asn Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Thr Gly
                165                 170                 175

Gly Gly Ala Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
            180                 185                 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp
        195                 200                 205

Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly Ala
    210                 215                 220

Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Ala Arg Ala Thr His
225                 230                 235                 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
                245                 250                 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
            260                 265                 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr His Cys Ala Arg Gly Gly Asn
        275                 280                 285

Ala Cys Asn Cys Ala Tyr Thr Gly Gly Cys Cys Asn Ala Cys Asn Ala
    290                 295                 300

Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys
305                 310                 315                 320

Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
                325                 330                 335

Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn Cys
            340                 345                 350

Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr Thr
        355                 360                 365

Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala Arg
    370                 375                 380

Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn Ala
385                 390                 395                 400

Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr Gly
                405                 410                 415
```

```
Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr Tyr
            420                 425                 430

Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn Ala
        435                 440                 445

Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly Thr
    450                 455                 460

Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala Arg
465                 470                 475                 480

Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg Gly
                485                 490                 495

Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys Ala
            500                 505                 510

Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser Asn
        515                 520                 525

Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp
    530                 535                 540

Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp Ser
545                 550                 555                 560

Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala Arg
                565                 570                 575

Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr Gly
            580                 585                 590

Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys Ala
        595                 600                 605

Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
    610                 615                 620

Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn Thr
625                 630                 635                 640

Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr Gly
                645                 650                 655

Tyr
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<210> 519
<211> 657
<212> PRT
<213> Homo Sapiens

2428

<400> 519

Gly Ala Tyr Gly Thr Asn Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Met Thr Asn Trp Ser Asn Met Thr
20 25 30

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Met Thr Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr Met Gly Asn Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Met Thr Asn Gly Thr Asn Thr Ala Tyr Trp Ser Asn
85 90 95

Gly Ala Tyr Gly Gly Asn Ala Ala Tyr Ala Cys Asn Thr Ala Tyr Met
100 105 110

Thr Asn Ala Ala Tyr Thr Gly Gly Met Thr Asn Cys Ala Arg Cys Ala
115 120 125

Arg Met Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala Arg Trp Ser Asn
130 135 140

Cys Cys Asn Met Gly Asn Met Gly Asn Met Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Thr Gly
165 170 175

Gly Gly Ala Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
180 185 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp
195 200 205

Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly Ala
210 215 220

Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Ala Arg Ala Thr His
225 230 235 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
245 250 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
260 265 270

2129

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Gly Gly Asn
275 280 285

Ala Cys Asn Cys Ala Tyr Thr Gly Gly Cys Cys Asn Ala Thr His Ala
290 295 300

Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys
305 310 315 320

Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
325 330 335

Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn Cys
340 345 350

Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr Thr
355 360 365

Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala Arg
370 375 380

Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn Ala
385 390 395 400

Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr Gly
405 410 415

Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr Tyr
420 425 430

Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn Ala
435 440 445

Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly Thr
450 455 460

Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala Arg
465 470 475 480

Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg Gly
485 490 495

Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys Ala
500 505 510

Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser Asn
515 520 525

Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp
530 535 540

Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp Ser
545 550 555 560

Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala Arg
565 570 575

Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr Gly
580 585 590

Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys Ala
595 600 605

Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
610 615 620

Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn Thr
625 630 635 640

Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr Gly
645 650 655

Tyr

<210> 520
<211> 657
<212> PRT
<213> Homo Sapiens

<400> 520

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Ala Cys Asn Cys Cys Asn Met Thr Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Thr Asn Ala Cys Asn Cys Cys Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Met Thr Asn Met Thr Asn Cys Ala Tyr Trp Ser Asn
85 90 95

Gly Ala Tyr Gly Gly Asn Ala Ala Arg Ala Cys Asn Thr Ala Tyr Met
100 105 110

Thr Asn Thr Ala Tyr Thr Gly Gly Thr Ala Tyr Met Thr Asn Cys Ala
115 120 125

```
Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn
    130                 135                 140

Cys Cys Asn Cys Ala Arg Met Thr Asn Met Thr Asn Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Gly Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Met Gly
                165                 170                 175

Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
            180                 185                 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp
        195                 200                 205

Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly Ala
    210                 215                 220

Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Ala Arg Ala Thr His
225                 230                 235                 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
                245                 250                 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
            260                 265                 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Gly Gly Asn
        275                 280                 285

Ala Thr His Cys Ala Arg Met Thr Asn Cys Cys Asn Thr Gly Tyr Trp
    290                 295                 300

Ser Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys
305                 310                 315                 320

Asn Ala Ala Arg Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
                325                 330                 335

Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn Cys
            340                 345                 350

Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr Thr
        355                 360                 365

Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala Arg
    370                 375                 380

Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn Ala
385                 390                 395                 400

Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr Gly
                405                 410                 415
```

Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr Tyr
420 425 430

Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn Ala
435 440 445

Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly Thr
450 455 460

Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala Arg
465 470 475 480

Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg Gly
485 490 495

Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys Ala
500 505 510

Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser Asn
515 520 525

Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp
530 535 540

Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp Ser
545 550 555 560

Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala Arg
565 570 575

Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr Gly
580 585 590

Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys Ala
595 600 605

Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
610 615 620

Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn Thr
625 630 635 640

Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr Gly
645 650 655

Tyr

<210> 521
<211> 657
<212> PRT
<213> Homo Sapiens

<400> 521

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Ala Cys Asn Cys Cys Asn Met Thr Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Thr Asn Ala Cys Asn Cys Cys Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Met Thr Asn Met Thr Asn Cys Ala Tyr Trp Ser Asn
85 90 95

Gly Ala Tyr Gly Gly Asn Ala Ala Arg Ala Cys Asn Thr Ala Tyr Met
100 105 110

Thr Asn Thr Ala Tyr Thr Gly Gly Thr Ala Tyr Met Thr Asn Cys Ala
115 120 125

Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn
130 135 140

Cys Cys Asn Cys Ala Arg Met Thr Asn Met Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Gly Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Met Gly
165 170 175

Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
180 185 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp
195 200 205

Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly Ala
210 215 220

Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Ala Arg Ala Thr His
225 230 235 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
245 250 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
260 265 270

```
Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Trp Ser Asn
        275                 280                 285

Ala Thr His Cys Ala Arg Met Thr Asn Cys Cys Asn Met Thr Asn Ala
    290                 295                 300

Cys Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Ala Cys
305                 310                 315                 320

Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
                325                 330                 335

Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn Cys
            340                 345                 350

Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr Thr
        355                 360                 365

Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala Arg
    370                 375                 380

Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn Ala
385                 390                 395                 400

Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr Gly
                405                 410                 415

Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr Tyr
            420                 425                 430

Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn Ala
        435                 440                 445

Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly Thr
    450                 455                 460

Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala Arg
465                 470                 475                 480

Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg Gly
                485                 490                 495

Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys Ala
            500                 505                 510

Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser Asn
        515                 520                 525

Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp
    530                 535                 540

Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp Ser
545                 550                 555                 560
```

Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala Arg
565 570 575

Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr Gly
580 585 590

Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys Ala
595 600 605

Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
610 615 620

Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn Thr
625 630 635 640

Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr Gly
645 650 655

Tyr

<210> 522
<211> 657
<212> PRT
<213> Homo Sapiens

<400> 522

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Ala Cys Asn Cys Cys Asn Met Thr Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Thr Asn Ala Cys Asn Cys Cys Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Met Thr Asn Met Thr Asn Cys Ala Tyr Trp Ser Asn
85 90 95

Gly Ala Tyr Gly Gly Asn Ala Ala Arg Ala Cys Asn Thr Ala Tyr Met
100 105 110

Thr Asn Thr Ala Tyr Thr Gly Gly Thr Thr Tyr Met Thr Asn Cys Ala
115 120 125

```
Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn
    130                 135                 140

Cys Cys Asn Cys Ala Arg Cys Cys Asn Met Thr Asn Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Gly Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Met Gly
                165                 170                 175

Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
            180                 185                 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp
        195                 200                 205

Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly Ala
    210                 215                 220

Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Ala Arg Ala Thr His
225                 230                 235                 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
                245                 250                 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
            260                 265                 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Trp Ser Asn
        275                 280                 285

Ala Thr His Cys Ala Arg Met Thr Asn Cys Cys Asn Ala Thr His Ala
    290                 295                 300

Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Tyr Gly Gly Asn Ala Cys
305                 310                 315                 320

Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
                325                 330                 335

Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn Cys
            340                 345                 350

Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr Thr
        355                 360                 365

Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala Arg
    370                 375                 380

Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn Ala
385                 390                 395                 400

Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr Gly
                405                 410                 415
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2127

Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr Tyr
420 425 430

Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn Ala
435 440 445

Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly Thr
450 455 460

Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala Arg
465 470 475 480

Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg Gly
485 490 495

Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys Ala
500 505 510

Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser Asn
515 520 525

Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp
530 535 540

Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp Ser
545 550 555 560

Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala Arg
565 570 575

Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr Gly
580 585 590

Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys Ala
595 600 605

Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
610 615 620

Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn Thr
625 630 635 640

Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr Gly
645 650 655

Tyr

<210> 523
<211> 642
<212> PRT
<213> Homo Sapiens

2128

<400> 523

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Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1               5                  10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
            20                  25                  30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
    50                  55                  60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Gly Gly Asn Ala Thr His Gly Cys Asn Ala Ala Tyr Thr Ala Tyr
                85                  90                  95

Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Thr
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Thr Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Met
145                 150                 155                 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Ala Cys Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Ala Ala Tyr Thr Ala
            260                 265                 270
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Tyr Ala Ala Tyr Trp Ser Asn Gly Cys Asn Cys Cys Asn Thr Thr Tyr
        275                 280                 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Ala
    290                 295                 300

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Thr His Ala Ala
305                 310                 315                 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
                325                 330                 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
            340                 345                 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
        355                 360                 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
    370                 375                 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385                 390                 395                 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
                405                 410                 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
            420                 425                 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
        435                 440                 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
    450                 455                 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465                 470                 475                 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
                485                 490                 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
            500                 505                 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
        515                 520                 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
    530                 535                 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545                 550                 555                 560
```

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 524
<211> 642
<212> PRT
<213> Homo Sapiens

<400> 524

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Thr His Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Gly Asn Ala Thr His Trp Ser Asn Ala Ala Tyr Gly Ala Tyr
85 90 95

Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Thr
115 120 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
130 135 140

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Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Met
145                 150                 155                 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Ala Cys Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Ala Ala Arg Thr Ala
            260                 265                 270

Tyr Ala Ala Tyr Trp Ser Asn Gly Thr Asn Cys Cys Asn Met Thr Asn
        275                 280                 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Ala
    290                 295                 300

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305                 310                 315                 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
                325                 330                 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
            340                 345                 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
        355                 360                 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
    370                 375                 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385                 390                 395                 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
                405                 410                 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
            420                 425                 430
```

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
435 440 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
450 455 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465 470 475 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
485 490 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
500 505 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 525
<211> 657
<212> PRT
<213> Homo Sapiens

<400> 525

Ala Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Ala Cys Asn Cys Cys Asn Met Thr Asn Trp Ser Asn Trp Ser
20 25 30

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Met Thr Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr Met Gly Asn Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Met Thr Asn Gly Thr Asn Cys Ala Tyr Trp Ser Asn
85 90 95

Gly Ala Tyr Gly Gly Asn Ala Ala Tyr Ala Cys Asn Thr Ala Tyr Met
100 105 110

Thr Asn Trp Ser Asn Thr Gly Gly Met Thr Asn Cys Ala Arg Cys Ala
115 120 125

Arg Met Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn
130 135 140

Cys Cys Asn Met Gly Asn Met Thr Asn Met Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Ala Ala Arg Ala Thr His Trp Ser Asn Ala Ala Tyr Met Gly
165 170 175

Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
180 185 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp
195 200 205

Ser Asn Gly Gly Asn Gly Cys Asn Gly Gly Asn Ala Cys Asn Gly Ala
210 215 220

Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Ala Arg Ala Thr His
225 230 235 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
245 250 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
260 265 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Gly Cys Asn
275 280 285

Ala Cys Asn Cys Ala Arg Thr Thr Tyr Cys Cys Asn Cys Ala Tyr Ala
290 295 300

2134

Cys Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Ala Cys
305 310 315 320

Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Thr His Ala Ala Arg
325 330 335

Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn Cys
340 345 350

Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr Thr
355 360 365

Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala Arg
370 375 380

Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn Ala
385 390 395 400

Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr Gly
405 410 415

Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr Tyr
420 425 430

Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn Ala
435 440 445

Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly Thr
450 455 460

Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala Arg
465 470 475 480

Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg Gly
485 490 495

Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys Ala
500 505 510

Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser Asn
515 520 525

Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp
530 535 540

Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp Ser
545 550 555 560

Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala Arg
565 570 575

Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr Gly
580 585 590

2138

Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys Ala
595 600 605

Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
610 615 620

Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn Thr
625 630 635 640

Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr Gly
645 650 655

Tyr

<210> 526
<211> 657
<212> PRT
<213> Homo Sapiens

<400> 526

Gly Ala Arg Ala Thr His Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Ala Cys Asn Cys Cys Asn Met Thr Asn Trp Ser Asn Trp Ser
20 25 30

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Met Thr Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr Met Gly Asn Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Met Thr Asn Gly Thr Asn Cys Ala Tyr Trp Ser Asn
85 90 95

Gly Ala Tyr Gly Gly Asn Ala Ala Tyr Ala Cys Asn Thr Ala Tyr Met
100 105 110

Thr Asn Trp Ser Asn Thr Gly Gly Met Thr Asn Cys Ala Arg Cys Ala
115 120 125

Arg Met Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn
130 135 140

Cys Cys Asn Met Gly Asn Met Thr Asn Met Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Ala Ala Arg Ala Thr His Trp Ser Asn Ala Ala Tyr Met Gly
165 170 175

Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
180 185 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Ala
195 200 205

Cys Asn Gly Gly Asn Gly Cys Asn Gly Gly Asn Ala Cys Asn Gly Ala
210 215 220

Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Ala Arg Ala Thr His
225 230 235 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
245 250 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
260 265 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Gly Cys Asn
275 280 285

Ala Cys Asn Cys Ala Arg Thr Thr Tyr Cys Cys Asn Cys Ala Tyr Ala
290 295 300

Cys Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Ala Cys
305 310 315 320

Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
325 330 335

Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn Cys
340 345 350

Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr Thr
355 360 365

Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala Arg
370 375 380

Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn Ala
385 390 395 400

Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr Gly
405 410 415

Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr Tyr
420 425 430

Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn Ala
435 440 445

2137

Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly Thr
450 455 460

Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala Arg
465 470 475 480

Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg Gly
485 490 495

Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys Ala
500 505 510

Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser Asn
515 520 525

Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp
530 535 540

Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp Ser
545 550 555 560

Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala Arg
565 570 575

Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr Gly
580 585 590

Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys Ala
595 600 605

Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
610 615 620

Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn Thr
625 630 635 640

Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr Gly
645 650 655

Tyr

<210> 527
<211> 645
<212> PRT
<213> Homo Sapiens

<400> 527

Gly Ala Arg Ala Thr His Gly Thr Asn Met Thr Asn Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Gly Asn Ala Cys Asn Met Thr
20 25 30

Asn Trp Ser Asn Met Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Ala Cys Asn Met Thr Asn Trp
50 55 60

Ser Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Ala Cys Asn Gly Thr Asn Ala Thr His Trp Ser Asn Trp Ser Asn
85 90 95

Thr Ala Tyr Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys
100 105 110

Ala Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala
115 120 125

Arg Gly Cys Asn Cys Cys Asn Met Gly Asn Met Thr Asn Met Thr Asn
130 135 140

Ala Thr His Trp Ser Asn Gly Gly Asn Gly Cys Asn Trp Ser Asn Trp
145 150 155 160

Ser Asn Met Gly Asn Gly Cys Asn Ala Cys Asn Gly Gly Asn Ala Thr
165 170 175

His Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn
180 185 190

Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala
195 200 205

Cys Asn Gly Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys
210 215 220

Asn Ala Thr His Trp Ser Asn Met Gly Asn Met Thr Asn Gly Ala Arg
225 230 235 240

Cys Cys Asn Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Gly
245 250 255

Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala
260 265 270

Arg Thr Ala Tyr Gly Gly Asn Trp Ser Asn Trp Ser Asn Cys Cys Asn
275 280 285

Met Gly Asn Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly
290 295 300

Gly Asn Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr
305 310 315 320

His Ala Ala Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn
325 330 335

Gly Cys Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala
340 345 350

Thr His Thr Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala
355 360 365

Tyr Gly Ala Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn
370 375 380

Gly Gly Asn Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly
385 390 395 400

Thr Asn Thr Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala
405 410 415

Tyr Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg
420 425 430

Gly Cys Asn Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala
435 440 445

Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr
450 455 460

Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn
465 470 475 480

Cys Ala Arg Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly
485 490 495

Ala Arg Cys Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala
500 505 510

Tyr Trp Ser Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn
515 520 525

Trp Ser Asn Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met
530 535 540

Thr Asn Trp Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala
545 550 555 560

Tyr Gly Ala Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn
565 570 575

Thr Ala Tyr Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala
580 585 590

2140

Cys Asn Cys Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser
595 600 605

Asn Trp Ser Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg
610 615 620

Trp Ser Asn Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly
625 630 635 640

Ala Arg Thr Gly Tyr
645

<210> 528
<211> 639
<212> PRT
<213> Homo Sapiens

<400> 528

Gly Ala Arg Ala Thr His Gly Thr Asn Met Thr Asn Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Gly Asn Ala Cys Asn Met Thr
20 25 30

Asn Trp Ser Asn Met Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Ala Cys Asn Met Thr Asn Trp
50 55 60

Ser Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Gly Thr Asn Trp Ser Asn Met Gly Asn Met Thr Asn
85 90 95

Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala
100 105 110

Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys
115 120 125

Asn Met Gly Asn Met Thr Asn Met Thr Asn Ala Thr His Thr Ala Tyr
130 135 140

Gly Gly Asn Gly Cys Asn Trp Ser Asn Met Gly Asn Met Gly Asn Gly
145 150 155 160

Cys Asn Ala Cys Asn Gly Gly Asn Ala Thr His Cys Cys Asn Gly Ala
165 170 175

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Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn
            180                 185                 190

Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly Ala Tyr Thr
        195                 200                 205

Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr His Trp Ser
    210                 215                 220

Asn Met Gly Asn Met Thr Asn Gly Ala Arg Cys Cys Asn Gly Ala Arg
225                 230                 235                 240

Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr
                245                 250                 255

Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala Tyr Gly Gly
            260                 265                 270

Asn Trp Ser Asn Trp Ser Asn Cys Cys Asn Met Gly Asn Trp Ser Asn
        275                 280                 285

Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Ala
    290                 295                 300

Ala Arg Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg Met Gly
305                 310                 315                 320

Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn Cys Cys Asn
                325                 330                 335

Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr Thr Tyr Cys
            340                 345                 350

Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala Arg Cys Ala
        355                 360                 365

Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn Ala Cys Asn
    370                 375                 380

Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr Gly Tyr Met
385                 390                 395                 400

Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr Tyr Thr Ala
                405                 410                 415

Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn Ala Ala Arg
            420                 425                 430

Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly Thr Asn Gly
        435                 440                 445

Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala Arg Trp Ser
    450                 455                 460
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2142

Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg Gly Ala Arg
465 470 475 480

Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys Ala Arg Gly
485 490 495

Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser Asn Ala Cys
500 505 510

Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
515 520 525

Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp Ser Asn Ala
530 535 540

Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala Arg Ala Ala
545 550 555 560

Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr Gly Cys Asn
565 570 575

Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys Ala Tyr Cys
580 585 590

Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Cys Cys
595 600 605

Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn Thr Thr Tyr
610 615 620

Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr Gly Tyr
625 630 635

<210> 529
<211> 642
<212> PRT
<213> Homo Sapiens

<400> 529

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Gly Asn Ala Thr His Met Gly Asn Ala Ala Tyr Gly Ala Tyr
85 90 95

Met Thr Asn Gly Gly Asn Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Met Gly Asn Met Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Met
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
195 200 205

Ala Arg Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Ala Cys Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Met Thr Asn Cys Ala Arg Cys Ala
260 265 270

Tyr Ala Ala Tyr Trp Ser Asn Thr Ala Tyr Cys Cys Asn Cys Cys Asn
275 280 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala
290 295 300

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
325 330 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
340 345 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
355 360 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
370 375 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385 390 395 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
405 410 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
420 425 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
435 440 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
450 455 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465 470 475 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
485 490 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
500 505 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

2148

Gly Tyr

<210> 530
<211> 660
<212> PRT
<213> Homo Sapiens

<400> 530

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Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
1               5                  10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Met Thr
            20                  25                  30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Met Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Arg Met Gly Asn Gly Cys Asn Ala Cys Asn Ala Thr His Ala
    50                  55                  60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Trp Ser Asn Gly Thr Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn
                85                  90                  95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
            100                 105                 110

Ala Tyr Met Thr Asn Gly Thr Asn Thr Gly Gly Thr Ala Tyr Cys Ala
        115                 120                 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
    130                 135                 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Thr Thr Tyr Ala
145                 150                 155                 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Ala Cys
                165                 170                 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
            180                 185                 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Ala Cys Asn Gly
        195                 200                 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys
    210                 215                 220
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Asn Gly Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn
225 230 235 240

Ala Thr His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Gly
245 250 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
260 265 270

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
275 280 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Thr Thr Tyr Cys Cys Asn Thr
290 295 300

Gly Gly Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly
305 310 315 320

Asn Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
325 330 335

Ala Ala Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly
340 345 350

Cys Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr
355 360 365

His Thr Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr
370 375 380

Gly Ala Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly
385 390 395 400

Gly Asn Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr
405 410 415

Asn Thr Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr
420 425 430

Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly
435 440 445

Cys Asn Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala
450 455 460

Arg Gly Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn
465 470 475 480

Cys Ala Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys
485 490 495

Ala Arg Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala
500 505 510

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Arg Cys Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr
        515                 520                 525

Trp Ser Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp
    530                 535                 540

Ser Asn Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr
545                 550                 555                 560

Asn Trp Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr
                565                 570                 575

Gly Ala Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr
            580                 585                 590

Ala Tyr Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys
        595                 600                 605

Asn Cys Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn
    610                 615                 620

Trp Ser Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp
625                 630                 635                 640

Ser Asn Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala
                645                 650                 655

Arg Thr Gly Tyr
            660

<210>  531
<211>  660
<212>  PRT
<213>  Homo Sapiens

<400>  531

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
1               5                   10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Met Thr
            20                  25                  30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Met Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Arg Met Gly Asn Gly Cys Asn Ala Cys Asn Ala Thr His Ala
    50                  55                  60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65                  70                  75                  80
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Arg Trp Ser Asn Gly Thr Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn
                85                  90                  95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
            100                 105                 110

Ala Tyr Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
        115                 120                 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
    130                 135                 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala
145                 150                 155                 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Ala Cys
                165                 170                 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
            180                 185                 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
        195                 200                 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys
    210                 215                 220

Asn Gly Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn
225                 230                 235                 240

Ala Thr His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Gly
                245                 250                 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
            260                 265                 270

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
        275                 280                 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Ala Cys Asn Ala Cys Asn Thr
    290                 295                 300

Gly Gly Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly
305                 310                 315                 320

Asn Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
                325                 330                 335

Ala Ala Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly
            340                 345                 350

Cys Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr
        355                 360                 365
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His Thr Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr
    370                 375                 380

Gly Ala Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly
385                 390                 395                 400

Gly Asn Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr
                405                 410                 415

Asn Thr Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr
            420                 425                 430

Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly
        435                 440                 445

Cys Asn Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala
    450                 455                 460

Arg Gly Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn
465                 470                 475                 480

Cys Ala Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys
                485                 490                 495

Ala Arg Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala
            500                 505                 510

Arg Cys Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr
        515                 520                 525

Trp Ser Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp
    530                 535                 540

Ser Asn Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr
545                 550                 555                 560

Asn Trp Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr
                565                 570                 575

Gly Ala Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr
            580                 585                 590

Ala Tyr Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys
        595                 600                 605

Asn Cys Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn
    610                 615                 620

Trp Ser Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp
625                 630                 635                 640

Ser Asn Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala
                645                 650                 655
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2150

Arg Thr Gly Tyr
660

<210> 532
<211> 660
<212> PRT
<213> Homo Sapiens

<400> 532

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Met Thr
20 25 30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Met Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Ala Ala Tyr Gly Thr Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn
85 90 95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
100 105 110

Ala Tyr Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
115 120 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
130 135 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala
145 150 155 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Ala Cys
165 170 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
180 185 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
195 200 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys
210 215 220

Asn Gly Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn
225 230 235 240

Ala Thr His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Gly
245 250 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
260 265 270

Asn Thr Ala Tyr Thr Thr Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
275 280 285

Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Cys Asn Cys Cys Asn Met
290 295 300

Gly Asn Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly
305 310 315 320

Asn Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
325 330 335

Ala Ala Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly
340 345 350

Cys Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr
355 360 365

His Thr Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr
370 375 380

Gly Ala Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly
385 390 395 400

Gly Asn Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr
405 410 415

Asn Thr Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr
420 425 430

Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly
435 440 445

Cys Asn Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala
450 455 460

Arg Gly Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn
465 470 475 480

Cys Ala Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys
485 490 495

Ala Arg Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala
500 505 510

Arg Cys Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr
515 520 525

Trp Ser Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp
530 535 540

Ser Asn Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr
545 550 555 560

Asn Trp Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr
565 570 575

Gly Ala Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr
580 585 590

Ala Tyr Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys
595 600 605

Asn Cys Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn
610 615 620

Trp Ser Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp
625 630 635 640

Ser Asn Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala
645 650 655

Arg Thr Gly Tyr
660

<210> 533
<211> 660
<212> PRT
<213> Homo Sapiens

<400> 533

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Met Thr
20 25 30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Met Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Ala Ala Tyr Gly Thr Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn
85 90 95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
100 105 110

Ala Tyr Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
115 120 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
130 135 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala
145 150 155 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Ala Cys
165 170 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
180 185 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
195 200 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys
210 215 220

Asn Gly Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn
225 230 235 240

Ala Thr His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Gly
245 250 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
260 265 270

Asn Thr Ala Tyr Thr Thr Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
275 280 285

Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Cys Asn Cys Cys Asn Met
290 295 300

Gly Asn Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly
305 310 315 320

Asn Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
325 330 335

Ala Ala Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly
340 345 350

Cys Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr
355 360 365

```
His Thr Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr
370                 375                 380

Gly Ala Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly
385                 390                 395                 400

Gly Asn Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr
                405                 410                 415

Asn Thr Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr
            420                 425                 430

Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly
        435                 440                 445

Cys Asn Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala
450                 455                 460

Arg Gly Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn
465                 470                 475                 480

Cys Ala Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys
                485                 490                 495

Ala Arg Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala
            500                 505                 510

Arg Cys Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr
        515                 520                 525

Trp Ser Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp
530                 535                 540

Ser Asn Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr
545                 550                 555                 560

Asn Trp Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr
                565                 570                 575

Gly Ala Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr
            580                 585                 590

Ala Tyr Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys
        595                 600                 605

Asn Cys Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn
610                 615                 620

Trp Ser Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp
625                 630                 635                 640

Ser Asn Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala
                645                 650                 655
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Arg Thr Gly Tyr
660

<210> 534
<211> 660
<212> PRT
<213> Homo Sapiens

<400> 534

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Met Thr
20 25 30

Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Met Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Gly Thr Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn
85 90 95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
100 105 110

Ala Tyr Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
115 120 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
130 135 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala
145 150 155 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Ala Cys
165 170 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
180 185 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Gly Gly Asn Gly
195 200 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys
210 215 220

```
Asn Gly Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn
225                 230                 235                 240

Ala Thr His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Gly
                245                 250                 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
            260                 265                 270

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
        275                 280                 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Ala Thr His Trp Ser Asn Met
    290                 295                 300

Gly Asn Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly
305                 310                 315                 320

Asn Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
                325                 330                 335

Ala Ala Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly
            340                 345                 350

Cys Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr
        355                 360                 365

His Thr Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr
    370                 375                 380

Gly Ala Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly
385                 390                 395                 400

Gly Asn Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr
                405                 410                 415

Asn Thr Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr
            420                 425                 430

Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly
        435                 440                 445

Cys Asn Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala
    450                 455                 460

Arg Gly Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn
465                 470                 475                 480

Cys Ala Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys
                485                 490                 495

Ala Arg Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala
            500                 505                 510
```

Arg Cys Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr
515 520 525

Trp Ser Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp
530 535 540

Ser Asn Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr
545 550 555 560

Asn Trp Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr
565 570 575

Gly Ala Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr
580 585 590

Ala Tyr Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys
595 600 605

Asn Cys Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn
610 615 620

Trp Ser Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp
625 630 635 640

Ser Asn Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala
645 650 655

Arg Thr Gly Tyr
660

<210> 535
<211> 660
<212> PRT
<213> Homo Sapiens

<400> 535

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Met Thr
20 25 30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Met Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

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Arg Trp Ser Asn Gly Thr Asn Met Thr Asn Thr Ala Tyr Ala Ala Tyr
                85                  90                  95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
            100                 105                 110

Ala Tyr Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
        115                 120                 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
    130                 135                 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala
145                 150                 155                 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Ala Cys
                165                 170                 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
            180                 185                 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
        195                 200                 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys
    210                 215                 220

Asn Gly Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn
225                 230                 235                 240

Ala Thr His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Gly
                245                 250                 255

Cys Asn Gly Ala Tyr Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
            260                 265                 270

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
        275                 280                 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Ala Cys Asn Ala Cys Asn Thr
    290                 295                 300

Gly Gly Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly
305                 310                 315                 320

Asn Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
                325                 330                 335

Ala Ala Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly
            340                 345                 350

Cys Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr
        355                 360                 365
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His Thr Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr
370 375 380

Gly Ala Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly
385 390 395 400

Gly Asn Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr
405 410 415

Asn Thr Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr
420 425 430

Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly
435 440 445

Cys Asn Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala
450 455 460

Arg Gly Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn
465 470 475 480

Cys Ala Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys
485 490 495

Ala Arg Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala
500 505 510

Arg Cys Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr
515 520 525

Trp Ser Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp
530 535 540

Ser Asn Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr
545 550 555 560

Asn Trp Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr
565 570 575

Gly Ala Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr
580 585 590

Ala Tyr Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys
595 600 605

Asn Cys Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn
610 615 620

Trp Ser Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp
625 630 635 640

Ser Asn Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala
645 650 655

2160

Arg Thr Gly Tyr
660

<210> 536
<211> 660
<212> PRT
<213> Homo Sapiens

<400> 536

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Met Thr
20 25 30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Met Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Gly Thr Asn Met Thr Asn Thr Ala Tyr Ala Ala Tyr
85 90 95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
100 105 110

Ala Tyr Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
115 120 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
130 135 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala
145 150 155 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Ala Cys
165 170 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
180 185 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
195 200 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys
210 215 220

```
Asn Gly Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn
225                 230                 235                 240

Ala Thr His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Gly
                245                 250                 255

Cys Asn Gly Ala Tyr Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
            260                 265                 270

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
        275                 280                 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Ala Cys Asn Ala Cys Asn Thr
    290                 295                 300

Gly Gly Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly
305                 310                 315                 320

Asn Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
                325                 330                 335

Ala Ala Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly
            340                 345                 350

Cys Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr
        355                 360                 365

His Thr Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr
    370                 375                 380

Gly Ala Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly
385                 390                 395                 400

Gly Asn Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr
                405                 410                 415

Asn Thr Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr
            420                 425                 430

Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly
        435                 440                 445

Cys Asn Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala
    450                 455                 460

Arg Gly Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn
465                 470                 475                 480

Cys Ala Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys
                485                 490                 495

Ala Arg Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala
            500                 505                 510
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Arg Cys Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr
515 520 525

Trp Ser Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp
530 535 540

Ser Asn Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr
545 550 555 560

Asn Trp Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr
565 570 575

Gly Ala Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr
580 585 590

Ala Tyr Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys
595 600 605

Asn Cys Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn
610 615 620

Trp Ser Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp
625 630 635 640

Ser Asn Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala
645 650 655

Arg Thr Gly Tyr
660

<210> 537
<211> 660
<212> PRT
<213> Homo Sapiens

<400> 537

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Met Thr
20 25 30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Met Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

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Arg Trp Ser Asn Gly Thr Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn
                85                  90                  95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
            100                 105                 110

Ala Tyr Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
        115                 120                 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
    130                 135                 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Gly Thr Asn Met Thr Asn Ala
145                 150                 155                 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Ala Cys
                165                 170                 175

Asn Met Gly Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
            180                 185                 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
        195                 200                 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys
    210                 215                 220

Asn Gly Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn
225                 230                 235                 240

Ala Thr His Trp Ser Asn Gly Gly Asn Met Thr Asn Cys Ala Arg Gly
                245                 250                 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Met Thr
            260                 265                 270

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
        275                 280                 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Ala Cys Asn Ala Thr Gly Thr
    290                 295                 300

Thr Tyr Trp Ser Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly
305                 310                 315                 320

Asn Ala Cys Asn Ala Ala Arg Met Thr Asn Gly Ala Arg Ala Thr His
                325                 330                 335

Ala Ala Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly
            340                 345                 350

Cys Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr
        355                 360                 365
```

```
His Thr Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr
370                 375                 380

Gly Ala Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly
385                 390                 395                 400

Gly Asn Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr
                405                 410                 415

Asn Thr Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr
            420                 425                 430

Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly
        435                 440                 445

Cys Asn Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala
450                 455                 460

Arg Gly Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn
465                 470                 475                 480

Cys Ala Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys
                485                 490                 495

Ala Arg Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala
            500                 505                 510

Arg Cys Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr
        515                 520                 525

Trp Ser Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp
530                 535                 540

Ser Asn Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr
545                 550                 555                 560

Asn Trp Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr
                565                 570                 575

Gly Ala Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr
            580                 585                 590

Ala Tyr Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys
        595                 600                 605

Asn Cys Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn
610                 615                 620

Trp Ser Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp
625                 630                 635                 640

Ser Asn Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala
                645                 650                 655
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2165

Arg Thr Gly Tyr
660

<210> 538
<211> 660
<212> PRT
<213> Homo Sapiens

<400> 538

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Met Thr
20 25 30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Met Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Gly Thr Asn Met Thr Asn Gly Ala Tyr Trp Ser Asn
85 90 95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
100 105 110

Ala Tyr Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
115 120 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
130 135 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala
145 150 155 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Ala Cys
165 170 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
180 185 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
195 200 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys
210 215 220

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Asn Gly Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn
225                 230                 235                 240

Ala Thr His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Gly
                245                 250                 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
            260                 265                 270

Asn Thr Thr Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Tyr Cys Ala Arg
        275                 280                 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Ala Cys Asn Cys Cys Asn Met
    290                 295                 300

Thr Asn Ala Cys Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly
305                 310                 315                 320

Asn Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Cys Asn Ala Thr His
                325                 330                 335

Ala Ala Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly
            340                 345                 350

Cys Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr
        355                 360                 365

His Thr Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr
    370                 375                 380

Gly Ala Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly
385                 390                 395                 400

Gly Asn Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr
                405                 410                 415

Asn Thr Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr
            420                 425                 430

Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly
        435                 440                 445

Cys Asn Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala
    450                 455                 460

Arg Gly Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn
465                 470                 475                 480

Cys Ala Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys
                485                 490                 495

Ala Arg Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala
            500                 505                 510
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Arg Cys Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr
515 520 525

Trp Ser Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp
530 535 540

Ser Asn Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr
545 550 555 560

Asn Trp Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr
565 570 575

Gly Ala Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr
580 585 590

Ala Tyr Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys
595 600 605

Asn Cys Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn
610 615 620

Trp Ser Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp
625 630 635 640

Ser Asn Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala
645 650 655

Arg Thr Gly Tyr
660

<210> 539
<211> 660
<212> PRT
<213> Homo Sapiens

<400> 539

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Met Thr
20 25 30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Met Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

```
Arg Trp Ser Asn Ala Thr His Met Thr Asn Thr Ala Tyr Met Gly Asn
                85                  90                  95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
            100                 105                 110

Ala Tyr Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
        115                 120                 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
    130                 135                 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala
145                 150                 155                 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Gly Cys
                165                 170                 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
            180                 185                 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
        195                 200                 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys
    210                 215                 220

Asn Gly Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn
225                 230                 235                 240

Ala Thr His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Gly
                245                 250                 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
            260                 265                 270

Asn Thr Ala Tyr Thr Thr Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
        275                 280                 285

Thr Ala Tyr Thr Thr Tyr Ala Thr His Ala Cys Asn Cys Cys Asn Met
    290                 295                 300

Thr Asn Ala Cys Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly
305                 310                 315                 320

Asn Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
                325                 330                 335

Ala Ala Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly
            340                 345                 350

Cys Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr
        355                 360                 365
```

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His Thr Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr
370                 375                 380

Gly Ala Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly
385                 390                 395                 400

Gly Asn Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr
                405                 410                 415

Asn Thr Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr
            420                 425                 430

Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly
        435                 440                 445

Cys Asn Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala
450                 455                 460

Arg Gly Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn
465                 470                 475                 480

Cys Ala Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys
                485                 490                 495

Ala Arg Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala
            500                 505                 510

Arg Cys Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr
        515                 520                 525

Trp Ser Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp
530                 535                 540

Ser Asn Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr
545                 550                 555                 560

Asn Trp Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr
                565                 570                 575

Gly Ala Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr
            580                 585                 590

Ala Tyr Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys
        595                 600                 605

Asn Cys Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn
610                 615                 620

Trp Ser Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp
625                 630                 635                 640

Ser Asn Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala
                645                 650                 655
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1170

Arg Thr Gly Tyr
660

<210> 540
<211> 642
<212> PRT
<213> Homo Sapiens

<400> 540

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Cys Ala Tyr Thr Ala Tyr
85 90 95

Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Thr Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Trp Ser Asn Met Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Met
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Ala Ala Arg Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
210 215 220

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His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Ala Cys Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala
            260                 265                 270

Tyr Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr Cys Cys Asn Thr Thr Tyr
        275                 280                 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Ala
    290                 295                 300

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Thr His Ala Ala
305                 310                 315                 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
                325                 330                 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
            340                 345                 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
        355                 360                 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
    370                 375                 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385                 390                 395                 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
                405                 410                 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
            420                 425                 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
        435                 440                 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
    450                 455                 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465                 470                 475                 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
                485                 490                 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
            500                 505                 510
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Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 541
<211> 642
<212> PRT
<213> Homo Sapiens

<400> 541

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Gly Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Thr Ala Tyr
85 90 95

2173

Met Thr Asn Gly Cys Asn Thr Gly Gly Met Thr Asn Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Trp Ser Asn Met Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Met
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Ala Cys Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala
260 265 270

Tyr Ala Ala Tyr Ala Cys Asn Thr Ala Tyr Cys Cys Asn Thr Thr Tyr
275 280 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Ala
290 295 300

Cys Asn Ala Ala Arg Ala Thr Gly Gly Ala Tyr Ala Thr His Ala Ala
305 310 315 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
325 330 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
340 345 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
355 360 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
370 375 380

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Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385                 390                 395                 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
                405                 410                 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
            420                 425                 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
        435                 440                 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
    450                 455                 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465                 470                 475                 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
                485                 490                 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
            500                 505                 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
        515                 520                 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
    530                 535                 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545                 550                 555                 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
                565                 570                 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
            580                 585                 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
        595                 600                 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
    610                 615                 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625                 630                 635                 640

Gly Tyr
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<210> 542
<211> 645

2178

<212> PRT
<213> Homo Sapiens

<400> 542

Gly Ala Arg Ala Thr His Gly Thr Asn Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Cys Asn Ala Cys Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Ala Cys Asn Met Thr Asn Trp
50 55 60

Ser Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr
85 90 95

Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Gly Ala Tyr Cys Cys Asn Gly Gly Asn Cys Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Met Gly Asn Met Thr Asn Met Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Gly Asn Gly Cys Asn Trp Ser Asn Met Gly Asn Met
145 150 155 160

Gly Asn Gly Cys Asn Ala Cys Asn Gly Gly Asn Ala Thr His Cys Cys
165 170 175

Asn Gly Cys Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
195 200 205

Ala Arg Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Trp Ser Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Gly Thr Asn Thr
245 250 255

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Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Cys Ala
            260                 265                 270

Tyr Ala Ala Tyr Ala Ala Tyr Thr Gly Gly Cys Cys Asn Cys Cys Asn
        275                 280                 285

Thr Gly Gly Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly
    290                 295                 300

Gly Asn Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr
305                 310                 315                 320

His Ala Ala Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn
                325                 330                 335

Gly Cys Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala
            340                 345                 350

Thr His Thr Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala
        355                 360                 365

Tyr Gly Ala Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn
    370                 375                 380

Gly Gly Asn Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly
385                 390                 395                 400

Thr Asn Thr Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala
                405                 410                 415

Tyr Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg
            420                 425                 430

Gly Cys Asn Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala
        435                 440                 445

Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr
    450                 455                 460

Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn
465                 470                 475                 480

Cys Ala Arg Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly
                485                 490                 495

Ala Arg Cys Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala
            500                 505                 510

Tyr Trp Ser Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn
        515                 520                 525

Trp Ser Asn Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met
    530                 535                 540
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2177

Thr Asn Trp Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala
545 550 555 560

Tyr Gly Ala Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn
565 570 575

Thr Ala Tyr Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala
580 585 590

Cys Asn Cys Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser
595 600 605

Asn Trp Ser Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg
610 615 620

Trp Ser Asn Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly
625 630 635 640

Ala Arg Thr Gly Tyr
645

<210> 543
<211> 642
<212> PRT
<213> Homo Sapiens

<400> 543

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Gly Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Met Gly Asn Thr Gly Gly
85 90 95

Met Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

2178

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Met
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Ala Cys Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Gly Cys
260 265 270

Asn Ala Ala Tyr Trp Ser Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn
275 280 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala
290 295 300

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Thr Thr Tyr Ala Ala
305 310 315 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
325 330 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
340 345 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
355 360 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
370 375 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385 390 395 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
405 410 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
420 425 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
435 440 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
450 455 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465 470 475 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
485 490 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
500 505 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 544
<211> 642
<212> PRT
<213> Homo Sapiens

<400> 544

2180

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Ala Thr His Trp Ser Asn Ala Cys Asn Thr Ala Tyr
85 90 95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Thr Thr Tyr Met Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Met
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Gly Cys Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
260 265 270

Asn Cys Ala Tyr Trp Ser Asn Gly Cys Asn Cys Cys Asn Thr Thr Tyr
275 280 285

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Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Ala
    290                 295                 300

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Thr His Ala Ala
305                 310                 315                 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
                325                 330                 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
            340                 345                 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
        355                 360                 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
    370                 375                 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385                 390                 395                 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
                405                 410                 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
            420                 425                 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
        435                 440                 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
    450                 455                 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465                 470                 475                 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
                485                 490                 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
            500                 505                 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
        515                 520                 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
    530                 535                 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545                 550                 555                 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
                565                 570                 575
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2182

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 545
<211> 639
<212> PRT
<213> Homo Sapiens

<400> 545

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Met Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Ala Cys Asn Ala Thr His Trp Ser Asn Ala Thr His Thr Ala Tyr
85 90 95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Met
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Ala Cys Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
260 265 270

Asn Thr Ala Tyr Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn
275 280 285

Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Ala Cys Asn Ala
290 295 300

Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg Met Gly
305 310 315 320

Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn Cys Cys Asn
325 330 335

Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr Thr Tyr Cys
340 345 350

Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala Arg Cys Ala
355 360 365

Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn Ala Cys Asn
370 375 380

Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr Gly Tyr Met
385 390 395 400

Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr Tyr Thr Ala
405 410 415

Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn Ala Ala Arg
420 425 430

Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly Thr Asn Gly
435 440 445

2184

Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala Arg Trp Ser
450 455 460

Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg Gly Ala Arg
465 470 475 480

Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys Ala Arg Gly
485 490 495

Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser Asn Ala Cys
500 505 510

Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
515 520 525

Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp Ser Asn Ala
530 535 540

Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala Arg Ala Ala
545 550 555 560

Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr Gly Cys Asn
565 570 575

Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys Ala Tyr Cys
580 585 590

Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Cys Cys
595 600 605

Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn Thr Thr Tyr
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625 630 635

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Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
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Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

2185

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Ala Thr His Met Gly Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Met Gly Asn Cys Cys Asn Gly Gly Asn Ala Ala Tyr Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Met
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
210 215 220

His Met Gly Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Ala Cys Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
260 265 270

Asn Thr Ala Tyr Trp Ser Asn Ala Thr His Cys Cys Asn Met Thr Asn
275 280 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Ala
290 295 300

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
325 330 335

2186

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
340 345 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
355 360 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
370 375 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385 390 395 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
405 410 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
420 425 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
435 440 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
450 455 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465 470 475 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
485 490 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
500 505 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

2187

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 547
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<400> 547

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Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Gly
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Ala Cys Asn Ala Thr His Trp Ser Asn Met Gly Asn Thr Ala Tyr
85 90 95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Met
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
195 200 205

2188

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Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr
    210                 215                 220

Asn Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Ala Cys Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Ala Thr
            260                 265                 270

His Thr Ala Tyr Trp Ser Asn Ala Cys Asn Trp Ser Asn Ala Thr His
        275                 280                 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala
    290                 295                 300

Cys Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305                 310                 315                 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
                325                 330                 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
            340                 345                 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
        355                 360                 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
    370                 375                 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385                 390                 395                 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
                405                 410                 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
            420                 425                 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
        435                 440                 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
    450                 455                 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465                 470                 475                 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
                485                 490                 495
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1189

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
500 505 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
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Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

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Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Met Gly Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Gly Thr Asn Met Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Cys Asn Gly Ala Arg Trp Ser Asn Trp Ser Asn Met
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Ala Cys Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
260 265 270

Asn Thr Ala Tyr Ala Thr His Ala Cys Asn Cys Cys Asn Ala Thr His
275 280 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala
290 295 300

Cys Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Thr
305 310 315 320

His Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
325 330 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
340 345 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
355 360 365

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Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
    370                 375                 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385                 390                 395                 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
                405                 410                 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
            420                 425                 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
        435                 440                 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
    450                 455                 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465                 470                 475                 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
                485                 490                 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
            500                 505                 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
        515                 520                 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
    530                 535                 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545                 550                 555                 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
                565                 570                 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
            580                 585                 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
        595                 600                 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
    610                 615                 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625                 630                 635                 640

Gly Tyr
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J192

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20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Ala Thr His Trp Ser Asn Met Gly Asn Thr Ala Tyr
85 90 95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Ala Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Met
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Ala Ala Tyr Thr Thr Tyr Gly Cys Asn Ala Cys Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
260 265 270

Asn Thr Ala Tyr Thr Thr Tyr Ala Cys Asn Cys Cys Asn Ala Thr His
275 280 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala
290 295 300

Cys Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
325 330 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
340 345 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
355 360 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
370 375 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385 390 395 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
405 410 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
420 425 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
435 440 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
450 455 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465 470 475 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
485 490 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
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Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
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Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 550
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Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
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Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Ala Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Met
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Thr Thr
210 215 220

Tyr Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Ala Cys Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
260 265 270

Asn Thr Ala Tyr Thr Thr Tyr Trp Ser Asn Cys Cys Asn Ala Thr His
275 280 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala
290 295 300

Cys Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
325 330 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
340 345 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
355 360 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
370 375 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385 390 395 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
405 410 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
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Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
435 440 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
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Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465 470 475 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
485 490 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
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Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

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Gly Tyr

<210> 551
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2197

<400> 551

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Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Ala Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Met
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr
210 215 220

Asn Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Trp Ser Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
260 265 270

Asn Thr Thr Tyr Thr Ala Tyr Ala Cys Asn Cys Cys Asn Ala Thr His
275 280 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala
290 295 300

Cys Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
325 330 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
340 345 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
355 360 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
370 375 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385 390 395 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
405 410 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
420 425 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
435 440 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
450 455 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465 470 475 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
485 490 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
500 505 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

1199

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

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Gly Tyr

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35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
130 135 140

1200

Thr Ala Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Met
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Ala Cys Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
260 265 270

Asn Thr Ala Tyr Thr Thr Tyr Ala Cys Asn Cys Cys Asn Ala Thr His
275 280 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala
290 295 300

Cys Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
325 330 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
340 345 350

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2204

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1205

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Cys Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala
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Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala
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Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
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Thr Asn Gly Ala Arg Ala Cys Asn Gly Gly Asn Gly Thr Asn Cys Cys
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Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
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2216

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His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

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Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala
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Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
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Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
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2918

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
405 410 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
420 425 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
435 440 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
450 455 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465 470 475 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
485 490 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
500 505 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 560
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<212> PRT
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2299

<400> 560

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
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Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Trp Ser Asn
85 90 95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Met
145 150 155 160

Thr Asn Gly Ala Arg Ala Cys Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Thr Thr Tyr Ala Cys Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Ala Cys Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala
260 265 270

2110

Tyr Gly Ala Tyr Ala Ala Tyr Met Thr Asn Cys Cys Asn Met Thr Asn
275 280 285

Gly Cys Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Ala
290 295 300

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Met Gly
305 310 315 320

Asn Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
325 330 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
340 345 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
355 360 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
370 375 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385 390 395 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
405 410 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
420 425 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
435 440 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
450 455 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465 470 475 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
485 490 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
500 505 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

2221

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 561
<211> 642
<212> PRT
<213> Homo Sapiens

<400> 561

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Gly Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Ala Cys Asn Ala Ala Tyr Thr Ala Tyr
85 90 95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
130 135 140

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Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Met
145                 150                 155                 160

Thr Asn Gly Ala Arg Ala Cys Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Thr Thr Tyr Ala Cys Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Ala Cys Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala
            260                 265                 270

Tyr Gly Ala Tyr Trp Ser Asn Met Thr Asn Cys Cys Asn Ala Thr His
        275                 280                 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala
    290                 295                 300

Cys Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305                 310                 315                 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
                325                 330                 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
            340                 345                 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
        355                 360                 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
    370                 375                 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385                 390                 395                 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
                405                 410                 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
            420                 425                 430
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1128

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
435 440 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
450 455 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465 470 475 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
485 490 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
500 505 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 562
<211> 642
<212> PRT
<213> Homo Sapiens

<400> 562

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Thr Ala Tyr
85 90 95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Met Thr Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
130 135 140

Cys Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Met
145 150 155 160

Thr Asn Gly Ala Arg Ala Cys Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Thr Thr Tyr Ala Cys Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Ala Cys Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala
260 265 270

Tyr Gly Ala Tyr Ala Ala Tyr Met Thr Asn Cys Cys Asn Ala Thr His
275 280 285

J223

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala
290 295 300

Cys Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
325 330 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
340 345 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
355 360 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
370 375 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385 390 395 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
405 410 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
420 425 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
435 440 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
450 455 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465 470 475 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
485 490 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
500 505 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 563
<211> 642
<212> PRT
<213> Homo Sapiens

<400> 563

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
50 55 60

Cys Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Gly Ala Tyr Thr Ala Tyr
85 90 95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Met
145 150 155 160

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Thr Asn Gly Ala Arg Ala Cys Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Thr Thr Tyr Ala Cys Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Ala Cys Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Tyr Thr Ala
            260                 265                 270

Tyr Gly Ala Tyr Ala Ala Tyr Met Thr Asn Cys Cys Asn Ala Thr His
        275                 280                 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala
    290                 295                 300

Cys Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305                 310                 315                 320

Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
                325                 330                 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
            340                 345                 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
        355                 360                 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
    370                 375                 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385                 390                 395                 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
                405                 410                 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
            420                 425                 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
        435                 440                 445
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2228

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
450 455 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465 470 475 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
485 490 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
500 505 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 564
<211> 642
<212> PRT
<213> Homo Sapiens

<400> 564

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Ala Cys Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Thr
20 25 30

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Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Ala
    50                  55                  60

Cys Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Trp Ser Asn
                85                  90                  95

Met Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Met Thr Asn Met Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Met
145                 150                 155                 160

Thr Asn Gly Ala Arg Ala Cys Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Ala Cys Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Ala Cys Asn Thr Thr Tyr Ala Cys Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Met Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Ala Cys Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Tyr Thr Ala
            260                 265                 270

Tyr Gly Ala Tyr Ala Ala Tyr Met Thr Asn Cys Cys Asn Ala Thr His
        275                 280                 285

Ala Cys Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala
    290                 295                 300

Cys Asn Met Gly Asn Met Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305                 310                 315                 320
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Arg Met Gly Asn Ala Cys Asn Gly Thr Asn Gly Cys Asn Gly Cys Asn
325 330 335

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Ala Thr His Thr
340 345 350

Thr Tyr Cys Cys Asn Cys Cys Asn Trp Ser Asn Gly Ala Tyr Gly Ala
355 360 365

Arg Cys Ala Arg Met Thr Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn
370 375 380

Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Thr
385 390 395 400

Gly Tyr Met Thr Asn Met Thr Asn Ala Ala Tyr Ala Ala Tyr Thr Thr
405 410 415

Tyr Thr Ala Tyr Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Cys Asn
420 425 430

Ala Ala Arg Gly Thr Asn Cys Ala Arg Thr Gly Gly Ala Ala Arg Gly
435 440 445

Thr Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Met Thr Asn Cys Ala
450 455 460

Arg Trp Ser Asn Gly Gly Asn Ala Ala Tyr Trp Ser Asn Cys Ala Arg
465 470 475 480

Gly Ala Arg Trp Ser Asn Gly Thr Asn Ala Cys Asn Gly Ala Arg Cys
485 490 495

Ala Arg Gly Ala Tyr Trp Ser Asn Ala Ala Arg Gly Ala Tyr Trp Ser
500 505 510

Asn Ala Cys Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
515 520 525

Trp Ser Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Trp
530 535 540

Ser Asn Ala Ala Arg Gly Cys Asn Gly Ala Tyr Thr Ala Tyr Gly Ala
545 550 555 560

Arg Ala Ala Arg Cys Ala Tyr Ala Ala Arg Gly Thr Asn Thr Ala Tyr
565 570 575

Gly Cys Asn Thr Gly Tyr Gly Ala Arg Gly Thr Asn Ala Cys Asn Cys
580 585 590

Ala Tyr Cys Ala Arg Gly Gly Asn Met Thr Asn Trp Ser Asn Trp Ser
595 600 605

Asn Cys Cys Asn Gly Thr Asn Ala Cys Asn Ala Ala Arg Trp Ser Asn
610 615 620

Thr Thr Tyr Ala Ala Tyr Met Gly Asn Gly Gly Asn Gly Ala Arg Thr
625 630 635 640

Gly Tyr

<210> 565
<211> 1338
<212> PRT
<213> Homo Sapiens

<400> 565

Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
20 25 30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Cys Asn
35 40 45

Trp Ser Asn Gly Thr Asn Ala Ala Arg Gly Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Ala
65 70 75 80

Tyr Ala Cys Asn Thr Thr Tyr Ala Cys Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Gly Asn Ala Thr His Trp Ser Asn Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Cys Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
130 135 140

Gly Gly Asn Thr Gly Gly Ala Thr His Trp Ser Asn Gly Cys Asn Trp
145 150 155 160

Ser Asn Ala Ala Tyr Gly Gly Asn Ala Ala Tyr Ala Cys Asn Ala Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Cys Ala Arg Ala Ala Arg Met Thr Asn
180 185 190

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Cys Ala Arg Gly Ala Tyr Met Gly Asn Gly Thr Asn Ala Cys Asn Ala
        195                 200                 205

Thr Gly Ala Cys Asn Ala Cys Asn Gly Ala Tyr Ala Cys Asn Trp Ser
    210                 215                 220

Asn Ala Cys Asn Trp Ser Asn Ala Cys Asn Gly Cys Asn Thr Ala Tyr
225                 230                 235                 240

Ala Thr Gly Gly Ala Arg Met Thr Asn Met Gly Asn Trp Ser Asn Met
                245                 250                 255

Thr Asn Met Gly Asn Trp Ser Asn Gly Ala Tyr Gly Ala Tyr Ala Cys
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Tyr Ala Ala Tyr Thr
    290                 295                 300

Gly Gly Ala Ala Tyr Thr Ala Tyr Gly Gly Asn Thr Thr Tyr Thr Thr
305                 310                 315                 320

Tyr Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg
                325                 330                 335

Gly Gly Asn Ala Cys Asn Met Thr Asn Gly Thr Asn Ala Cys Asn Gly
            340                 345                 350

Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys
        355                 360                 365

Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn
    370                 375                 380

Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr
385                 390                 395                 400

Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser
                405                 410                 415

Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn
            420                 425                 430

Met Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala
        435                 440                 445

Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala
    450                 455                 460

Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn
465                 470                 475                 480
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2133

Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met
485 490 495

Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala
500 505 510

Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn
515 520 525

Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met
530 535 540

Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser
545 550 555 560

Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn
565 570 575

Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala
580 585 590

Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly
595 600 605

Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg
610 615 620

Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly
625 630 635 640

Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala
645 650 655

Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn
660 665 670

Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys
675 680 685

Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys
690 695 700

Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr
705 710 715 720

Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys
725 730 735

Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr
740 745 750

Gly Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn
755 760 765

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Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly
    770                 775                 780

Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala
785                 790                 795                 800

Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn
                805                 810                 815

Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly
            820                 825                 830

Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr
        835                 840                 845

Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn
    850                 855                 860

Ala Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys
865                 870                 875                 880

Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr
                885                 890                 895

Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn
            900                 905                 910

Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys
        915                 920                 925

Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly
    930                 935                 940

Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr
945                 950                 955                 960

Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly
                965                 970                 975

Gly Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr
            980                 985                 990

His Gly Ala Arg Ala Ala Arg Ala  Cys Asn Ala Thr His  Trp Ser Asn
        995                 1000                1005

Ala Ala  Arg Ala Cys Asn Ala  Ala Arg Gly Gly Asn  Cys Ala Arg
    1010                1015                1020

Cys Cys  Asn Met Gly Asn Gly  Ala Arg Cys Cys Asn  Cys Ala Arg
    1025                1030                1035

Gly Thr  Asn Thr Ala Tyr Ala  Cys Asn Met Thr Asn  Cys Cys Asn
    1040                1045                1050
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Cys Cys Asn Trp Ser Asn Met Gly Asn Gly Ala Arg Gly Ala Arg
1055 1060 1065

Ala Thr Gly Ala Cys Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg
1070 1075 1080

Gly Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr Gly Tyr
1085 1090 1095

Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Gly Asn Thr Thr Tyr
1100 1105 1110

Thr Ala Tyr Cys Cys Asn Trp Ser Asn Gly Ala Tyr Ala Thr His
1115 1120 1125

Gly Cys Asn Gly Thr Asn Gly Ala Arg Thr Gly Gly Gly Ala Arg
1130 1135 1140

Trp Ser Asn Ala Ala Tyr Gly Gly Asn Cys Ala Arg Cys Cys Asn
1145 1150 1155

Gly Ala Arg Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr Ala Ala Arg
1160 1165 1170

Ala Cys Asn Ala Cys Asn Cys Cys Asn Cys Cys Asn Ala Thr Gly
1175 1180 1185

Met Thr Asn Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Gly Asn
1190 1195 1200

Trp Ser Asn Thr Thr Tyr Thr Thr Tyr Met Thr Asn Thr Ala Tyr
1205 1210 1215

Trp Ser Asn Ala Ala Arg Met Thr Asn Ala Cys Asn Gly Thr Asn
1220 1225 1230

Gly Ala Tyr Ala Ala Arg Trp Ser Asn Met Gly Asn Thr Gly Gly
1235 1240 1245

Cys Ala Arg Cys Ala Arg Gly Gly Asn Ala Ala Tyr Gly Thr Asn
1250 1255 1260

Thr Thr Tyr Trp Ser Asn Thr Gly Tyr Trp Ser Asn Gly Thr Asn
1265 1270 1275

Ala Thr Gly Cys Ala Tyr Gly Ala Arg Gly Cys Asn Met Thr Asn
1280 1285 1290

Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr Thr Ala Tyr Ala Cys Asn
1295 1300 1305

Cys Ala Arg Ala Ala Arg Trp Ser Asn Met Thr Asn Trp Ser Asn
1310 1315 1320

Met Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn Ala Ala Arg
1325 1330 1335

<210> 566
<211> 1329
<212> PRT
<213> Homo Sapiens

<400> 566

Cys Ala Arg Gly Thr Asn Cys Ala Tyr Met Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
20 25 30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Cys Asn
35 40 45

Trp Ser Asn Gly Thr Asn Ala Ala Arg Gly Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Gly Gly Asn Thr Ala
65 70 75 80

Tyr Ala Cys Asn Thr Thr Tyr Ala Cys Asn Gly Gly Asn Cys Ala Tyr
85 90 95

Thr Ala Tyr Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Cys Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
130 135 140

Gly Gly Asn Thr Gly Gly Ala Thr His Ala Ala Tyr Cys Cys Asn Ala
145 150 155 160

Ala Tyr Trp Ser Asn Gly Gly Asn Gly Gly Asn Ala Cys Asn Ala Ala
165 170 175

Tyr Thr Gly Tyr Gly Cys Asn Cys Ala Arg Ala Ala Arg Thr Thr Tyr
180 185 190

Cys Ala Arg Gly Gly Asn Met Gly Asn Gly Thr Asn Ala Cys Asn Ala
195 200 205

Thr Gly Ala Cys Asn Met Gly Asn Gly Ala Tyr Ala Cys Asn Trp Ser
210 215 220

```
Asn Ala Thr His Trp Ser Asn Ala Cys Asn Gly Cys Asn Thr Ala Tyr
225                 230                 235                 240

Ala Thr Gly Gly Ala Arg Met Thr Asn Trp Ser Asn Met Gly Asn Met
                245                 250                 255

Thr Asn Met Gly Asn Trp Ser Asn Gly Ala Tyr Gly Ala Tyr Ala Cys
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Met Gly Asn Trp Ser Asn Ala Thr His Gly Cys Asn Gly
    290                 295                 300

Thr Asn Gly Cys Asn Met Thr Asn Gly Ala Tyr Thr Ala Tyr Thr Gly
305                 310                 315                 320

Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Met Thr Asn
                325                 330                 335

Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly
            340                 345                 350

Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys
        355                 360                 365

Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn
    370                 375                 380

Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp
385                 390                 395                 400

Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys
                405                 410                 415

Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr
            420                 425                 430

Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr
        435                 440                 445

Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys
    450                 455                 460

Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn
465                 470                 475                 480

Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser Asn Gly
                485                 490                 495

Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys
            500                 505                 510
```

Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp Ser Asn
515 520 525

Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn Met
530 535 540

Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys
545 550 555 560

Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr
565 570 575

Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr
580 585 590

Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala
595 600 605

Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr
610 615 620

Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala
625 630 635 640

Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg Thr Gly
645 650 655

Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn
660 665 670

Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys
675 680 685

Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser
690 695 700

Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn
705 710 715 720

Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala
725 730 735

Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn Met Gly
740 745 750

Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn
755 760 765

Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly
770 775 780

Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys
785 790 795 800

2229

```
Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr
                805                 810                 815

Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly
            820                 825                 830

Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys
        835                 840                 845

Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met Gly Asn
    850                 855                 860

Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp
865                 870                 875                 880

Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr
                885                 890                 895

Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly Thr Asn
            900                 905                 910

Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met
        915                 920                 925

Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala
    930                 935                 940

Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn
945                 950                 955                 960

Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys Cys Asn Gly
                965                 970                 975

Cys Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala Arg Ala Cys
            980                 985                 990

Asn Ala Thr His Trp Ser Asn Ala  Ala Arg Ala Cys Asn  Ala Ala Arg
        995                 1000                1005

Gly Gly  Asn Cys Ala Arg Cys  Cys Asn Met Gly Asn  Gly Ala Arg
    1010                1015                1020

Cys Cys  Asn Cys Ala Arg Gly  Thr Asn Thr Ala Tyr  Ala Cys Asn
    1025                1030                1035

Met Thr  Asn Cys Cys Asn Cys  Cys Asn Trp Ser Asn  Met Gly Asn
    1040                1045                1050

Gly Ala  Arg Gly Ala Arg Ala  Thr Gly Ala Cys Asn  Ala Ala Arg
    1055                1060                1065

Ala Ala  Tyr Cys Ala Arg Gly  Thr Asn Trp Ser Asn  Met Thr Asn
    1070                1075                1080
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2140

Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg
1085 1090 1095

Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Trp Ser Asn
1100 1105 1110

Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn Gly Ala Arg
1115 1120 1125

Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr Gly Gly Asn
1130 1135 1140

Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr Ala Ala Tyr
1145 1150 1155

Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn Cys Cys Asn
1160 1165 1170

Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr Trp Ser Asn
1175 1180 1185

Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr Thr Thr Tyr
1190 1195 1200

Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg Met Thr Asn
1205 1210 1215

Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg Trp Ser Asn
1220 1225 1230

Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg Gly Gly Asn
1235 1240 1245

Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn Thr Gly Tyr
1250 1255 1260

Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr Gly Ala Arg
1265 1270 1275

Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr
1280 1285 1290

Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg Trp Ser Asn
1295 1300 1305

Met Thr Asn Trp Ser Asn Met Thr Asn Trp Ser Asn Cys Cys Asn
1310 1315 1320

Gly Gly Asn Ala Ala Arg
1325

<210> 567
<211> 1329

2141

<212> PRT
<213> Homo Sapiens

<400> 567

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Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Gly Thr Asn Cys
1               5                  10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
            20                  25                  30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Cys Asn
        35                  40                  45

Trp Ser Asn Gly Thr Asn Ala Ala Arg Gly Thr Asn Trp Ser Asn Thr
    50                  55                  60

Gly Tyr Ala Ala Arg Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Ala
65                  70                  75                  80

Tyr Ala Cys Asn Thr Thr Tyr Ala Cys Asn Gly Gly Asn Thr Ala Tyr
                85                  90                  95

Thr Ala Tyr Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
            100                 105                 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Cys Ala
        115                 120                 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
    130                 135                 140

Gly Gly Asn Thr Gly Gly Ala Thr His Ala Ala Tyr Cys Cys Asn Ala
145                 150                 155                 160

Ala Tyr Trp Ser Asn Gly Gly Asn Gly Gly Asn Ala Cys Asn Ala Ala
                165                 170                 175

Tyr Cys Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg Thr Thr Tyr
            180                 185                 190

Cys Ala Arg Gly Gly Asn Met Gly Asn Gly Thr Asn Ala Cys Asn Ala
        195                 200                 205

Thr Gly Ala Cys Asn Met Gly Asn Gly Ala Tyr Ala Cys Asn Trp Ser
    210                 215                 220

Asn Ala Thr His Trp Ser Asn Ala Cys Asn Gly Cys Asn Thr Ala Tyr
225                 230                 235                 240

Ala Thr Gly Gly Ala Arg Met Thr Asn Trp Ser Asn Met Gly Asn Met
                245                 250                 255
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2242

Thr Asn Met Gly Asn Trp Ser Asn Gly Ala Tyr Gly Ala Tyr Ala Cys
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Trp Ser Asn Ala Thr His Gly Cys Asn Gly
290 295 300

Thr Asn Gly Cys Asn Met Thr Asn Gly Ala Tyr Thr Ala Tyr Thr Gly
305 310 315 320

Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Met Thr Asn
325 330 335

Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly
340 345 350

Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys
355 360 365

Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn
370 375 380

Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp
385 390 395 400

Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys
405 410 415

Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr
420 425 430

Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr
435 440 445

Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys
450 455 460

Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn
465 470 475 480

Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser Asn Gly
485 490 495

Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys
500 505 510

Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp Ser Asn
515 520 525

Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn Met
530 535 540

2245

Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys
545 550 555 560

Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr
565 570 575

Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr
580 585 590

Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala
595 600 605

Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr
610 615 620

Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala
625 630 635 640

Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg Thr Gly
645 650 655

Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn
660 665 670

Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys
675 680 685

Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser
690 695 700

Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn
705 710 715 720

Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala
725 730 735

Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn Met Gly
740 745 750

Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn
755 760 765

Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly
770 775 780

Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys
785 790 795 800

Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr
805 810 815

Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly
820 825 830

2144

```
Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys
        835                 840                 845

Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met Gly Asn
    850                 855                 860

Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp
865                 870                 875                 880

Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr
                885                 890                 895

Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly Thr Asn
            900                 905                 910

Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met
        915                 920                 925

Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala
    930                 935                 940

Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn
945                 950                 955                 960

Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys Cys Asn Gly
                965                 970                 975

Cys Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala Arg Ala Cys
            980                 985                 990

Asn Ala Thr His Trp Ser Asn Ala  Ala Arg Ala Cys Asn  Ala Ala Arg
        995                 1000                1005

Gly Gly  Asn Cys Ala Arg Cys  Cys Asn Met Gly Asn  Gly Ala Arg
    1010                1015                1020

Cys Cys  Asn Cys Ala Arg Gly  Thr Asn Thr Ala Tyr  Ala Cys Asn
    1025                1030                1035

Met Thr  Asn Cys Cys Asn Cys  Cys Asn Trp Ser Asn  Met Gly Asn
    1040                1045                1050

Gly Ala  Arg Gly Ala Arg Ala  Thr Gly Ala Cys Asn  Ala Ala Arg
    1055                1060                1065

Ala Ala  Tyr Cys Ala Arg Gly  Thr Asn Trp Ser Asn  Met Thr Asn
    1070                1075                1080

Ala Cys  Asn Thr Gly Tyr Met  Thr Asn Gly Thr Asn  Ala Ala Arg
    1085                1090                1095

Gly Gly  Asn Thr Thr Tyr Thr  Ala Tyr Cys Cys Asn  Trp Ser Asn
    1100                1105                1110
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Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn Gly Ala Arg
1115 1120 1125

Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr Gly Gly Asn
1130 1135 1140

Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr Ala Ala Tyr
1145 1150 1155

Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn Cys Cys Asn
1160 1165 1170

Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr Trp Ser Asn
1175 1180 1185

Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr Thr Thr Tyr
1190 1195 1200

Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg Met Thr Asn
1205 1210 1215

Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg Trp Ser Asn
1220 1225 1230

Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg Gly Gly Asn
1235 1240 1245

Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn Thr Gly Tyr
1250 1255 1260

Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr Gly Ala Arg
1265 1270 1275

Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr
1280 1285 1290

Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg Trp Ser Asn
1295 1300 1305

Met Thr Asn Trp Ser Asn Met Thr Asn Trp Ser Asn Cys Cys Asn
1310 1315 1320

Gly Gly Asn Ala Ala Arg
1325

<210> 568
<211> 1344
<212> PRT
<213> Homo Sapiens

<400> 568

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Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Gly Thr Asn Cys
1               5                  10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
            20                  25                  30

Asn Met Gly Asn Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Cys Asn
        35                  40                  45

Trp Ser Asn Gly Thr Asn Ala Ala Arg Gly Thr Asn Trp Ser Asn Thr
    50                  55                  60

Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Gly Gly Asn Thr Ala
65                  70                  75                  80

Tyr Ala Cys Asn Met Thr Asn Ala Cys Asn Gly Ala Arg Met Thr Asn
                85                  90                  95

Trp Ser Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
            100                 105                 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
        115                 120                 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
    130                 135                 140

Gly Gly Asn Trp Ser Asn Thr Thr Tyr Gly Ala Tyr Cys Cys Asn Gly
145                 150                 155                 160

Ala Arg Gly Ala Tyr Gly Gly Asn Gly Ala Arg Ala Cys Asn Ala Thr
                165                 170                 175

His Thr Ala Tyr Gly Cys Asn Cys Ala Arg Ala Ala Arg Thr Thr Tyr
            180                 185                 190

Cys Ala Arg Gly Gly Asn Met Gly Asn Gly Thr Asn Ala Cys Asn Ala
        195                 200                 205

Thr Gly Met Thr Asn Gly Ala Arg Gly Ala Tyr Ala Cys Asn Trp Ser
    210                 215                 220

Asn Ala Cys Asn Gly Ala Tyr Ala Cys Asn Gly Cys Asn Thr Ala Tyr
225                 230                 235                 240

Ala Thr Gly Gly Ala Arg Met Thr Asn Trp Ser Asn Trp Ser Asn Met
                245                 250                 255

Thr Asn Met Gly Asn Trp Ser Asn Gly Ala Arg Gly Ala Tyr Ala Cys
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285
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Gly Cys Asn Ala Cys Asn Gly Ala Arg Gly Gly Asn Gly Ala Tyr Gly
290 295 300

Gly Asn Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala
305 310 315 320

Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr Gly Gly
325 330 335

Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Ala Cys Asn Gly
340 345 350

Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys
355 360 365

Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn
370 375 380

Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly
385 390 395 400

Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser
405 410 415

Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn
420 425 430

Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr Met
435 440 445

Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr
450 455 460

Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn
465 470 475 480

Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly
485 490 495

Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly
500 505 510

Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn
515 520 525

Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp Ser Asn Trp
530 535 540

Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr
545 550 555 560

Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn
565 570 575

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Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr
            580                 585                 590

Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala
        595                 600                 605

Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr
    610                 615                 620

Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala
625                 630                 635                 640

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys
                645                 650                 655

Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr
            660                 665                 670

Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys
        675                 680                 685

Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys
    690                 695                 700

Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn
705                 710                 715                 720

Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys
                725                 730                 735

Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys
            740                 745                 750

Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn Met Gly Asn
        755                 760                 765

Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr
    770                 775                 780

Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr
785                 790                 795                 800

Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn
                805                 810                 815

Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr
            820                 825                 830

Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr
        835                 840                 845

Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn
    850                 855                 860
```

Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met Gly Asn Gly
865 870 875 880

Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser
885 890 895

Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn
900 905 910

Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly Thr Asn Gly
915 920 925

Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr
930 935 940

Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr
945 950 955 960

Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala
965 970 975

Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys Cys Asn Gly Cys
980 985 990

Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala Arg Ala Cys Asn
995 1000 1005

Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg
1010 1015 1020

Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg
1025 1030 1035

Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr Ala Cys Asn
1040 1045 1050

Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn Met Gly Asn
1055 1060 1065

Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn Ala Ala Arg
1070 1075 1080

Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn Met Thr Asn
1085 1090 1095

Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg
1100 1105 1110

Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Trp Ser Asn
1115 1120 1125

Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn Gly Ala Arg
1130 1135 1140

1150

```
Thr Gly  Gly Gly Ala Arg Trp  Ser Asn Ala Ala Tyr  Gly Gly Asn
     1145                 1150                 1155

Cys Ala  Arg Cys Cys Asn Gly  Ala Arg Ala Ala Tyr  Ala Ala Tyr
     1160                 1165                 1170

Thr Ala  Tyr Ala Ala Arg Ala  Cys Asn Ala Cys Asn  Cys Cys Asn
     1175                 1180                 1185

Cys Cys  Asn Ala Thr Gly Met  Thr Asn Gly Ala Tyr  Trp Ser Asn
     1190                 1195                 1200

Gly Ala  Tyr Gly Gly Asn Trp  Ser Asn Thr Thr Tyr  Thr Thr Tyr
     1205                 1210                 1215

Met Thr  Asn Thr Ala Tyr Trp  Ser Asn Ala Ala Arg  Met Thr Asn
     1220                 1225                 1230

Ala Cys  Asn Gly Thr Asn Gly  Ala Tyr Ala Ala Arg  Trp Ser Asn
     1235                 1240                 1245

Met Gly  Asn Thr Gly Gly Cys  Ala Arg Cys Ala Arg  Gly Gly Asn
     1250                 1255                 1260

Ala Ala  Tyr Gly Thr Asn Thr  Thr Tyr Trp Ser Asn  Thr Gly Tyr
     1265                 1270                 1275

Trp Ser  Asn Gly Thr Asn Ala  Thr Gly Cys Ala Tyr  Gly Ala Arg
     1280                 1285                 1290

Gly Cys  Asn Met Thr Asn Cys  Ala Tyr Ala Ala Tyr  Cys Ala Tyr
     1295                 1300                 1305

Thr Ala  Tyr Ala Cys Asn Cys  Ala Arg Ala Ala Arg  Trp Ser Asn
     1310                 1315                 1320

Met Thr  Asn Trp Ser Asn Met  Thr Asn Trp Ser Asn  Cys Cys Asn
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Gly Gly  Asn Ala Ala Arg
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<400> 569

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Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Ala Cys Asn Gly Ala Arg
35 40 45

Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Thr
50 55 60

Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Ala Ala Tyr Gly Cys Asn
85 90 95

Met Gly Asn Ala Thr Gly Gly Gly Asn Gly Thr Asn Trp Ser Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Met Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Met Thr Asn Gly Cys Asn Cys Ala Tyr Ala Thr His Thr
145 150 155 160

Thr Tyr Trp Ser Asn Ala Ala Tyr Gly Ala Tyr Gly Ala Arg Ala Ala
165 170 175

Arg Trp Ser Asn Thr Ala Tyr Trp Ser Asn Ala Cys Asn Trp Ser Asn
180 185 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Met Thr Asn Ala
195 200 205

Cys Asn Ala Thr His Trp Ser Asn Ala Ala Arg Gly Ala Tyr Ala Cys
210 215 220

Asn Trp Ser Asn Ala Ala Arg Trp Ser Asn Cys Ala Arg Gly Thr Asn
225 230 235 240

Gly Thr Asn Met Thr Asn Ala Cys Asn Ala Thr Gly Ala Cys Asn Ala
245 250 255

Ala Tyr Ala Thr Gly Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
260 265 270

Tyr Ala Cys Asn Gly Cys Asn Ala Cys Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Ala Thr Gly Thr Ala Tyr Trp
290 295 300

Ser Asn Trp Ser Asn Gly Gly Asn Thr Gly Gly Thr Ala Tyr Gly Gly
305 310 315 320

Asn Gly Thr Asn Thr Thr Tyr Gly Ala Tyr Thr Ala Tyr Thr Gly Gly
325 330 335

Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Met Thr Asn Gly
340 345 350

Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys
355 360 365

Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn
370 375 380

Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly
385 390 395 400

Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser
405 410 415

Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn
420 425 430

Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr Met
435 440 445

Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr
450 455 460

Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn
465 470 475 480

Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly
485 490 495

Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly
500 505 510

Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn
515 520 525

Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp Ser Asn Trp
530 535 540

Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr
545 550 555 560

Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn
565 570 575

Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr
580 585 590

Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala
595 600 605

Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr
610 615 620

Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala
625 630 635 640

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys
645 650 655

Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr
660 665 670

Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys
675 680 685

Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys
690 695 700

Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn
705 710 715 720

Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys
725 730 735

Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys
740 745 750

Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn Met Gly Asn
755 760 765

Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr
770 775 780

Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr
785 790 795 800

Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn
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Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr
820 825 830

Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr
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Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn
850 855 860

Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met Gly Asn Gly
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Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser
885 890 895

Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn
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Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly Thr Asn Gly
915 920 925

Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr
930 935 940

Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr
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Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala
965 970 975

Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys Cys Asn Gly Cys
980 985 990

Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala Arg Ala Cys Asn
995 1000 1005

Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg
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Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg
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Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr Ala Cys Asn
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Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn Met Gly Asn
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Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn Ala Ala Arg
1070 1075 1080

Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn Met Thr Asn
1085 1090 1095

Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg
1100 1105 1110

Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Trp Ser Asn
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Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn Gly Ala Arg
1130 1135 1140

Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr Gly Gly Asn
1145 1150 1155

Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr Ala Ala Tyr
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Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn Cys Cys Asn
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Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr Trp Ser Asn
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Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr Thr Thr Tyr
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Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg Met Thr Asn
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Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg Trp Ser Asn
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Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg Gly Gly Asn
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Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn Thr Gly Tyr
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Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr Gly Ala Arg
1280 1285 1290

Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr
1295 1300 1305

Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg Trp Ser Asn
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1325 1330 1335

Gly Gly Asn Ala Ala Arg
1340

<210> 570
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35 40 45

Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Thr
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Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Thr Thr
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Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Ala Ala Tyr Gly Cys Asn
85 90 95

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100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Met Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Met Thr Asn Gly Thr Asn Met Thr Asn Ala Thr His Thr
145 150 155 160

Thr Tyr Trp Ser Asn Ala Ala Tyr Gly Ala Tyr Gly Ala Arg Ala Ala
165 170 175

Arg Trp Ser Asn Thr Ala Tyr Trp Ser Asn Ala Cys Asn Trp Ser Asn
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Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Met Thr Asn Ala
195 200 205

Cys Asn Ala Thr His Trp Ser Asn Ala Ala Arg Gly Ala Tyr Ala Cys
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225 230 235 240

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Ala Tyr Ala Thr Gly Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
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Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn
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Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Ala
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Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser
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Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn
370 375 380

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met
385 390 395 400

Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly
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Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn
420 425 430

Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr
435 440 445

Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala
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Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn
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Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp
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Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr
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530 535 540

Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser
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Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn
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580 585 590

Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys
595 600 605

Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn
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Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala
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645 650 655

Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg
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675 680 685

Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys
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Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys
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Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala
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Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn
755 760 765

Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala
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Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala
785 790 795 800

Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr
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Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala
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Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly
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Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr
850 855 860

Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met
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Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala
885 890 895

Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn
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Gly Thr Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly
915 920 925

Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly
930 935 940

Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg
945 950 955 960

Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp
965 970 975

Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys Cys
980 985 990

Asn Gly Cys Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala Arg
995 1000 1005

Ala Cys Asn Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn
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Ala Ala Arg Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn
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Gly Ala Arg Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr
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Ala Cys Asn Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn
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1070 1075 1080

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1100 1105 1110

Ala Ala Arg Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn
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Trp Ser Asn Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn
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Gly Ala Arg Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr
1145 1150 1155

Gly Gly Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr
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Ala Ala Tyr Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn
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Cys Cys Asn Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr
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Trp Ser Asn Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr
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Thr Thr Tyr Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg
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Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg
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Trp Ser Asn Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg
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Gly Gly Asn Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn
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Thr Gly Tyr Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr
1280 1285 1290

Gly Ala Arg Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr
1295 1300 1305

Cys Ala Tyr Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg
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Cys Cys Asn Gly Gly Asn Ala Ala Arg
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Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Ala Cys Asn Cys Ala Arg
35 40 45

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Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Thr
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Gly Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Thr
65                  70                  75                  80

Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Ala Cys Asn Gly Gly Asn
                85                  90                  95

Gly Gly Asn Gly Thr Asn Gly Gly Asn Gly Thr Asn Gly Gly Asn Thr
            100                 105                 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Met Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Met Thr Asn Gly Cys Asn Met Thr Asn Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Thr Gly Gly Ala Ala Tyr Gly Ala Tyr Gly Ala Tyr Ala Ala
                165                 170                 175

Arg Met Gly Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn
            180                 185                 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Met Thr Asn Ala
        195                 200                 205

Cys Asn Ala Thr His Ala Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn
225                 230                 235                 240

Gly Thr Asn Met Thr Asn Ala Cys Asn Ala Thr Gly Ala Cys Asn Ala
                245                 250                 255

Ala Tyr Ala Thr Gly Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
            260                 265                 270

Tyr Ala Cys Asn Gly Cys Asn Ala Cys Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Cys Ala Tyr Met Gly Asn Met Gly Asn Gly
    290                 295                 300

Ala Arg Met Thr Asn Cys Cys Asn Thr Thr Tyr Gly Ala Tyr Thr Ala
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Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn
                325                 330                 335
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Met Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp
340 345 350

Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly
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Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn
370 375 380

Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met
385 390 395 400

Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser
405 410 415

Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn
420 425 430

Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr
435 440 445

Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr
450 455 460

Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr
465 470 475 480

Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp
485 490 495

Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr
500 505 510

Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg
515 520 525

Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp
530 535 540

Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr
545 550 555 560

Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn
565 570 575

Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala
580 585 590

Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr
595 600 605

Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn
610 615 620

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Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala
625                 630                 635                 640

Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala
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Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr
            660                 665                 670

Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys
        675                 680                 685

Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys
    690                 695                 700

Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr
705                 710                 715                 720

Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly
                725                 730                 735

Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser
            740                 745                 750

Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn
        755                 760                 765

Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly
    770                 775                 780

Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala
785                 790                 795                 800

Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr
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Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly
            820                 825                 830

Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala
        835                 840                 845

Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn
    850                 855                 860

Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala
865                 870                 875                 880

Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr
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Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn
            900                 905                 910
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2264

Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr
915 920 925

Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala
930 935 940

Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn
945 950 955 960

Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys
965 970 975

Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala
980 985 990

Arg Ala Cys Asn Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn
995 1000 1005

Ala Ala Arg Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn
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Gly Ala Arg Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr
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Ala Cys Asn Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn
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Met Gly Asn Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn
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Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn
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Ala Ala Arg Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn
1100 1105 1110

Trp Ser Asn Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn
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Gly Ala Arg Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr
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Gly Gly Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr
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Ala Ala Tyr Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn
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Cys Cys Asn Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr
1175 1180 1185

Trp Ser Asn Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr
1190 1195 1200

Thr Thr Tyr Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg
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Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg
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Trp Ser Asn Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg
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Thr Gly Tyr Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr
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Gly Ala Arg Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr
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Cys Ala Tyr Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg
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35 40 45

Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Thr
50 55 60

Gly Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

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Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Ala Cys Asn Gly Gly Asn
                85                  90                  95

Gly Gly Asn Gly Thr Asn Gly Gly Asn Gly Thr Asn Gly Gly Asn Thr
            100                 105                 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Met Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Met Thr Asn Gly Cys Asn Met Thr Asn Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Thr Gly Gly Ala Ala Tyr Gly Ala Tyr Gly Ala Tyr Ala Ala
                165                 170                 175

Arg Met Gly Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn
            180                 185                 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Met Thr Asn Ala
        195                 200                 205

Cys Asn Ala Thr His Ala Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Cys Asn Cys Ala Arg Gly Thr Asn
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Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr
705 710 715 720

Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly
725 730 735

Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser
740 745 750

Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn
755 760 765

Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly
770 775 780

Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala
785 790 795 800

Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr
805 810 815

Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly
820 825 830

Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala
835 840 845

Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn
850 855 860

Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala
865 870 875 880

Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr
885 890 895

Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn
900 905 910

Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr
915 920 925

Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala
930 935 940

Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn
945 950 955 960

Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys
965 970 975

Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala
980 985 990

Arg Ala Cys Asn Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn
995 1000 1005

Ala Ala Arg Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn
1010 1015 1020

Gly Ala Arg Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr
1025 1030 1035

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Ala Cys Asn Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn
    1040                1045                1050

Met Gly Asn Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn
    1055                1060                1065

Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn
    1070                1075                1080

Met Thr Asn Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn
    1085                1090                1095

Ala Ala Arg Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn
    1100                1105                1110

Trp Ser Asn Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn
    1115                1120                1125

Gly Ala Arg Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr
    1130                1135                1140

Gly Gly Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr
    1145                1150                1155

Ala Ala Tyr Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn
    1160                1165                1170

Cys Cys Asn Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr
    1175                1180                1185

Trp Ser Asn Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr
    1190                1195                1200

Thr Thr Tyr Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg
    1205                1210                1215

Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg
    1220                1225                1230

Trp Ser Asn Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg
    1235                1240                1245

Gly Gly Asn Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn
    1250                1255                1260

Thr Gly Tyr Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr
    1265                1270                1275

Gly Ala Arg Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr
    1280                1285                1290

Cys Ala Tyr Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg
    1295                1300                1305
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Trp Ser  Asn Met Thr Asn Trp  Ser Asn Met Thr Asn  Trp Ser Asn
    1310                 1315                 1320

Cys Cys  Asn Gly Gly Asn Ala  Ala Arg
    1325                 1330
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<210> 576
<211> 1332
<212> PRT
<213> Homo Sapiens

<400> 576

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Cys Ala Arg Ala Thr His Ala Cys Asn Met Thr Asn Ala Ala Arg Gly
1               5                  10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Ala Cys Asn Met Thr
            20                  25                  30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Ala Cys Asn Cys Ala Arg
        35                  40                  45

Ala Cys Asn Met Thr Asn Ala Cys Asn Met Thr Asn Ala Cys Asn Thr
    50                  55                  60

Gly Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Thr
65                  70                  75                  80

Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Ala Cys Asn Gly Gly Asn
                85                  90                  95

Gly Gly Asn Gly Thr Asn Gly Gly Asn Gly Thr Asn Gly Gly Asn Thr
            100                 105                 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Met Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Met Thr Asn Gly Cys Asn Met Thr Asn Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Thr Gly Gly Ala Ala Tyr Gly Ala Tyr Gly Ala Tyr Ala Ala
                165                 170                 175

Arg Met Gly Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn
            180                 185                 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Met Thr Asn Ala
        195                 200                 205
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Cys Asn Ala Thr His Ala Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn
225                 230                 235                 240

Gly Thr Asn Met Thr Asn Ala Cys Asn Ala Thr Gly Ala Cys Asn Ala
                245                 250                 255

Ala Tyr Ala Thr Gly Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
            260                 265                 270

Tyr Ala Cys Asn Gly Cys Asn Ala Cys Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Cys Ala Tyr Met Gly Asn Gly Gly Asn Gly
    290                 295                 300

Ala Arg Met Thr Asn Cys Cys Asn Thr Thr Tyr Gly Ala Tyr Thr Ala
305                 310                 315                 320

Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn
                325                 330                 335

Met Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp
            340                 345                 350

Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly
        355                 360                 365

Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn
    370                 375                 380

Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met
385                 390                 395                 400

Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser
                405                 410                 415

Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn
            420                 425                 430

Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr
        435                 440                 445

Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr
    450                 455                 460

Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr
465                 470                 475                 480
```

```
Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp
                485                 490                 495

Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr
            500                 505                 510

Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg
        515                 520                 525

Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp
    530                 535                 540

Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr
545                 550                 555                 560

Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn
                565                 570                 575

Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala
            580                 585                 590

Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr
        595                 600                 605

Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn
    610                 615                 620

Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala
625                 630                 635                 640

Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala
                645                 650                 655

Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr
            660                 665                 670

Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys
        675                 680                 685

Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys
    690                 695                 700

Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr
705                 710                 715                 720

Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly
                725                 730                 735

Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser
            740                 745                 750

Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn
        755                 760                 765
```

Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly
770 775 780

Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala
785 790 795 800

Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr
805 810 815

Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly
820 825 830

Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala
835 840 845

Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn
850 855 860

Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala
865 870 875 880

Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr
885 890 895

Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn
900 905 910

Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr
915 920 925

Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala
930 935 940

Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn
945 950 955 960

Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys
965 970 975

Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala
980 985 990

Arg Ala Cys Asn Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn
995 1000 1005

Ala Ala Arg Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn
1010 1015 1020

Gly Ala Arg Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr
1025 1030 1035

Ala Cys Asn Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn
1040 1045 1050

Met Gly Asn Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn
1055 1060 1065

Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn
1070 1075 1080

Met Thr Asn Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn
1085 1090 1095

Ala Ala Arg Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn
1100 1105 1110

Trp Ser Asn Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn
1115 1120 1125

Gly Ala Arg Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr
1130 1135 1140

Gly Gly Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr
1145 1150 1155

Ala Ala Tyr Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn
1160 1165 1170

Cys Cys Asn Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr
1175 1180 1185

Trp Ser Asn Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr
1190 1195 1200

Thr Thr Tyr Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg
1205 1210 1215

Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg
1220 1225 1230

Trp Ser Asn Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg
1235 1240 1245

Gly Gly Asn Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn
1250 1255 1260

Thr Gly Tyr Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr
1265 1270 1275

Gly Ala Arg Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr
1280 1285 1290

Cys Ala Tyr Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg
1295 1300 1305

Trp Ser Asn Met Thr Asn Trp Ser Asn Met Thr Asn Trp Ser Asn
1310 1315 1320

Cys Cys Asn Gly Gly Asn Ala Ala Arg
1325 1330

<210> 577
<211> 1341
<212> PRT
<213> Homo Sapiens

<400> 577

Gly Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Met Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
35 40 45

Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Cys Cys Asn Thr Thr Tyr Trp Ser Asn Met Gly Asn Thr Ala Tyr
85 90 95

Trp Ser Asn Ala Thr Gly Ala Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Trp Ser Asn Gly Cys Asn Ala Thr His Trp Ser Asn Trp Ser Asn Trp
145 150 155 160

Ser Asn Trp Ser Asn Trp Ser Asn Thr Ala Tyr Ala Thr His Thr Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Ala Cys Asn Ala
195 200 205

```
Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Gly Cys
    210                 215                 220

Asn Ala Ala Arg Ala Ala Tyr Trp Ser Asn Met Thr Asn Thr Ala Tyr
225                 230                 235                 240

Met Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Met
                245                 250                 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Ala Cys
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Met Gly Asn Gly Ala Tyr Met Gly Asn Gly Thr Asn Gly
    290                 295                 300

Gly Asn Gly Cys Asn Ala Cys Asn Cys Cys Asn Gly Ala Tyr Gly Cys
305                 310                 315                 320

Asn Thr Thr Tyr Gly Ala Tyr Ala Thr His Thr Gly Gly Gly Gly Asn
                325                 330                 335

Cys Ala Arg Gly Gly Asn Ala Cys Asn Ala Thr Gly Gly Thr Asn Ala
            340                 345                 350

Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser
        355                 360                 365

Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn
    370                 375                 380

Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys
385                 390                 395                 400

Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys
                405                 410                 415

Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn
            420                 425                 430

Gly Cys Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly
        435                 440                 445

Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys
    450                 455                 460

Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn
465                 470                 475                 480

Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly
                485                 490                 495
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Cys Asn Met Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr
500 505 510

Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn
515 520 525

Gly Thr Asn Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly
530 535 540

Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser
545 550 555 560

Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn
565 570 575

Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly
580 585 590

Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys
595 600 605

Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr
610 615 620

Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala
625 630 635 640

Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr
645 650 655

Asn Gly Ala Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr
660 665 670

Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr
675 680 685

Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr
690 695 700

Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn
705 710 715 720

Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala
725 730 735

Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr
740 745 750

Asn Ala Thr Gly Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn
755 760 765

Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly
770 775 780

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Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser
785                 790                 795                 800

Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg
                805                 810                 815

Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr
            820                 825                 830

Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala
        835                 840                 845

Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg
    850                 855                 860

Ala Cys Asn Ala Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly
865                 870                 875                 880

Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys
                885                 890                 895

Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn
            900                 905                 910

Gly Thr Asn Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys
        915                 920                 925

Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala
    930                 935                 940

Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg
945                 950                 955                 960

Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala
                965                 970                 975

Ala Arg Gly Gly Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys
            980                 985                 990

Asn Ala Thr His Gly Ala Arg Ala  Ala Arg Ala Cys Asn  Ala Thr His
        995                 1000                1005

Trp Ser  Asn Ala Ala Arg Ala  Cys Asn Ala Ala Arg  Gly Gly Asn
    1010                1015                1020

Cys Ala  Arg Cys Cys Asn Met  Gly Asn Gly Ala Arg  Cys Cys Asn
    1025                1030                1035

Cys Ala  Arg Gly Thr Asn Thr  Ala Tyr Ala Cys Asn  Met Thr Asn
    1040                1045                1050

Cys Cys  Asn Cys Cys Asn Trp  Ser Asn Met Gly Asn  Gly Ala Arg
    1055                1060                1065
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Gly Ala Arg Ala Thr Gly Ala Cys Asn Ala Ala Arg Ala Ala Tyr
1070 1075 1080

Cys Ala Arg Gly Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn
1085 1090 1095

Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Gly Asn
1100 1105 1110

Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Trp Ser Asn Gly Ala Tyr
1115 1120 1125

Ala Thr His Gly Cys Asn Gly Thr Asn Gly Ala Arg Thr Gly Gly
1130 1135 1140

Gly Ala Arg Trp Ser Asn Ala Ala Tyr Gly Gly Asn Cys Ala Arg
1145 1150 1155

Cys Cys Asn Gly Ala Arg Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr
1160 1165 1170

Ala Ala Arg Ala Cys Asn Ala Cys Asn Cys Cys Asn Cys Cys Asn
1175 1180 1185

Ala Thr Gly Met Thr Asn Gly Ala Tyr Trp Ser Asn Gly Ala Tyr
1190 1195 1200

Gly Gly Asn Trp Ser Asn Thr Thr Tyr Thr Thr Tyr Met Thr Asn
1205 1210 1215

Thr Ala Tyr Trp Ser Asn Ala Ala Arg Met Thr Asn Ala Cys Asn
1220 1225 1230

Gly Thr Asn Gly Ala Tyr Ala Ala Arg Trp Ser Asn Met Gly Asn
1235 1240 1245

Thr Gly Gly Cys Ala Arg Cys Ala Arg Gly Gly Asn Ala Ala Tyr
1250 1255 1260

Gly Thr Asn Thr Thr Tyr Trp Ser Asn Thr Gly Tyr Trp Ser Asn
1265 1270 1275

Gly Thr Asn Ala Thr Gly Cys Ala Tyr Gly Ala Arg Gly Cys Asn
1280 1285 1290

Met Thr Asn Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr Thr Ala Tyr
1295 1300 1305

Ala Cys Asn Cys Ala Arg Ala Ala Arg Trp Ser Asn Met Thr Asn
1310 1315 1320

Trp Ser Asn Met Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn
1325 1330 1335

Ala Ala Arg
1340

<210> 578
<211> 1362
<212> PRT
<213> Homo Sapiens

<400> 578

Gly Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Met Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Met Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
35 40 45

Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Cys Asn Ala Thr Gly Ala Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Trp Ser Asn Gly Cys Asn Ala Thr His Trp Ser Asn Gly Gly Asn Trp
145 150 155 160

Ser Asn Gly Gly Asn Gly Gly Asn Trp Ser Asn Ala Cys Asn Thr Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Ala Cys Asn Ala
195 200 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
210 215 220

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Asn Ala Ala Arg Ala Ala Tyr Ala Cys Asn Met Thr Asn Thr Ala Tyr
225                 230                 235                 240

Met Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Met
                245                 250                 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Ala Cys
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Ala Ala Arg Gly Ala Arg Gly Gly Asn Ala Thr His Gly
    290                 295                 300

Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Ala Cys Asn Gly Cys
305                 310                 315                 320

Asn Gly Ala Arg Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr
                325                 330                 335

Thr Ala Tyr Gly Cys Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr
            340                 345                 350

Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Ala Cys
        355                 360                 365

Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
    370                 375                 380

Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys
385                 390                 395                 400

Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr
                405                 410                 415

Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn
            420                 425                 430

Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala
        435                 440                 445

Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr Gly
    450                 455                 460

Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr
465                 470                 475                 480

Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala
                485                 490                 495

Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser
            500                 505                 510
```

Asn Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser Asn
515 520 525

Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys
530 535 540

Cys Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp Ser
545 550 555 560

Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn
565 570 575

Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala
580 585 590

Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala
595 600 605

Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn
610 615 620

Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly
625 630 635 640

Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala
645 650 655

Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg
660 665 670

Ala Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg Thr
675 680 685

Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys
690 695 700

Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn
705 710 715 720

Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp
725 730 735

Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys
740 745 750

Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr
755 760 765

Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn Met
770 775 780

Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys
785 790 795 800

```
Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr
                805                 810                 815

Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys
            820                 825                 830

Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala
        835                 840                 845

Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn
    850                 855                 860

Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly
865                 870                 875                 880

Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met Gly
                885                 890                 895

Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr
            900                 905                 910

Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly
        915                 920                 925

Thr Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly Thr
    930                 935                 940

Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly Gly
945                 950                 955                 960

Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg Thr
                965                 970                 975

Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser
            980                 985                 990

Asn Ala Ala Tyr Ala Ala Arg Gly  Gly Asn Met Thr Asn  Cys Cys Asn
        995                 1000                1005

Gly Cys  Asn Cys Cys Asn Ala  Thr His Gly Ala Arg  Ala Ala Arg
    1010                1015                1020

Ala Cys  Asn Ala Thr His Trp  Ser Asn Ala Ala Arg  Ala Cys Asn
    1025                1030                1035

Ala Ala  Arg Gly Gly Asn Cys  Ala Arg Cys Cys Asn  Met Gly Asn
    1040                1045                1050

Gly Ala  Arg Cys Cys Asn Cys  Ala Arg Gly Thr Asn  Thr Ala Tyr
    1055                1060                1065

Ala Cys  Asn Met Thr Asn Cys  Cys Asn Cys Cys Asn  Trp Ser Asn
    1070                1075                1080
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Met Gly Asn Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn
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Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn
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Met Thr Asn Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn
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Ala Ala Arg Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn
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Trp Ser Asn Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn
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Gly Ala Arg Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr
1160 1165 1170

Gly Gly Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr
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Ala Ala Tyr Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn
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Cys Cys Asn Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr
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Trp Ser Asn Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr
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Thr Thr Tyr Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg
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Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg
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Trp Ser Asn Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg
1265 1270 1275

Gly Gly Asn Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn
1280 1285 1290

Thr Gly Tyr Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr
1295 1300 1305

Gly Ala Arg Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr
1310 1315 1320

Cys Ala Tyr Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg
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Trp Ser Asn Met Thr Asn Trp Ser Asn Met Thr Asn Trp Ser Asn
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Cys Cys Asn Gly Gly Asn Ala Ala Arg
1355 1360

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35 40 45

Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Cys Asn Ala Thr Gly Trp Ser Asn Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Trp Ser Asn Gly Cys Asn Ala Thr His Trp Ser Asn Gly Gly Asn Trp
145 150 155 160

Ser Asn Gly Gly Asn Gly Gly Asn Trp Ser Asn Ala Cys Asn Thr Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Ala Cys Asn Ala
195 200 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
210 215 220

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Asn Ala Ala Arg Ala Ala Tyr Ala Cys Asn Met Thr Asn Thr Ala Tyr
225                 230                 235                 240

Met Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Met
                245                 250                 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Ala Cys
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Ala Ala Arg Gly Ala Arg Gly Gly Asn Ala Thr His Gly
    290                 295                 300

Cys Asn Gly Cys Asn Met Gly Asn Gly Ala Tyr Trp Ser Asn Thr Ala
305                 310                 315                 320

Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Cys Asn Ala Thr Gly
                325                 330                 335

Gly Ala Tyr Gly Thr Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly
            340                 345                 350

Gly Asn Ala Cys Asn Ala Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr
        355                 360                 365

Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn
    370                 375                 380

Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr
385                 390                 395                 400

Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly
                405                 410                 415

Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn
            420                 425                 430

Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met
        435                 440                 445

Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala
    450                 455                 460

Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg
465                 470                 475                 480

Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr
                485                 490                 495

Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr
            500                 505                 510
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Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr
515 520 525

Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met
530 535 540

Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr
545 550 555 560

Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
565 570 575

Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp
580 585 590

Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys
595 600 605

Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr
610 615 620

Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys
625 630 635 640

Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr
645 650 655

Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg
660 665 670

Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly
675 680 685

Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys
690 695 700

Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn
705 710 715 720

Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met
725 730 735

Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys
740 745 750

Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly
755 760 765

Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly
770 775 780

Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr
785 790 795 800

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Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr
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Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys
            820                 825                 830

Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr
        835                 840                 845

Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn
    850                 855                 860

Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala
865                 870                 875                 880

Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala
                885                 890                 895

Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr
            900                 905                 910

Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met
        915                 920                 925

Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala
    930                 935                 940

Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn
945                 950                 955                 960

Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala
                965                 970                 975

Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly
            980                 985                 990

Asn Met Thr Asn Cys Cys Asn Gly  Cys Asn Cys Cys Asn  Ala Thr His
        995                 1000                1005

Gly Ala  Arg Ala Ala Arg Ala  Cys Asn Ala Thr His  Trp Ser Asn
    1010                1015                1020

Ala Ala  Arg Ala Cys Asn Ala  Ala Arg Gly Gly Asn  Cys Ala Arg
    1025                1030                1035

Cys Cys  Asn Met Gly Asn Gly  Ala Arg Cys Cys Asn  Cys Ala Arg
    1040                1045                1050

Gly Thr  Asn Thr Ala Tyr Ala  Cys Asn Met Thr Asn  Cys Cys Asn
    1055                1060                1065

Cys Cys  Asn Trp Ser Asn Met  Gly Asn Gly Ala Arg  Gly Ala Arg
    1070                1075                1080
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Ala Thr Gly Ala Cys Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg
1085 1090 1095

Gly Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr Gly Tyr
1100 1105 1110

Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Gly Asn Thr Thr Tyr
1115 1120 1125

Thr Ala Tyr Cys Cys Asn Trp Ser Asn Gly Ala Tyr Ala Thr His
1130 1135 1140

Gly Cys Asn Gly Thr Asn Gly Ala Arg Thr Gly Gly Gly Ala Arg
1145 1150 1155

Trp Ser Asn Ala Ala Tyr Gly Gly Asn Cys Ala Arg Cys Cys Asn
1160 1165 1170

Gly Ala Arg Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr Ala Ala Arg
1175 1180 1185

Ala Cys Asn Ala Cys Asn Cys Cys Asn Cys Cys Asn Ala Thr Gly
1190 1195 1200

Met Thr Asn Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Gly Asn
1205 1210 1215

Trp Ser Asn Thr Thr Tyr Thr Thr Tyr Met Thr Asn Thr Ala Tyr
1220 1225 1230

Trp Ser Asn Ala Ala Arg Met Thr Asn Ala Cys Asn Gly Thr Asn
1235 1240 1245

Gly Ala Tyr Ala Ala Arg Trp Ser Asn Met Gly Asn Thr Gly Gly
1250 1255 1260

Cys Ala Arg Cys Ala Arg Gly Gly Asn Ala Ala Tyr Gly Thr Asn
1265 1270 1275

Thr Thr Tyr Trp Ser Asn Thr Gly Tyr Trp Ser Asn Gly Thr Asn
1280 1285 1290

Ala Thr Gly Cys Ala Tyr Gly Ala Arg Gly Cys Asn Met Thr Asn
1295 1300 1305

Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr Thr Ala Tyr Ala Cys Asn
1310 1315 1320

Cys Ala Arg Ala Ala Arg Trp Ser Asn Met Thr Asn Trp Ser Asn
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2304

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1340 1345 1350

<210> 580
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20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
35 40 45

Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Cys Asn Ala Thr Gly Trp Ser Asn Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Trp Ser Asn Gly Cys Asn Ala Thr His Trp Ser Asn Gly Gly Asn Trp
145 150 155 160

Ser Asn Gly Gly Asn Gly Gly Asn Trp Ser Asn Ala Cys Asn Thr Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Ala Cys Asn Ala
195 200 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
210 215 220

Asn Ala Ala Arg Ala Ala Tyr Ala Cys Asn Met Thr Asn Thr Ala Tyr
225 230 235 240

Met Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Met
245 250 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Ala Cys
260 265 270

Asn Gly Cys Asn Gly Ala Arg Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Ala Ala Arg Gly Ala Arg Gly Gly Asn Ala Thr His Gly
290 295 300

Cys Asn Gly Gly Asn Met Gly Asn Gly Ala Tyr Trp Ser Asn Thr Ala
305 310 315 320

Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly
325 330 335

Gly Ala Tyr Gly Thr Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly
340 345 350

Gly Asn Ala Cys Asn Ala Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr
355 360 365

Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn
370 375 380

Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr
385 390 395 400

Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly
405 410 415

Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn
420 425 430

Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met
435 440 445

Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala
450 455 460

Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg
465 470 475 480

Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr
485 490 495

Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr
500 505 510

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Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr
        515                 520                 525

Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met
    530                 535                 540

Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr
545                 550                 555                 560

Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
                565                 570                 575

Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp
            580                 585                 590

Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys
        595                 600                 605

Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr
    610                 615                 620

Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys
625                 630                 635                 640

Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr
                645                 650                 655

Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg
            660                 665                 670

Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly
        675                 680                 685

Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys
    690                 695                 700

Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn
705                 710                 715                 720

Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met
                725                 730                 735

Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys
            740                 745                 750

Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly
        755                 760                 765

Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly
    770                 775                 780

Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr
785                 790                 795                 800
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Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr
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Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys
            820                 825                 830

Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr
        835                 840                 845

Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn
    850                 855                 860

Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala
865                 870                 875                 880

Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala
                885                 890                 895

Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr
            900                 905                 910

Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met
        915                 920                 925

Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala
    930                 935                 940

Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn
945                 950                 955                 960

Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala
                965                 970                 975

Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly
            980                 985                 990

Asn Met Thr Asn Cys Cys Asn Gly  Cys Asn Cys Cys Asn  Ala Thr His
        995                 1000                1005

Gly Ala  Arg Ala Ala Arg Ala  Cys Asn Ala Thr His  Trp Ser Asn
    1010                1015                1020

Ala Ala  Arg Ala Cys Asn Ala  Ala Arg Gly Gly Asn  Cys Ala Arg
    1025                1030                1035

Cys Cys  Asn Met Gly Asn Gly  Ala Arg Cys Cys Asn  Cys Ala Arg
    1040                1045                1050

Gly Thr  Asn Thr Ala Tyr Ala  Cys Asn Met Thr Asn  Cys Cys Asn
    1055                1060                1065

Cys Cys  Asn Trp Ser Asn Met  Gly Asn Gly Ala Arg  Gly Ala Arg
    1070                1075                1080
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Ala Thr Gly Ala Cys Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg
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Gly Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr Gly Tyr
1100 1105 1110

Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Gly Asn Thr Thr Tyr
1115 1120 1125

Thr Ala Tyr Cys Cys Asn Trp Ser Asn Gly Ala Tyr Ala Thr His
1130 1135 1140

Gly Cys Asn Gly Thr Asn Gly Ala Arg Thr Gly Gly Gly Ala Arg
1145 1150 1155

Trp Ser Asn Ala Ala Tyr Gly Gly Asn Cys Ala Arg Cys Cys Asn
1160 1165 1170

Gly Ala Arg Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr Ala Ala Arg
1175 1180 1185

Ala Cys Asn Ala Cys Asn Cys Cys Asn Cys Cys Asn Ala Thr Gly
1190 1195 1200

Met Thr Asn Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Gly Asn
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Trp Ser Asn Thr Thr Tyr Thr Thr Tyr Met Thr Asn Thr Ala Tyr
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Trp Ser Asn Ala Ala Arg Met Thr Asn Ala Cys Asn Gly Thr Asn
1235 1240 1245

Gly Ala Tyr Ala Ala Arg Trp Ser Asn Met Gly Asn Thr Gly Gly
1250 1255 1260

Cys Ala Arg Cys Ala Arg Gly Gly Asn Ala Ala Tyr Gly Thr Asn
1265 1270 1275

Thr Thr Tyr Trp Ser Asn Thr Gly Tyr Trp Ser Asn Gly Thr Asn
1280 1285 1290

Ala Thr Gly Cys Ala Tyr Gly Ala Arg Gly Cys Asn Met Thr Asn
1295 1300 1305

Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr Thr Ala Tyr Ala Cys Asn
1310 1315 1320

Cys Ala Arg Ala Ala Arg Trp Ser Asn Met Thr Asn Trp Ser Asn
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Met Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn Ala Ala Arg
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Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
35 40 45

Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Gly Cys Asn Thr Thr Tyr Ala Thr His Trp Ser Asn Gly Ala Tyr Gly
145 150 155 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Thr Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Ala Cys Asn Ala
195 200 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
210 215 220

Asn Ala Thr Gly Ala Ala Tyr Ala Cys Asn Met Thr Asn Thr Ala Tyr
225 230 235 240

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Met Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Met
                245                 250                 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Ala Cys
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Met Gly Asn Trp Ser Asn Thr Ala Tyr Thr Ala Tyr Gly
    290                 295                 300

Ala Tyr Trp Ser Asn Trp Ser Asn Gly Gly Asn Thr Ala Tyr Thr Ala
305                 310                 315                 320

Tyr Thr Ala Tyr Gly Gly Asn Thr Thr Tyr Gly Ala Tyr Thr Ala Tyr
                325                 330                 335

Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Met
            340                 345                 350

Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser
        355                 360                 365

Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn
    370                 375                 380

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met
385                 390                 395                 400

Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly
                405                 410                 415

Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn
            420                 425                 430

Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr
        435                 440                 445

Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala
    450                 455                 460

Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn
465                 470                 475                 480

Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp
                485                 490                 495

Ser Asn Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser
            500                 505                 510

Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr
        515                 520                 525
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2311

Cys Cys Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp
530 535 540

Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser
545 550 555 560

Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn
565 570 575

Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala
580 585 590

Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys
595 600 605

Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn
610 615 620

Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala
625 630 635 640

Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala
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Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg
660 665 670

Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys
675 680 685

Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys
690 695 700

Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn
705 710 715 720

Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys
725 730 735

Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala
740 745 750

Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn
755 760 765

Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala
770 775 780

Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala
785 790 795 800

Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr
805 810 815

2312

Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala
820 825 830

Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly
835 840 845

Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr
850 855 860

Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met
865 870 875 880

Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala
885 890 895

Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn
900 905 910

Gly Thr Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly
915 920 925

Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly
930 935 940

Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg
945 950 955 960

Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp
965 970 975

Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys Cys
980 985 990

Asn Gly Cys Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala Arg
995 1000 1005

Ala Cys Asn Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn
1010 1015 1020

Ala Ala Arg Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn
1025 1030 1035

Gly Ala Arg Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr
1040 1045 1050

Ala Cys Asn Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn
1055 1060 1065

Met Gly Asn Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn
1070 1075 1080

Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn
1085 1090 1095

2313

Met Thr Asn Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn
1100 1105 1110

Ala Ala Arg Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn
1115 1120 1125

Trp Ser Asn Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn
1130 1135 1140

Gly Ala Arg Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr
1145 1150 1155

Gly Gly Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr
1160 1165 1170

Ala Ala Tyr Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn
1175 1180 1185

Cys Cys Asn Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr
1190 1195 1200

Trp Ser Asn Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr
1205 1210 1215

Thr Thr Tyr Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg
1220 1225 1230

Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg
1235 1240 1245

Trp Ser Asn Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg
1250 1255 1260

Gly Gly Asn Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn
1265 1270 1275

Thr Gly Tyr Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr
1280 1285 1290

Gly Ala Arg Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr
1295 1300 1305

Cys Ala Tyr Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg
1310 1315 1320

Trp Ser Asn Met Thr Asn Trp Ser Asn Met Thr Asn Trp Ser Asn
1325 1330 1335

Cys Cys Asn Gly Gly Asn Ala Ala Arg
1340 1345

<210> 582
<211> 1320

<212> PRT
<213> Homo Sapiens

<400> 582

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1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
35 40 45

Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly
145 150 155 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Thr Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Ala Cys Asn Ala
195 200 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
210 215 220

Asn Ala Ala Arg Ala Ala Tyr Ala Cys Asn Met Thr Asn Thr Ala Tyr
225 230 235 240

Met Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Met
245 250 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Ala Cys
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Ala Ala Tyr Gly Thr Asn Ala Thr His Gly
290 295 300

Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly
305 310 315 320

Asn Ala Cys Asn Met Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn
325 330 335

Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala
340 345 350

Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr
355 360 365

Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr
370 375 380

Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly
385 390 395 400

Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr
405 410 415

Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg
420 425 430

Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys
435 440 445

Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly
450 455 460

Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr Asn
465 470 475 480

Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala
485 490 495

Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met Thr
500 505 510

Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn
515 520 525

Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly
530 535 540

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Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser
545                 550                 555                 560

Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn
                565                 570                 575

Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala
            580                 585                 590

Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys
        595                 600                 605

Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn
    610                 615                 620

Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg Met
625                 630                 635                 640

Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala
                645                 650                 655

Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn
            660                 665                 670

Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly
        675                 680                 685

Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr
    690                 695                 700

Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn
705                 710                 715                 720

Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala
                725                 730                 735

Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala
            740                 745                 750

Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn
        755                 760                 765

Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly
    770                 775                 780

Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala
785                 790                 795                 800

Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn
                805                 810                 815

Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys
            820                 825                 830
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2317

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Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala
        835                 840                 845

Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg
    850                 855                 860

Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met
865                 870                 875                 880

Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met Thr
                885                 890                 895

Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg
            900                 905                 910

Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala
        915                 920                 925

Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala
    930                 935                 940

Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn
945                 950                 955                 960

Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His Gly
                965                 970                 975

Ala Arg Ala Ala Arg Ala Cys Asn Ala Thr His Trp Ser Asn Ala Ala
            980                 985                 990

Arg Ala Cys Asn Ala Ala Arg Gly  Gly Asn Cys Ala Arg  Cys Cys Asn
        995                 1000                1005

Met Gly  Asn Gly Ala Arg Cys  Cys Asn Cys Ala Arg  Gly Thr Asn
    1010                1015                1020

Thr Ala  Tyr Ala Cys Asn Met  Thr Asn Cys Cys Asn  Cys Cys Asn
    1025                1030                1035

Trp Ser  Asn Met Gly Asn Gly  Ala Arg Gly Ala Arg  Ala Thr Gly
    1040                1045                1050

Ala Cys  Asn Ala Ala Arg Ala  Ala Tyr Cys Ala Arg  Gly Thr Asn
    1055                1060                1065

Trp Ser  Asn Met Thr Asn Ala  Cys Asn Thr Gly Tyr  Met Thr Asn
    1070                1075                1080

Gly Thr  Asn Ala Ala Arg Gly  Gly Asn Thr Thr Tyr  Thr Ala Tyr
    1085                1090                1095

Cys Cys  Asn Trp Ser Asn Gly  Ala Tyr Ala Thr His  Gly Cys Asn
    1100                1105                1110
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Gly Thr  Asn Gly Ala Arg Thr  Gly Gly Gly Ala Arg  Trp Ser Asn
    1115                 1120                 1125

Ala Ala  Tyr Gly Gly Asn Cys  Ala Arg Cys Cys Asn  Gly Ala Arg
    1130                 1135                 1140

Ala Ala  Tyr Ala Ala Tyr Thr  Ala Tyr Ala Ala Arg  Ala Cys Asn
    1145                 1150                 1155

Ala Cys  Asn Cys Cys Asn Cys  Cys Asn Ala Thr Gly  Met Thr Asn
    1160                 1165                 1170

Gly Ala  Tyr Trp Ser Asn Gly  Ala Tyr Gly Gly Asn  Trp Ser Asn
    1175                 1180                 1185

Thr Thr  Tyr Thr Thr Tyr Met  Thr Asn Thr Ala Tyr  Trp Ser Asn
    1190                 1195                 1200

Ala Ala  Arg Met Thr Asn Ala  Cys Asn Gly Thr Asn  Gly Ala Tyr
    1205                 1210                 1215

Ala Ala  Arg Trp Ser Asn Met  Gly Asn Thr Gly Gly  Cys Ala Arg
    1220                 1225                 1230

Cys Ala  Arg Gly Gly Asn Ala  Ala Tyr Gly Thr Asn  Thr Thr Tyr
    1235                 1240                 1245

Trp Ser  Asn Thr Gly Tyr Trp  Ser Asn Gly Thr Asn  Ala Thr Gly
    1250                 1255                 1260

Cys Ala  Tyr Gly Ala Arg Gly  Cys Asn Met Thr Asn  Cys Ala Tyr
    1265                 1270                 1275

Ala Ala  Tyr Cys Ala Tyr Thr  Ala Tyr Ala Cys Asn  Cys Ala Arg
    1280                 1285                 1290

Ala Ala  Arg Trp Ser Asn Met  Thr Asn Trp Ser Asn  Met Thr Asn
    1295                 1300                 1305

Trp Ser  Asn Cys Cys Asn Gly  Gly Asn Ala Ala Arg
    1310                 1315                 1320

<210>  583
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<212>  PRT
<213>  Homo Sapiens

<400>  583

Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Gly Thr Asn Gly
1               5                  10                  15
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2319

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
35 40 45

Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Ala Tyr Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly
145 150 155 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Thr His Ala Ala Arg Thr Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Ala Cys Asn Ala
195 200 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
210 215 220

Asn Ala Ala Arg Ala Ala Tyr Ala Cys Asn Met Thr Asn Thr Ala Tyr
225 230 235 240

Met Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Met
245 250 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Ala Cys
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Gly Gly Asn Gly Gly Asn Gly Cys Asn Ala
290 295 300

Cys Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Thr Ala Tyr Thr Thr
305 310 315 320

Tyr Cys Ala Arg Cys Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg
325 330 335

Gly Gly Asn Ala Cys Asn Met Thr Asn Gly Thr Asn Ala Cys Asn Gly
340 345 350

Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys
355 360 365

Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn
370 375 380

Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr
385 390 395 400

Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser
405 410 415

Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn
420 425 430

Met Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala
435 440 445

Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala
450 455 460

Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn
465 470 475 480

Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met
485 490 495

Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala
500 505 510

Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn
515 520 525

Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met
530 535 540

Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser
545 550 555 560

Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn
565 570 575

Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala
580 585 590

2321

Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly
595 600 605

Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg
610 615 620

Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly
625 630 635 640

Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala
645 650 655

Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn
660 665 670

Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys
675 680 685

Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys
690 695 700

Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr
705 710 715 720

Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys
725 730 735

Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr
740 745 750

Gly Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn
755 760 765

Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly
770 775 780

Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala
785 790 795 800

Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn
805 810 815

Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly
820 825 830

Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr
835 840 845

Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn
850 855 860

Ala Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys
865 870 875 880

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Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr
               885                 890                 895

Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn
            900                 905                 910

Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys
        915                 920                 925

Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly
    930                 935                 940

Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr
945                 950                 955                 960

Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly
               965                 970                 975

Gly Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr
            980                 985                 990

His Gly Ala Arg Ala Ala Arg Ala  Cys Asn Ala Thr His  Trp Ser Asn
        995                 1000                1005

Ala Ala  Arg Ala Cys Asn Ala  Ala Arg Gly Gly Asn  Cys Ala Arg
    1010                1015                1020

Cys Cys  Asn Met Gly Asn Gly  Ala Arg Cys Cys Asn  Cys Ala Arg
    1025                1030                1035

Gly Thr  Asn Thr Ala Tyr Ala  Cys Asn Met Thr Asn  Cys Cys Asn
    1040                1045                1050

Cys Cys  Asn Trp Ser Asn Met  Gly Asn Gly Ala Arg  Gly Ala Arg
    1055                1060                1065

Ala Thr  Gly Ala Cys Asn Ala  Ala Arg Ala Ala Tyr  Cys Ala Arg
    1070                1075                1080

Gly Thr  Asn Trp Ser Asn Met  Thr Asn Ala Cys Asn  Thr Gly Tyr
    1085                1090                1095

Met Thr  Asn Gly Thr Asn Ala  Ala Arg Gly Gly Asn  Thr Thr Tyr
    1100                1105                1110

Thr Ala  Tyr Cys Cys Asn Trp  Ser Asn Gly Ala Tyr  Ala Thr His
    1115                1120                1125

Gly Cys  Asn Gly Thr Asn Gly  Ala Arg Thr Gly Gly  Gly Ala Arg
    1130                1135                1140

Trp Ser  Asn Ala Ala Tyr Gly  Gly Asn Cys Ala Arg  Cys Cys Asn
    1145                1150                1155
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Gly Ala Arg Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr Ala Ala Arg
1160 1165 1170

Ala Cys Asn Ala Cys Asn Cys Cys Asn Cys Cys Asn Ala Thr Gly
1175 1180 1185

Met Thr Asn Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Gly Asn
1190 1195 1200

Trp Ser Asn Thr Thr Tyr Thr Thr Tyr Met Thr Asn Thr Ala Tyr
1205 1210 1215

Trp Ser Asn Ala Ala Arg Met Thr Asn Ala Cys Asn Gly Thr Asn
1220 1225 1230

Gly Ala Tyr Ala Ala Arg Trp Ser Asn Met Gly Asn Thr Gly Gly
1235 1240 1245

Cys Ala Arg Cys Ala Arg Gly Gly Asn Ala Ala Tyr Gly Thr Asn
1250 1255 1260

Thr Thr Tyr Trp Ser Asn Thr Gly Tyr Trp Ser Asn Gly Thr Asn
1265 1270 1275

Ala Thr Gly Cys Ala Tyr Gly Ala Arg Gly Cys Asn Met Thr Asn
1280 1285 1290

Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr Thr Ala Tyr Ala Cys Asn
1295 1300 1305

Cys Ala Arg Ala Ala Arg Trp Ser Asn Met Thr Asn Trp Ser Asn
1310 1315 1320

Met Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn Ala Ala Arg
1325 1330 1335

<210> 584
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<400> 584

Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
35 40 45

1324

Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly
145 150 155 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Thr Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Ala Cys Asn Ala
195 200 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
210 215 220

Asn Ala Ala Arg Ala Ala Tyr Ala Cys Asn Met Thr Asn Thr Ala Tyr
225 230 235 240

Met Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Met
245 250 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Ala Cys
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Thr Asn Met Thr Asn Met Thr Asn Thr Gly Gly Thr Thr Tyr Gly
290 295 300

Gly Asn Gly Ala Arg Ala Cys Asn Thr Thr Tyr Gly Ala Tyr Thr Ala
305 310 315 320

Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Trp Ser Asn
325 330 335

Met Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Cys
340 345 350

Cys Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly
355 360 365

Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn
370 375 380

Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met
385 390 395 400

Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser
405 410 415

Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn
420 425 430

Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr
435 440 445

Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr
450 455 460

Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr
465 470 475 480

Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp
485 490 495

Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr
500 505 510

Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg
515 520 525

Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp
530 535 540

Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr
545 550 555 560

Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn
565 570 575

Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala
580 585 590

Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr
595 600 605

Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn
610 615 620

Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala
625 630 635 640

Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala
645 650 655

Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr
660 665 670

Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys
675 680 685

Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys
690 695 700

Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr
705 710 715 720

Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly
725 730 735

Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser
740 745 750

Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn
755 760 765

Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly
770 775 780

Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala
785 790 795 800

Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr
805 810 815

Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly
820 825 830

Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala
835 840 845

Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn
850 855 860

Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala
865 870 875 880

Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr
885 890 895

Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn
900 905 910

2324

Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr
915 920 925

Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala
930 935 940

Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn
945 950 955 960

Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys
965 970 975

Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala
980 985 990

Arg Ala Cys Asn Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn
995 1000 1005

Ala Ala Arg Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn
1010 1015 1020

Gly Ala Arg Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr
1025 1030 1035

Ala Cys Asn Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn
1040 1045 1050

Met Gly Asn Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn
1055 1060 1065

Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn
1070 1075 1080

Met Thr Asn Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn
1085 1090 1095

Ala Ala Arg Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn
1100 1105 1110

Trp Ser Asn Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn
1115 1120 1125

Gly Ala Arg Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr
1130 1135 1140

Gly Gly Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr
1145 1150 1155

Ala Ala Tyr Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn
1160 1165 1170

Cys Cys Asn Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr
1175 1180 1185

Trp Ser Asn Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr
1190 1195 1200

Thr Thr Tyr Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg
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Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg
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Trp Ser Asn Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg
1235 1240 1245

Gly Gly Asn Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn
1250 1255 1260

Thr Gly Tyr Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr
1265 1270 1275

Gly Ala Arg Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr
1280 1285 1290

Cys Ala Tyr Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg
1295 1300 1305

Trp Ser Asn Met Thr Asn Trp Ser Asn Met Thr Asn Trp Ser Asn
1310 1315 1320

Cys Cys Asn Gly Gly Asn Ala Ala Arg
1325 1330

<210> 585
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<400> 585

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Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
35 40 45

Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

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Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
                85                  90                  95

Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
            100                 105                 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
        115                 120                 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
    130                 135                 140

Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Trp Ser Asn Gly
145                 150                 155                 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Thr Ala
                165                 170                 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
            180                 185                 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Ala Cys Asn Ala
        195                 200                 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
    210                 215                 220

Asn Ala Ala Arg Ala Ala Tyr Ala Cys Asn Met Thr Asn Thr Ala Tyr
225                 230                 235                 240

Met Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Met
                245                 250                 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Ala Cys
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Met Gly Asn Ala Ala Tyr Met Thr Asn Cys Cys Asn Thr
    290                 295                 300

Thr Tyr Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala
305                 310                 315                 320

Arg Gly Gly Asn Ala Cys Asn Met Thr Asn Gly Thr Asn Ala Cys Asn
                325                 330                 335

Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala
            340                 345                 350

Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr
        355                 360                 365
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Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn
    370                 375                 380

Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp
385                 390                 395                 400

Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys
                405                 410                 415

Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn
            420                 425                 430

Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly
        435                 440                 445

Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser
    450                 455                 460

Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn
465                 470                 475                 480

Met Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys
                485                 490                 495

Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr
            500                 505                 510

Asn Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn
        515                 520                 525

Met Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp
    530                 535                 540

Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys
545                 550                 555                 560

Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn
                565                 570                 575

Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr
            580                 585                 590

Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala
        595                 600                 605

Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg
    610                 615                 620

Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly
625                 630                 635                 640

Ala Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr
                645                 650                 655
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Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr
            660                 665                 670

Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly
        675                 680                 685

Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr
    690                 695                 700

Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg
705                 710                 715                 720

Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala
                725                 730                 735

Thr Gly Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys
            740                 745                 750

Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn
        755                 760                 765

Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys
    770                 775                 780

Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr
785                 790                 795                 800

Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr
                805                 810                 815

Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly
            820                 825                 830

Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys
        835                 840                 845

Asn Ala Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg
    850                 855                 860

Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr
865                 870                 875                 880

Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr
                885                 890                 895

Asn Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr
            900                 905                 910

Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly
        915                 920                 925

Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly
    930                 935                 940
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Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg
945 950 955 960

Gly Gly Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala
965 970 975

Thr His Gly Ala Arg Ala Ala Arg Ala Cys Asn Ala Thr His Trp Ser
980 985 990

Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Ala Arg
995 1000 1005

Cys Cys Asn Met Gly Asn Gly Ala Arg Cys Cys Asn Cys Ala Arg
1010 1015 1020

Gly Thr Asn Thr Ala Tyr Ala Cys Asn Met Thr Asn Cys Cys Asn
1025 1030 1035

Cys Cys Asn Trp Ser Asn Met Gly Asn Gly Ala Arg Gly Ala Arg
1040 1045 1050

Ala Thr Gly Ala Cys Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg
1055 1060 1065

Gly Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr Gly Tyr
1070 1075 1080

Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Gly Asn Thr Thr Tyr
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Thr Ala Tyr Cys Cys Asn Trp Ser Asn Gly Ala Tyr Ala Thr His
1100 1105 1110

Gly Cys Asn Gly Thr Asn Gly Ala Arg Thr Gly Gly Gly Ala Arg
1115 1120 1125

Trp Ser Asn Ala Ala Tyr Gly Gly Asn Cys Ala Arg Cys Cys Asn
1130 1135 1140

Gly Ala Arg Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr Ala Ala Arg
1145 1150 1155

Ala Cys Asn Ala Cys Asn Cys Cys Asn Cys Cys Asn Ala Thr Gly
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Met Thr Asn Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Gly Asn
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Trp Ser Asn Thr Thr Tyr Thr Thr Tyr Met Thr Asn Thr Ala Tyr
1190 1195 1200

Trp Ser Asn Ala Ala Arg Met Thr Asn Ala Cys Asn Gly Thr Asn
1205 1210 1215

2333

Gly Ala Tyr Ala Ala Arg Trp Ser Asn Met Gly Asn Thr Gly Gly
1220 1225 1230

Cys Ala Arg Cys Ala Arg Gly Gly Asn Ala Ala Tyr Gly Thr Asn
1235 1240 1245

Thr Thr Tyr Trp Ser Asn Thr Gly Tyr Trp Ser Asn Gly Thr Asn
1250 1255 1260

Ala Thr Gly Cys Ala Tyr Gly Ala Arg Gly Cys Asn Met Thr Asn
1265 1270 1275

Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr Thr Ala Tyr Ala Cys Asn
1280 1285 1290

Cys Ala Arg Ala Ala Arg Trp Ser Asn Met Thr Asn Trp Ser Asn
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Met Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn Ala Ala Arg
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<210> 586
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20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
35 40 45

Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Gly Ala Tyr Gly
145 150 155 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Ala Tyr Cys Ala Arg Thr Ala
165 170 175

Tyr Thr Ala Tyr Ala Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Ala Cys Asn Gly
195 200 205

Thr Asn Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
210 215 220

Asn Ala Ala Arg Ala Ala Tyr Ala Cys Asn Met Thr Asn Thr Thr Tyr
225 230 235 240

Met Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Met
245 250 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Ala Cys
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Trp Ser Asn Cys Ala Tyr Thr Ala Tyr Gly
290 295 300

Gly Asn Gly Gly Asn Gly Ala Tyr Thr Ala Tyr Gly Ala Tyr Thr Ala
305 310 315 320

Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn
325 330 335

Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Ala
340 345 350

Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser
355 360 365

Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn
370 375 380

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met
385 390 395 400

Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly
405 410 415

Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn
420 425 430

Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr
435 440 445

Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala
450 455 460

Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn
465 470 475 480

Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp
485 490 495

Ser Asn Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser
500 505 510

Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr
515 520 525

Cys Cys Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp
530 535 540

Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser
545 550 555 560

Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn
565 570 575

Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala
580 585 590

Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys
595 600 605

Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn
610 615 620

Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala
625 630 635 640

Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala
645 650 655

Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg
660 665 670

Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys
675 680 685

Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys
690 695 700

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Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn
705                 710                 715                 720

Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys
                725                 730                 735

Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala
            740                 745                 750

Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn
        755                 760                 765

Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala
    770                 775                 780

Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala
785                 790                 795                 800

Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr
                805                 810                 815

Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala
            820                 825                 830

Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly
        835                 840                 845

Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr
    850                 855                 860

Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met
865                 870                 875                 880

Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala
                885                 890                 895

Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn
            900                 905                 910

Gly Thr Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly
        915                 920                 925

Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly
    930                 935                 940

Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg
945                 950                 955                 960

Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp
                965                 970                 975

Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys Cys
            980                 985                 990
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Asn Gly Cys Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala Arg
995 1000 1005

Ala Cys Asn Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn
1010 1015 1020

Ala Ala Arg Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn
1025 1030 1035

Gly Ala Arg Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr
1040 1045 1050

Ala Cys Asn Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn
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Met Gly Asn Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn
1070 1075 1080

Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn
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Met Thr Asn Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn
1100 1105 1110

Ala Ala Arg Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn
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Trp Ser Asn Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn
1130 1135 1140

Gly Ala Arg Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr
1145 1150 1155

Gly Gly Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr
1160 1165 1170

Ala Ala Tyr Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn
1175 1180 1185

Cys Cys Asn Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr
1190 1195 1200

Trp Ser Asn Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr
1205 1210 1215

Thr Thr Tyr Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg
1220 1225 1230

Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg
1235 1240 1245

Trp Ser Asn Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg
1250 1255 1260

Gly Gly Asn Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn
1265 1270 1275

Thr Gly Tyr Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr
1280 1285 1290

Gly Ala Arg Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr
1295 1300 1305

Cys Ala Tyr Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg
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Trp Ser Asn Met Thr Asn Trp Ser Asn Met Thr Asn Trp Ser Asn
1325 1330 1335

Cys Cys Asn Gly Gly Asn Ala Ala Arg
1340 1345

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20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
35 40 45

Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

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Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly
145                 150                 155                 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Met Gly
                165                 170                 175

Asn Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
            180                 185                 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Ala Cys Asn Ala
        195                 200                 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
    210                 215                 220

Asn Ala Ala Arg Ala Ala Tyr Ala Cys Asn Met Thr Asn Thr Ala Tyr
225                 230                 235                 240

Met Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Met
                245                 250                 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Ala Cys
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Met Gly Asn Gly Ala Tyr Gly Gly Asn Thr Gly Gly Cys
    290                 295                 300

Ala Arg Cys Ala Arg Cys Ala Arg Gly Cys Asn Cys Cys Asn Thr Thr
305                 310                 315                 320

Tyr Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg
                325                 330                 335

Gly Gly Asn Ala Cys Asn Met Thr Asn Gly Thr Asn Ala Cys Asn Gly
            340                 345                 350

Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys
        355                 360                 365

Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn
    370                 375                 380

Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr
385                 390                 395                 400

Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser
                405                 410                 415

Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn
            420                 425                 430
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2340

Met Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala
435 440 445

Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala
450 455 460

Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn
465 470 475 480

Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met
485 490 495

Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala
500 505 510

Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn
515 520 525

Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met
530 535 540

Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser
545 550 555 560

Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn
565 570 575

Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala
580 585 590

Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly
595 600 605

Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg
610 615 620

Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly
625 630 635 640

Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala
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Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn
660 665 670

Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys
675 680 685

Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys
690 695 700

Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr
705 710 715 720

Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys
725 730 735

Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr
740 745 750

Gly Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn
755 760 765

Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly
770 775 780

Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala
785 790 795 800

Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn
805 810 815

Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly
820 825 830

Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr
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Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn
850 855 860

Ala Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys
865 870 875 880

Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr
885 890 895

Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn
900 905 910

Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys
915 920 925

Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly
930 935 940

Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr
945 950 955 960

Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly
965 970 975

Gly Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr
980 985 990

His Gly Ala Arg Ala Ala Arg Ala Cys Asn Ala Thr His Trp Ser Asn
995 1000 1005

Ala Ala Arg Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Ala Arg
1010 1015 1020

Cys Cys Asn Met Gly Asn Gly Ala Arg Cys Cys Asn Cys Ala Arg
1025 1030 1035

Gly Thr Asn Thr Ala Tyr Ala Cys Asn Met Thr Asn Cys Cys Asn
1040 1045 1050

Cys Cys Asn Trp Ser Asn Met Gly Asn Gly Ala Arg Gly Ala Arg
1055 1060 1065

Ala Thr Gly Ala Cys Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg
1070 1075 1080

Gly Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr Gly Tyr
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Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Gly Asn Thr Thr Tyr
1100 1105 1110

Thr Ala Tyr Cys Cys Asn Trp Ser Asn Gly Ala Tyr Ala Thr His
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Gly Cys Asn Gly Thr Asn Gly Ala Arg Thr Gly Gly Gly Ala Arg
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Trp Ser Asn Ala Ala Tyr Gly Gly Asn Cys Ala Arg Cys Cys Asn
1145 1150 1155

Gly Ala Arg Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr Ala Ala Arg
1160 1165 1170

Ala Cys Asn Ala Cys Asn Cys Cys Asn Cys Cys Asn Ala Thr Gly
1175 1180 1185

Met Thr Asn Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Gly Asn
1190 1195 1200

Trp Ser Asn Thr Thr Tyr Thr Thr Tyr Met Thr Asn Thr Ala Tyr
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Trp Ser Asn Ala Ala Arg Met Thr Asn Ala Cys Asn Gly Thr Asn
1220 1225 1230

Gly Ala Tyr Ala Ala Arg Trp Ser Asn Met Gly Asn Thr Gly Gly
1235 1240 1245

Cys Ala Arg Cys Ala Arg Gly Gly Asn Ala Ala Tyr Gly Thr Asn
1250 1255 1260

Thr Thr Tyr Trp Ser Asn Thr Gly Tyr Trp Ser Asn Gly Thr Asn
1265 1270 1275

Ala Thr Gly Cys Ala Tyr Gly Ala Arg Gly Cys Asn Met Thr Asn
1280 1285 1290

Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr Thr Ala Tyr Ala Cys Asn
1295 1300 1305

Cys Ala Arg Ala Ala Arg Trp Ser Asn Met Thr Asn Trp Ser Asn
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Met Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn Ala Ala Arg
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<400> 588

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1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
35 40 45

Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Ala Cys Asn Thr Thr Tyr Met Gly Asn Trp Ser Asn Cys Ala Tyr
85 90 95

Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly
145 150 155 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Ala Ala
165 170 175

2344

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Met Gly Asn Gly Gly Asn Met Gly Asn Thr Thr Tyr Ala Cys Asn Ala
195 200 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
210 215 220

Asn Ala Ala Arg Ala Ala Tyr Ala Cys Asn Met Thr Asn Gly Ala Tyr
225 230 235 240

Met Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Met
245 250 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Ala Cys
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Thr Gly Gly Gly Gly Asn Ala Thr His Trp
290 295 300

Ser Asn Gly Cys Asn Cys Cys Asn Thr Thr Tyr Gly Ala Tyr Thr Gly
305 310 315 320

Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn
325 330 335

Met Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp
340 345 350

Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly
355 360 365

Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn
370 375 380

Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met
385 390 395 400

Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser
405 410 415

Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn
420 425 430

Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr
435 440 445

Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr
450 455 460

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Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr
465                 470                 475                 480

Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp
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Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr
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Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg
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Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp
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Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr
545                 550                 555                 560

Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn
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Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala
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Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr
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Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn
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Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala
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Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala
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Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr
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Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys
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Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys
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Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr
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Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr
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Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala
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Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala
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Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala
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Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn
945                 950                 955                 960

Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys
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Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala
            980                 985                 990

Arg Ala Cys Asn Ala Thr His Trp  Ser Asn Ala Ala Arg  Ala Cys Asn
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Ala Ala  Arg Gly Gly Asn Cys  Ala Arg Cys Cys Asn  Met Gly Asn
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Gly Ala  Arg Cys Cys Asn Cys  Ala Arg Gly Thr Asn  Thr Ala Tyr
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Ala Ala Arg Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn
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Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
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Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Gly Cys Asn Thr Ala Tyr
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Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
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Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
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Trp Ser Asn Thr Ala Tyr Ala Thr His Trp Ser Asn Trp Ser Asn Trp
145 150 155 160

Ser Asn Gly Gly Asn Met Gly Asn Ala Cys Asn Ala Thr His Thr Ala
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Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
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Thr Asn Met Gly Asn Gly Ala Tyr Gly Ala Arg Gly Ala Tyr Ala Cys
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Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr
355 360 365

Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn
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Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp
385 390 395 400

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Met Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys
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Asn Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn
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Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly
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Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg
945 950 955 960

Gly Gly Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala
965 970 975

Thr His Gly Ala Arg Ala Ala Arg Ala Cys Asn Ala Thr His Trp Ser
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Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Ala Arg
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Cys Cys Asn Met Gly Asn Gly Ala Arg Cys Cys Asn Cys Ala Arg
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Cys Cys Asn Trp Ser Asn Met Gly Asn Gly Ala Arg Gly Ala Arg
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Ser Asn Trp Ser Asn Met Gly Asn Ala Cys Asn Ala Thr His Thr Ala
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Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn
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Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met
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Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala
450 455 460

Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg
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Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr
485 490 495

Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr
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Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr
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Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met
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2353

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580 585 590

Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys
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Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr
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Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys
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Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr
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Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg
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Gly Thr  Asn Thr Ala Tyr Ala  Cys Asn Met Thr Asn  Cys Cys Asn
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Cys Cys  Asn Trp Ser Asn Met  Gly Asn Gly Ala Arg  Gly Ala Arg
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Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
        35                  40                  45

Trp Ser Asn Met Thr Asn Met Gly Asn Met Thr Asn Trp Ser Asn Thr
    50                  55                  60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65                  70                  75                  80

Tyr Ala Cys Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
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Trp Ser Asn Ala Thr Gly Ala Ala Tyr Thr Gly Gly Gly Thr Asn Met
            100                 105                 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
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Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
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Trp Ser Asn Cys Ala Tyr Ala Thr His Trp Ser Asn Met Gly Asn Trp
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Ser Asn Trp Ser Asn Met Gly Asn Ala Cys Asn Ala Thr His Thr Ala
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Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
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Gly Ala Tyr Gly Thr Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly
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Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn
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Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr
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485 490 495

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Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr
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Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly
675 680 685

Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys
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Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly
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785 790 795 800

Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr
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Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys
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Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr
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Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn
    850                 855                 860

Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala
865                 870                 875                 880

Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala
                885                 890                 895

Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr
            900                 905                 910

Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met
        915                 920                 925

Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala
    930                 935                 940

Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn
945                 950                 955                 960

Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala
                965                 970                 975

Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly
            980                 985                 990

Asn Met Thr Asn Cys Cys Asn Gly  Cys Asn Cys Cys Asn  Ala Thr His
        995                 1000                1005

Gly Ala  Arg Ala Ala Arg Ala  Cys Asn Ala Thr His  Trp Ser Asn
    1010                1015                1020

Ala Ala  Arg Ala Cys Asn Ala  Ala Arg Gly Gly Asn  Cys Ala Arg
    1025                1030                1035

Cys Cys  Asn Met Gly Asn Gly  Ala Arg Cys Cys Asn  Cys Ala Arg
    1040                1045                1050

Gly Thr  Asn Thr Ala Tyr Ala  Cys Asn Met Thr Asn  Cys Cys Asn
    1055                1060                1065

Cys Cys  Asn Trp Ser Asn Met  Gly Asn Gly Ala Arg  Gly Ala Arg
    1070                1075                1080

Ala Thr  Gly Ala Cys Asn Ala  Ala Arg Ala Ala Tyr  Cys Ala Arg
    1085                1090                1095

Gly Thr  Asn Trp Ser Asn Met  Thr Asn Ala Cys Asn  Thr Gly Tyr
    1100                1105                1110

Met Thr  Asn Gly Thr Asn Ala  Ala Arg Gly Gly Asn  Thr Thr Tyr
    1115                1120                1125
```

```
Thr Ala  Tyr Cys Cys Asn Trp  Ser Asn Gly Ala Tyr  Ala Thr His
    1130                 1135                 1140

Gly Cys  Asn Gly Thr Asn Gly  Ala Arg Thr Gly Gly  Gly Ala Arg
    1145                 1150                 1155

Trp Ser  Asn Ala Ala Tyr Gly  Gly Asn Cys Ala Arg  Cys Cys Asn
    1160                 1165                 1170

Gly Ala  Arg Ala Ala Tyr Ala  Ala Tyr Thr Ala Tyr  Ala Ala Arg
    1175                 1180                 1185

Ala Cys  Asn Ala Cys Asn Cys  Cys Asn Cys Cys Asn  Ala Thr Gly
    1190                 1195                 1200

Met Thr  Asn Gly Ala Tyr Trp  Ser Asn Gly Ala Tyr  Gly Gly Asn
    1205                 1210                 1215

Trp Ser  Asn Thr Thr Tyr Thr  Thr Tyr Met Thr Asn  Thr Ala Tyr
    1220                 1225                 1230

Trp Ser  Asn Ala Ala Arg Met  Thr Asn Ala Cys Asn  Gly Thr Asn
    1235                 1240                 1245

Gly Ala  Tyr Ala Ala Arg Trp  Ser Asn Met Gly Asn  Thr Gly Gly
    1250                 1255                 1260

Cys Ala  Arg Cys Ala Arg Gly  Gly Asn Ala Ala Tyr  Gly Thr Asn
    1265                 1270                 1275

Thr Thr  Tyr Trp Ser Asn Thr  Gly Tyr Trp Ser Asn  Gly Thr Asn
    1280                 1285                 1290

Ala Thr  Gly Cys Ala Tyr Gly  Ala Arg Gly Cys Asn  Met Thr Asn
    1295                 1300                 1305

Cys Ala  Tyr Ala Ala Tyr Cys  Ala Tyr Thr Ala Tyr  Ala Cys Asn
    1310                 1315                 1320

Cys Ala  Arg Ala Ala Arg Trp  Ser Asn Met Thr Asn  Trp Ser Asn
    1325                 1330                 1335

Met Thr  Asn Trp Ser Asn Cys  Cys Asn Gly Gly Asn  Ala Ala Arg
    1340                 1345                 1350
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<210> 592
<211> 1332
<212> PRT
<213> Homo Sapiens

<400> 592

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Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Cys Ala Arg Gly
1               5                  10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Met Thr
            20                  25                  30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
        35                  40                  45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr
    50                  55                  60

Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65                  70                  75                  80

Asn Trp Ser Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Gly Asn
                85                  90                  95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
            100                 105                 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Met Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Cys
145                 150                 155                 160

Ala Tyr Trp Ser Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Ala Cys
                165                 170                 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
            180                 185                 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Ala
        195                 200                 205

Cys Asn Ala Thr His Trp Ser Asn Gly Thr Asn Gly Ala Tyr Ala Cys
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225                 230                 235                 240

Trp Ser Asn Met Thr Asn Ala Ala Tyr Met Thr Asn Trp Ser Asn Trp
                245                 250                 255

Ser Asn Gly Thr Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala
            260                 265                 270

Tyr Ala Cys Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285
```

2364

Thr Gly Tyr Gly Cys Asn Met Gly Asn Gly Gly Asn Cys Cys Asn Thr
290 295 300

Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr
305 310 315 320

Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn
325 330 335

Ala Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp
340 345 350

Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly
355 360 365

Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn
370 375 380

Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met
385 390 395 400

Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser
405 410 415

Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn
420 425 430

Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr
435 440 445

Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr
450 455 460

Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr
465 470 475 480

Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp
485 490 495

Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr
500 505 510

Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg
515 520 525

Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp
530 535 540

Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr
545 550 555 560

Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn
565 570 575

2363

Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala
580 585 590

Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr
595 600 605

Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn
610 615 620

Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala
625 630 635 640

Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala
645 650 655

Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr
660 665 670

Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys
675 680 685

Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys
690 695 700

Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr
705 710 715 720

Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly
725 730 735

Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser
740 745 750

Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn
755 760 765

Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly
770 775 780

Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala
785 790 795 800

Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr
805 810 815

Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly
820 825 830

Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala
835 840 845

Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn
850 855 860

```
Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala
865                 870                 875                 880

Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr
                885                 890                 895

Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn
            900                 905                 910

Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr
        915                 920                 925

Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala
    930                 935                 940

Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn
945                 950                 955                 960

Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys
                965                 970                 975

Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala
            980                 985                 990

Arg Ala Cys Asn Ala Thr His Trp  Ser Asn Ala Ala Arg  Ala Cys Asn
        995                 1000                1005

Ala Ala  Arg Gly Gly Asn Cys  Ala Arg Cys Cys Asn  Met Gly Asn
    1010                1015                1020

Gly Ala  Arg Cys Cys Asn Cys  Ala Arg Gly Thr Asn  Thr Ala Tyr
    1025                1030                1035

Ala Cys  Asn Met Thr Asn Cys  Cys Asn Cys Cys Asn  Trp Ser Asn
    1040                1045                1050

Met Gly  Asn Gly Ala Arg Gly  Ala Arg Ala Thr Gly  Ala Cys Asn
    1055                1060                1065

Ala Ala  Arg Ala Ala Tyr Cys  Ala Arg Gly Thr Asn  Trp Ser Asn
    1070                1075                1080

Met Thr  Asn Ala Cys Asn Thr  Gly Tyr Met Thr Asn  Gly Thr Asn
    1085                1090                1095

Ala Ala  Arg Gly Gly Asn Thr  Thr Tyr Thr Ala Tyr  Cys Cys Asn
    1100                1105                1110

Trp Ser  Asn Gly Ala Tyr Ala  Thr His Gly Cys Asn  Gly Thr Asn
    1115                1120                1125

Gly Ala  Arg Thr Gly Gly Gly  Ala Arg Trp Ser Asn  Ala Ala Tyr
    1130                1135                1140
```

2367

Gly Gly Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr
1145 1150 1155

Ala Ala Tyr Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn
1160 1165 1170

Cys Cys Asn Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr
1175 1180 1185

Trp Ser Asn Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr
1190 1195 1200

Thr Thr Tyr Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg
1205 1210 1215

Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg
1220 1225 1230

Trp Ser Asn Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg
1235 1240 1245

Gly Gly Asn Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn
1250 1255 1260

Thr Gly Tyr Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr
1265 1270 1275

Gly Ala Arg Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr
1280 1285 1290

Cys Ala Tyr Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg
1295 1300 1305

Trp Ser Asn Met Thr Asn Trp Ser Asn Met Thr Asn Trp Ser Asn
1310 1315 1320

Cys Cys Asn Gly Gly Asn Ala Ala Arg
1325 1330

<210> 593
<211> 1359
<212> PRT
<213> Homo Sapiens

<400> 593

Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Met Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr
50 55 60

Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Met Gly Asn Gly Gly Asn
85 90 95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Met Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Thr
145 150 155 160

Ala Tyr Cys Ala Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Ala Cys
165 170 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
180 185 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Ala
195 200 205

Ala Tyr Ala Thr Gly Trp Ser Asn Gly Thr Asn Gly Ala Tyr Ala Cys
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225 230 235 240

Trp Ser Asn Met Thr Asn Ala Ala Arg Met Thr Asn Trp Ser Asn Trp
245 250 255

Ser Asn Gly Thr Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala
260 265 270

Tyr Ala Cys Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Gly Cys Asn Met Thr Asn Met
290 295 300

Gly Asn Gly Gly Asn Ala Thr His Gly Thr Asn Met Thr Asn Ala Thr
305 310 315 320

2369

Gly Gly Thr Asn Thr Ala Tyr Gly Thr Asn Met Thr Asn Gly Gly Asn
325 330 335

Gly Cys Asn Met Thr Asn Gly Ala Tyr Ala Thr His Thr Gly Gly Gly
340 345 350

Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Ala Ala Arg Gly Thr
355 360 365

Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn
370 375 380

Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp
385 390 395 400

Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys
405 410 415

Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn
420 425 430

Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly
435 440 445

Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr
450 455 460

Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr
465 470 475 480

Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly
485 490 495

Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly
500 505 510

Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn
515 520 525

Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly
530 535 540

Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser
545 550 555 560

Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn
565 570 575

Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly
580 585 590

Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr
595 600 605

2370.

Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr
610 615 620

Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys
625 630 635 640

Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys
645 650 655

Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn
660 665 670

Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr
675 680 685

Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys
690 695 700

Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn
705 710 715 720

Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly
725 730 735

Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys
740 745 750

Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn
755 760 765

Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn Met Gly Asn Ala
770 775 780

Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly
785 790 795 800

Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn
805 810 815

Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly
820 825 830

Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly
835 840 845

Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn
850 855 860

Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala
865 870 875 880

Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met Gly Asn Gly Ala
885 890 895

2371

Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn
900 905 910

Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn Trp
915 920 925

Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr
930 935 940

Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn
945 950 955 960

Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala
965 970 975

Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala
980 985 990

Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys Cys Asn Gly Cys Asn
995 1000 1005

Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala Arg Ala Cys Asn
1010 1015 1020

Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg
1025 1030 1035

Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg
1040 1045 1050

Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr Ala Cys Asn
1055 1060 1065

Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn Met Gly Asn
1070 1075 1080

Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn Ala Ala Arg
1085 1090 1095

Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn Met Thr Asn
1100 1105 1110

Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg
1115 1120 1125

Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Trp Ser Asn
1130 1135 1140

Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn Gly Ala Arg
1145 1150 1155

Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr Gly Gly Asn
1160 1165 1170

```
Cys Ala  Arg Cys Cys Asn Gly  Ala Arg Ala Ala Tyr  Ala Ala Tyr
    1175                 1180                 1185

Thr Ala  Tyr Ala Ala Arg Ala  Cys Asn Ala Cys Asn  Cys Cys Asn
    1190                 1195                 1200

Cys Cys  Asn Ala Thr Gly Met  Thr Asn Gly Ala Tyr  Trp Ser Asn
    1205                 1210                 1215

Gly Ala  Tyr Gly Gly Asn Trp  Ser Asn Thr Thr Tyr  Thr Thr Tyr
    1220                 1225                 1230

Met Thr  Asn Thr Ala Tyr Trp  Ser Asn Ala Ala Arg  Met Thr Asn
    1235                 1240                 1245

Ala Cys  Asn Gly Thr Asn Gly  Ala Tyr Ala Ala Arg  Trp Ser Asn
    1250                 1255                 1260

Met Gly  Asn Thr Gly Gly Cys  Ala Arg Cys Ala Arg  Gly Gly Asn
    1265                 1270                 1275

Ala Ala  Tyr Gly Thr Asn Thr  Thr Tyr Trp Ser Asn  Thr Gly Tyr
    1280                 1285                 1290

Trp Ser  Asn Gly Thr Asn Ala  Thr Gly Cys Ala Tyr  Gly Ala Arg
    1295                 1300                 1305

Gly Cys  Asn Met Thr Asn Cys  Ala Tyr Ala Ala Tyr  Cys Ala Tyr
    1310                 1315                 1320

Thr Ala  Tyr Ala Cys Asn Cys  Ala Arg Ala Ala Arg  Trp Ser Asn
    1325                 1330                 1335

Met Thr  Asn Trp Ser Asn Met  Thr Asn Trp Ser Asn  Cys Cys Asn
    1340                 1345                 1350

Gly Gly  Asn Ala Ala Arg
    1355
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<210> 594
<211> 1359
<212> PRT
<213> Homo Sapiens

<400> 594

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Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Cys Ala Arg Gly
1               5                  10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Met Thr
            20                  25                  30
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Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr
50 55 60

Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
85 90 95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Met Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Thr
145 150 155 160

Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Ala Cys
165 170 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
180 185 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Ala
195 200 205

Cys Asn Ala Thr His Trp Ser Asn Gly Thr Asn Gly Ala Tyr Ala Cys
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225 230 235 240

Trp Ser Asn Met Thr Asn Ala Ala Arg Met Thr Asn Trp Ser Asn Trp
245 250 255

Ser Asn Gly Thr Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala
260 265 270

Tyr Ala Cys Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Gly Ala Tyr Gly Ala Arg Ala
290 295 300

Cys Asn Gly Thr Asn Gly Thr Asn Met Gly Asn Gly Gly Asn Met Thr
305 310 315 320

Asn Ala Thr His Met Gly Asn Thr Ala Tyr Thr Gly Tyr Thr Ala Tyr
325 330 335

Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr Gly Gly Gly
340 345 350

Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Ala Cys Asn Gly Thr
355 360 365

Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn
370 375 380

Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp
385 390 395 400

Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys
405 410 415

Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn
420 425 430

Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly
435 440 445

Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr
450 455 460

Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr
465 470 475 480

Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly
485 490 495

Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly
500 505 510

Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn
515 520 525

Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly
530 535 540

Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser
545 550 555 560

Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn
565 570 575

Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly
580 585 590

Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr
595 600 605

```
Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr
    610                 615                 620

Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys
625                 630                 635                 640

Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys
                645                 650                 655

Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn
            660                 665                 670

Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr
        675                 680                 685

Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys
    690                 695                 700

Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn
705                 710                 715                 720

Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly
                725                 730                 735

Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys
            740                 745                 750

Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn
        755                 760                 765

Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn Met Gly Asn Ala
    770                 775                 780

Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly
785                 790                 795                 800

Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn
                805                 810                 815

Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly
            820                 825                 830

Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly
        835                 840                 845

Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn
    850                 855                 860

Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala
865                 870                 875                 880

Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met Gly Asn Gly Ala
                885                 890                 895
```

Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn
900 905 910

Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn Trp
915 920 925

Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr
930 935 940

Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn
945 950 955 960

Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala
965 970 975

Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala
980 985 990

Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys Cys Asn Gly Cys Asn
995 1000 1005

Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala Arg Ala Cys Asn
1010 1015 1020

Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg
1025 1030 1035

Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg
1040 1045 1050

Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr Ala Cys Asn
1055 1060 1065

Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn Met Gly Asn
1070 1075 1080

Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn Ala Ala Arg
1085 1090 1095

Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn Met Thr Asn
1100 1105 1110

Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg
1115 1120 1125

Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Trp Ser Asn
1130 1135 1140

Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn Gly Ala Arg
1145 1150 1155

Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr Gly Gly Asn
1160 1165 1170

Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr Ala Ala Tyr
1175 1180 1185

Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn Cys Cys Asn
1190 1195 1200

Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr Trp Ser Asn
1205 1210 1215

Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr Thr Thr Tyr
1220 1225 1230

Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg Met Thr Asn
1235 1240 1245

Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg Trp Ser Asn
1250 1255 1260

Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg Gly Gly Asn
1265 1270 1275

Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn Thr Gly Tyr
1280 1285 1290

Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr Gly Ala Arg
1295 1300 1305

Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr
1310 1315 1320

Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg Trp Ser Asn
1325 1330 1335

Met Thr Asn Trp Ser Asn Met Thr Asn Trp Ser Asn Cys Cys Asn
1340 1345 1350

Gly Gly Asn Ala Ala Arg
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<400> 595

Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Met Thr
20 25 30

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Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
        35                  40                  45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Ala Tyr Thr
    50                  55                  60

Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65                  70                  75                  80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
                85                  90                  95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
            100                 105                 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Met Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Cys
145                 150                 155                 160

Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Ala Cys
                165                 170                 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
            180                 185                 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Ala Thr His Ala
        195                 200                 205

Cys Asn Ala Thr His Trp Ser Asn Gly Cys Asn Gly Ala Tyr Ala Cys
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225                 230                 235                 240

Trp Ser Asn Met Thr Asn Ala Ala Arg Met Thr Asn Ala Ala Tyr Trp
                245                 250                 255

Ser Asn Gly Thr Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala
            260                 265                 270

Tyr Ala Cys Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Gly Ala Tyr Met Gly Asn Gly
    290                 295                 300

Gly Asn Gly Gly Asn Gly Gly Asn Gly Ala Tyr Thr Ala Tyr Gly Gly
305                 310                 315                 320
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Asn Met Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr Gly Gly
                325                 330                 335

Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Ala Cys Asn Gly
            340                 345                 350

Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys
        355                 360                 365

Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn
    370                 375                 380

Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly
385                 390                 395                 400

Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser
                405                 410                 415

Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn
            420                 425                 430

Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr Met
        435                 440                 445

Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr
    450                 455                 460

Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn
465                 470                 475                 480

Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly
                485                 490                 495

Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly
            500                 505                 510

Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn
        515                 520                 525

Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp Ser Asn Trp
    530                 535                 540

Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr
545                 550                 555                 560

Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn
                565                 570                 575

Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr
            580                 585                 590

Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala
        595                 600                 605
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Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr
    610                 615                 620

Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala
625                 630                 635                 640

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys
                645                 650                 655

Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr
            660                 665                 670

Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys
        675                 680                 685

Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys
    690                 695                 700

Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn
705                 710                 715                 720

Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys
                725                 730                 735

Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys
            740                 745                 750

Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn Met Gly Asn
        755                 760                 765

Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr
    770                 775                 780

Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr
785                 790                 795                 800

Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn
                805                 810                 815

Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr
            820                 825                 830

Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr
        835                 840                 845

Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn
    850                 855                 860

Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met Gly Asn Gly
865                 870                 875                 880

Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser
                885                 890                 895
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Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn
900 905 910

Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly Thr Asn Gly
915 920 925

Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr
930 935 940

Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr
945 950 955 960

Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala
965 970 975

Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys Cys Asn Gly Cys
980 985 990

Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala Arg Ala Cys Asn
995 1000 1005

Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg
1010 1015 1020

Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg
1025 1030 1035

Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr Ala Cys Asn
1040 1045 1050

Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn Met Gly Asn
1055 1060 1065

Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn Ala Ala Arg
1070 1075 1080

Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn Met Thr Asn
1085 1090 1095

Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg
1100 1105 1110

Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Trp Ser Asn
1115 1120 1125

Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn Gly Ala Arg
1130 1135 1140

Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr Gly Gly Asn
1145 1150 1155

Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr Ala Ala Tyr
1160 1165 1170

Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn Cys Cys Asn
1175 1180 1185

Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr Trp Ser Asn
1190 1195 1200

Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr Thr Thr Tyr
1205 1210 1215

Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg Met Thr Asn
1220 1225 1230

Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg Trp Ser Asn
1235 1240 1245

Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg Gly Gly Asn
1250 1255 1260

Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn Thr Gly Tyr
1265 1270 1275

Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr Gly Ala Arg
1280 1285 1290

Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr
1295 1300 1305

Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg Trp Ser Asn
1310 1315 1320

Met Thr Asn Trp Ser Asn Met Thr Asn Trp Ser Asn Cys Cys Asn
1325 1330 1335

Gly Gly Asn Ala Ala Arg
1340

<210> 596
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<400> 596

Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Met Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

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Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Ala Tyr Thr
    50                  55                  60

Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65                  70                  75                  80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
                85                  90                  95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
            100                 105                 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Met Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Cys
145                 150                 155                 160

Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Ala Cys
                165                 170                 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
            180                 185                 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Ala Thr His Ala
        195                 200                 205

Cys Asn Ala Thr His Trp Ser Asn Gly Cys Asn Gly Ala Tyr Ala Cys
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225                 230                 235                 240

Trp Ser Asn Met Thr Asn Ala Ala Arg Met Thr Asn Ala Ala Tyr Trp
                245                 250                 255

Ser Asn Gly Thr Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala
            260                 265                 270

Tyr Ala Cys Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Gly Ala Tyr Met Gly Asn Gly
    290                 295                 300

Gly Asn Gly Gly Asn Gly Gly Asn Gly Ala Tyr Thr Ala Tyr Gly Gly
305                 310                 315                 320

Asn Met Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr Gly Gly
                325                 330                 335
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Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Ala Cys Asn Gly
            340                 345                 350

Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys
        355                 360                 365

Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn
    370                 375                 380

Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly
385                 390                 395                 400

Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser
                405                 410                 415

Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn
            420                 425                 430

Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr Met
        435                 440                 445

Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr
    450                 455                 460

Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn
465                 470                 475                 480

Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly
                485                 490                 495

Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly
            500                 505                 510

Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn
        515                 520                 525

Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp Ser Asn Trp
    530                 535                 540

Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr
545                 550                 555                 560

Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn
                565                 570                 575

Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr
            580                 585                 590

Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala
        595                 600                 605

Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr
    610                 615                 620
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Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala
625 630 635 640

Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys
645 650 655

Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr
660 665 670

Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys
675 680 685

Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys
690 695 700

Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn
705 710 715 720

Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys
725 730 735

Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys
740 745 750

Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn Met Gly Asn
755 760 765

Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr
770 775 780

Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr
785 790 795 800

Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn
805 810 815

Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr
820 825 830

Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr
835 840 845

Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn
850 855 860

Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met Gly Asn Gly
865 870 875 880

Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser
885 890 895

Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn
900 905 910

Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly Thr Asn Gly
915 920 925

Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr
930 935 940

Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr
945 950 955 960

Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala
965 970 975

Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys Cys Asn Gly Cys
980 985 990

Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala Arg Ala Cys Asn
995 1000 1005

Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg
1010 1015 1020

Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg
1025 1030 1035

Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr Ala Cys Asn
1040 1045 1050

Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn Met Gly Asn
1055 1060 1065

Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn Ala Ala Arg
1070 1075 1080

Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn Met Thr Asn
1085 1090 1095

Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg
1100 1105 1110

Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Trp Ser Asn
1115 1120 1125

Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn Gly Ala Arg
1130 1135 1140

Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr Gly Gly Asn
1145 1150 1155

Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr Ala Ala Tyr
1160 1165 1170

Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn Cys Cys Asn
1175 1180 1185

1387

Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr Trp Ser Asn
1190 1195 1200

Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr Thr Thr Tyr
1205 1210 1215

Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg Met Thr Asn
1220 1225 1230

Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg Trp Ser Asn
1235 1240 1245

Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg Gly Gly Asn
1250 1255 1260

Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn Thr Gly Tyr
1265 1270 1275

Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr Gly Ala Arg
1280 1285 1290

Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr
1295 1300 1305

Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg Trp Ser Asn
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Met Thr Asn Trp Ser Asn Met Thr Asn Trp Ser Asn Cys Cys Asn
1325 1330 1335

Gly Gly Asn Ala Ala Arg
1340

<210> 597
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Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Met Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr
50 55 60

Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
85 90 95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Met Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Cys
145 150 155 160

Ala Tyr Trp Ser Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Ala Cys
165 170 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
180 185 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Ala Thr His Ala
195 200 205

Cys Asn Ala Ala Arg Trp Ser Asn Gly Thr Asn Gly Ala Tyr Ala Cys
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225 230 235 240

Trp Ser Asn Met Thr Asn Ala Ala Arg Met Thr Asn Trp Ser Asn Trp
245 250 255

Ser Asn Gly Thr Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala
260 265 270

Tyr Ala Cys Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Trp Ser Asn Ala Ala Tyr Ala
290 295 300

Ala Tyr Thr Ala Tyr Gly Gly Asn Thr Gly Tyr Thr Thr Tyr Gly Cys
305 310 315 320

Asn Met Thr Asn Thr Gly Gly Gly Gly Asn Met Gly Asn Gly Gly Asn
325 330 335

Ala Cys Asn Met Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp
340 345 350

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Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala
        355                 360                 365

Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr
    370                 375                 380

Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp
385                 390                 395                 400

Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala
                405                 410                 415

Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn
            420                 425                 430

Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly
        435                 440                 445

Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys
    450                 455                 460

Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly
465                 470                 475                 480

Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr Asn Ala
                485                 490                 495

Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys
            500                 505                 510

Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met Thr Asn
        515                 520                 525

Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr
    530                 535                 540

Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr
545                 550                 555                 560

Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn
                565                 570                 575

Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys
            580                 585                 590

Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala
        595                 600                 605

Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn
    610                 615                 620

Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly
625                 630                 635                 640
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1390

Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg Met Gly
645 650 655

Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg
660 665 670

Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly
675 680 685

Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly
690 695 700

Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn
705 710 715 720

Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala
725 730 735

Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr
740 745 750

His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg
755 760 765

Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly
770 775 780

Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala
785 790 795 800

Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg
805 810 815

Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly
820 825 830

Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala
835 840 845

Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg
850 855 860

Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr
865 870 875 880

Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly
885 890 895

Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met Thr Asn
900 905 910

Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly
915 920 925

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Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala
    930                 935                 940

Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg
945                 950                 955                 960

Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met
                965                 970                 975

Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His Gly Ala
            980                 985                 990

Arg Ala Ala Arg Ala Cys Asn Ala  Thr His Trp Ser Asn  Ala Ala Arg
        995                 1000                1005

Ala Cys  Asn Ala Ala Arg Gly  Gly Asn Cys Ala Arg  Cys Cys Asn
    1010                1015                1020

Met Gly  Asn Gly Ala Arg Cys  Cys Asn Cys Ala Arg  Gly Thr Asn
    1025                1030                1035

Thr Ala  Tyr Ala Cys Asn Met  Thr Asn Cys Cys Asn  Cys Cys Asn
    1040                1045                1050

Trp Ser  Asn Met Gly Asn Gly  Ala Arg Gly Ala Arg  Ala Thr Gly
    1055                1060                1065

Ala Cys  Asn Ala Ala Arg Ala  Ala Tyr Cys Ala Arg  Gly Thr Asn
    1070                1075                1080

Trp Ser  Asn Met Thr Asn Ala  Cys Asn Thr Gly Tyr  Met Thr Asn
    1085                1090                1095

Gly Thr  Asn Ala Ala Arg Gly  Gly Asn Thr Thr Tyr  Thr Ala Tyr
    1100                1105                1110

Cys Cys  Asn Trp Ser Asn Gly  Ala Tyr Ala Thr His  Gly Cys Asn
    1115                1120                1125

Gly Thr  Asn Gly Ala Arg Thr  Gly Gly Gly Ala Arg  Trp Ser Asn
    1130                1135                1140

Ala Ala  Tyr Gly Gly Asn Cys  Ala Arg Cys Cys Asn  Gly Ala Arg
    1145                1150                1155

Ala Ala  Tyr Ala Ala Tyr Thr  Ala Tyr Ala Ala Arg  Ala Cys Asn
    1160                1165                1170

Ala Cys  Asn Cys Cys Asn Cys  Cys Asn Ala Thr Gly  Met Thr Asn
    1175                1180                1185

Gly Ala  Tyr Trp Ser Asn Gly  Ala Tyr Gly Gly Asn  Trp Ser Asn
    1190                1195                1200
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Thr Thr Tyr Thr Thr Tyr Met Thr Asn Thr Ala Tyr Trp Ser Asn
1205 1210 1215

Ala Ala Arg Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Ala Tyr
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Ala Ala Arg Trp Ser Asn Met Gly Asn Thr Gly Gly Cys Ala Arg
1235 1240 1245

Cys Ala Arg Gly Gly Asn Ala Ala Tyr Gly Thr Asn Thr Thr Tyr
1250 1255 1260

Trp Ser Asn Thr Gly Tyr Trp Ser Asn Gly Thr Asn Ala Thr Gly
1265 1270 1275

Cys Ala Tyr Gly Ala Arg Gly Cys Asn Met Thr Asn Cys Ala Tyr
1280 1285 1290

Ala Ala Tyr Cys Ala Tyr Thr Ala Tyr Ala Cys Asn Cys Ala Arg
1295 1300 1305

Ala Ala Arg Trp Ser Asn Met Thr Asn Trp Ser Asn Met Thr Asn
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Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr
50 55 60

Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
85 90 95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Met Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Cys
145 150 155 160

Ala Tyr Trp Ser Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Ala Cys
165 170 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
180 185 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Ala Thr His Ala
195 200 205

Cys Asn Ala Ala Arg Trp Ser Asn Gly Thr Asn Gly Ala Tyr Ala Cys
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225 230 235 240

Trp Ser Asn Met Thr Asn Ala Ala Arg Met Thr Asn Trp Ser Asn Trp
245 250 255

Ser Asn Gly Thr Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala
260 265 270

Tyr Ala Cys Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Trp Ser Asn Ala Ala Tyr Ala
290 295 300

Ala Tyr Thr Ala Tyr Gly Gly Asn Thr Gly Tyr Thr Thr Tyr Gly Cys
305 310 315 320

Asn Met Thr Asn Thr Gly Gly Gly Gly Asn Met Gly Asn Gly Gly Asn
325 330 335

Ala Cys Asn Met Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp
340 345 350

Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala
355 360 365

Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr
370 375 380

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Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp
385                 390                 395                 400

Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala
                405                 410                 415

Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn
            420                 425                 430

Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly
        435                 440                 445

Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys
    450                 455                 460

Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly
465                 470                 475                 480

Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr Asn Ala
                485                 490                 495

Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys
            500                 505                 510

Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met Thr Asn
        515                 520                 525

Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr
    530                 535                 540

Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr
545                 550                 555                 560

Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn
                565                 570                 575

Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys
            580                 585                 590

Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala
        595                 600                 605

Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn
    610                 615                 620

Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly
625                 630                 635                 640

Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg Met Gly
                645                 650                 655

Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg
            660                 665                 670
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Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly
675 680 685

Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly
690 695 700

Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn
705 710 715 720

Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala
725 730 735

Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr
740 745 750

His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg
755 760 765

Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly
770 775 780

Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala
785 790 795 800

Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg
805 810 815

Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly
820 825 830

Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala
835 840 845

Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg
850 855 860

Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr
865 870 875 880

Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly
885 890 895

Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met Thr Asn
900 905 910

Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly
915 920 925

Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala
930 935 940

Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg
945 950 955 960

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Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met
               965                 970                 975

Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His Gly Ala
           980                 985                 990

Arg Ala Ala Arg Ala Cys Asn Ala  Thr His Trp Ser Asn  Ala Ala Arg
       995                 1000                1005

Ala Cys  Asn Ala Ala Arg Gly  Gly Asn Cys Ala Arg  Cys Cys Asn
    1010                1015                1020

Met Gly  Asn Gly Ala Arg Cys  Cys Asn Cys Ala Arg  Gly Thr Asn
    1025                1030                1035

Thr Ala  Tyr Ala Cys Asn Met  Thr Asn Cys Cys Asn  Cys Cys Asn
    1040                1045                1050

Trp Ser  Asn Met Gly Asn Gly  Ala Arg Gly Ala Arg  Ala Thr Gly
    1055                1060                1065

Ala Cys  Asn Ala Ala Arg Ala  Ala Tyr Cys Ala Arg  Gly Thr Asn
    1070                1075                1080

Trp Ser  Asn Met Thr Asn Ala  Cys Asn Thr Gly Tyr  Met Thr Asn
    1085                1090                1095

Gly Thr  Asn Ala Ala Arg Gly  Gly Asn Thr Thr Tyr  Thr Ala Tyr
    1100                1105                1110

Cys Cys  Asn Trp Ser Asn Gly  Ala Tyr Ala Thr His  Gly Cys Asn
    1115                1120                1125

Gly Thr  Asn Gly Ala Arg Thr  Gly Gly Gly Ala Arg  Trp Ser Asn
    1130                1135                1140

Ala Ala  Tyr Gly Gly Asn Cys  Ala Arg Cys Cys Asn  Gly Ala Arg
    1145                1150                1155

Ala Ala  Tyr Ala Ala Tyr Thr  Ala Tyr Ala Ala Arg  Ala Cys Asn
    1160                1165                1170

Ala Cys  Asn Cys Cys Asn Cys  Cys Asn Ala Thr Gly  Met Thr Asn
    1175                1180                1185

Gly Ala  Tyr Trp Ser Asn Gly  Ala Tyr Gly Gly Asn  Trp Ser Asn
    1190                1195                1200

Thr Thr  Tyr Thr Thr Tyr Met  Thr Asn Thr Ala Tyr  Trp Ser Asn
    1205                1210                1215
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Ala Ala Arg Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Ala Tyr
1220 1225 1230

Ala Ala Arg Trp Ser Asn Met Gly Asn Thr Gly Gly Cys Ala Arg
1235 1240 1245

Cys Ala Arg Gly Gly Asn Ala Ala Tyr Gly Thr Asn Thr Thr Tyr
1250 1255 1260

Trp Ser Asn Thr Gly Tyr Trp Ser Asn Gly Thr Asn Ala Thr Gly
1265 1270 1275

Cys Ala Tyr Gly Ala Arg Gly Cys Asn Met Thr Asn Cys Ala Tyr
1280 1285 1290

Ala Ala Tyr Cys Ala Tyr Thr Ala Tyr Ala Cys Asn Cys Ala Arg
1295 1300 1305

Ala Ala Arg Trp Ser Asn Met Thr Asn Trp Ser Asn Met Thr Asn
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Trp Ser Asn Cys Cys Asn Gly Gly Asn Ala Ala Arg
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<210> 599
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20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr
50 55 60

Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
85 90 95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
100 105 110

2398

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Met Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Cys
145 150 155 160

Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Ala Cys
165 170 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
180 185 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Ala
195 200 205

Cys Asn Ala Thr His Trp Ser Asn Gly Thr Asn Gly Ala Tyr Ala Cys
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225 230 235 240

Trp Ser Asn Met Thr Asn Ala Ala Arg Met Thr Asn Trp Ser Asn Trp
245 250 255

Ser Asn Gly Thr Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala
260 265 270

Tyr Ala Cys Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Ala Tyr Ala
290 295 300

Ala Tyr Thr Ala Tyr Gly Gly Asn Met Thr Asn Thr Ala Tyr Thr Ala
305 310 315 320

Tyr Thr Ala Tyr Gly Ala Tyr Trp Ser Asn Trp Ser Asn Gly Gly Asn
325 330 335

Thr Ala Tyr Cys Cys Asn Trp Ser Asn Thr Ala Tyr Thr Ala Tyr Thr
340 345 350

Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr Gly
355 360 365

Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Ala Cys Asn
370 375 380

Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly
385 390 395 400

Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys
405 410 415

Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn
420 425 430

Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp
435 440 445

Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys
450 455 460

Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr
465 470 475 480

Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr
485 490 495

Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys
500 505 510

Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn
515 520 525

Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser Asn Gly
530 535 540

Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys
545 550 555 560

Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp Ser Asn
565 570 575

Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn Met
580 585 590

Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys
595 600 605

Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr
610 615 620

Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr
625 630 635 640

Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala
645 650 655

Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr
660 665 670

Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala
675 680 685

Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg Thr Gly
690 695 700

Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn
705 710 715 720

Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys
725 730 735

Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser
740 745 750

Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn
755 760 765

Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala
770 775 780

Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn Met Gly
785 790 795 800

Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn
805 810 815

Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly
820 825 830

Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys
835 840 845

Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr
850 855 860

Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly
865 870 875 880

Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys
885 890 895

Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met Gly Asn
900 905 910

Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp
915 920 925

Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr
930 935 940

Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly Thr Asn
945 950 955 960

Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met
965 970 975

Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala
980 985 990

Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn
995 1000 1005

Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys Cys Asn
1010 1015 1020

Gly Cys Asn Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala Arg
1025 1030 1035

Ala Cys Asn Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn
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Ala Ala Arg Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn
1055 1060 1065

Gly Ala Arg Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr
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Ala Cys Asn Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn
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Met Gly Asn Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn
1100 1105 1110

Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn
1115 1120 1125

Met Thr Asn Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn
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Ala Ala Arg Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn
1145 1150 1155

Trp Ser Asn Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn
1160 1165 1170

Gly Ala Arg Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr
1175 1180 1185

Gly Gly Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr
1190 1195 1200

Ala Ala Tyr Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn
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Cys Cys Asn Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr
1220 1225 1230

Trp Ser Asn Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr
1235 1240 1245

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Thr Thr  Tyr Met Thr Asn Thr  Ala Tyr Trp Ser Asn  Ala Ala Arg
    1250                 1255                 1260

Met Thr  Asn Ala Cys Asn Gly  Thr Asn Gly Ala Tyr  Ala Ala Arg
    1265                 1270                 1275

Trp Ser  Asn Met Gly Asn Thr  Gly Gly Cys Ala Arg  Cys Ala Arg
    1280                 1285                 1290

Gly Gly  Asn Ala Ala Tyr Gly  Thr Asn Thr Thr Tyr  Trp Ser Asn
    1295                 1300                 1305

Thr Gly  Tyr Trp Ser Asn Gly  Thr Asn Ala Thr Gly  Cys Ala Tyr
    1310                 1315                 1320

Gly Ala  Arg Gly Cys Asn Met  Thr Asn Cys Ala Tyr  Ala Ala Tyr
    1325                 1330                 1335

Cys Ala  Tyr Thr Ala Tyr Ala  Cys Asn Cys Ala Arg  Ala Ala Arg
    1340                 1345                 1350

Trp Ser  Asn Met Thr Asn Trp  Ser Asn Met Thr Asn  Trp Ser Asn
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Cys Cys  Asn Gly Gly Asn Ala  Ala Arg
    1370                 1375

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1               5                  10                  15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Met Thr
            20                  25                  30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
        35                  40                  45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr
    50                  55                  60

Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65                  70                  75                  80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
                85                  90                  95
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Gly Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Ala Ala Tyr Thr
           100                 105                 110

Gly Gly Gly Thr Asn Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Met Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Gly Gly Asn Ala Cys
                165                 170                 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
           180                 185                 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Ala
        195                 200                 205

Cys Asn Ala Thr His Trp Ser Asn Gly Thr Asn Gly Ala Tyr Ala Cys
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225                 230                 235                 240

Trp Ser Asn Met Thr Asn Ala Ala Arg Met Thr Asn Thr Thr Tyr Trp
                245                 250                 255

Ser Asn Gly Thr Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala
           260                 265                 270

Tyr Ala Cys Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Thr Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Ala Cys Asn Thr Ala Tyr Thr
    290                 295                 300

Ala Tyr Gly Ala Tyr Ala Thr His Met Thr Asn Ala Cys Asn Gly Gly
305                 310                 315                 320

Asn Thr Ala Tyr Cys Cys Asn Thr Thr Tyr Thr Ala Tyr Thr Thr Tyr
                325                 330                 335

Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly
           340                 345                 350

Gly Asn Ala Cys Asn Met Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr
        355                 360                 365

Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn
    370                 375                 380
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Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr
385 390 395 400

Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly
405 410 415

Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn
420 425 430

Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met
435 440 445

Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala
450 455 460

Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg
465 470 475 480

Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr
485 490 495

Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr
500 505 510

Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr
515 520 525

Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met
530 535 540

Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr
545 550 555 560

Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
565 570 575

Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp
580 585 590

Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys
595 600 605

Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr
610 615 620

Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys
625 630 635 640

Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr
645 650 655

Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg
660 665 670

Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly
675 680 685

Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys
690 695 700

Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn
705 710 715 720

Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met
725 730 735

Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys
740 745 750

Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly
755 760 765

Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly
770 775 780

Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr
785 790 795 800

Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr
805 810 815

Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys
820 825 830

Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr
835 840 845

Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn
850 855 860

Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala
865 870 875 880

Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala
885 890 895

Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr
900 905 910

Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met
915 920 925

Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala
930 935 940

Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn
945 950 955 960

Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala
965 970 975

Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly
980 985 990

Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His
995 1000 1005

Gly Ala Arg Ala Ala Arg Ala Cys Asn Ala Thr His Trp Ser Asn
1010 1015 1020

Ala Ala Arg Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Ala Arg
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Cys Cys Asn Met Gly Asn Gly Ala Arg Cys Cys Asn Cys Ala Arg
1040 1045 1050

Gly Thr Asn Thr Ala Tyr Ala Cys Asn Met Thr Asn Cys Cys Asn
1055 1060 1065

Cys Cys Asn Trp Ser Asn Met Gly Asn Gly Ala Arg Gly Ala Arg
1070 1075 1080

Ala Thr Gly Ala Cys Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg
1085 1090 1095

Gly Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr Gly Tyr
1100 1105 1110

Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Gly Asn Thr Thr Tyr
1115 1120 1125

Thr Ala Tyr Cys Cys Asn Trp Ser Asn Gly Ala Tyr Ala Thr His
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Gly Cys Asn Gly Thr Asn Gly Ala Arg Thr Gly Gly Gly Ala Arg
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Trp Ser Asn Ala Ala Tyr Gly Gly Asn Cys Ala Arg Cys Cys Asn
1160 1165 1170

Gly Ala Arg Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr Ala Ala Arg
1175 1180 1185

Ala Cys Asn Ala Cys Asn Cys Cys Asn Cys Cys Asn Ala Thr Gly
1190 1195 1200

Met Thr Asn Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Gly Asn
1205 1210 1215

Trp Ser Asn Thr Thr Tyr Thr Thr Tyr Met Thr Asn Thr Ala Tyr
1220 1225 1230

Trp Ser Asn Ala Ala Arg Met Thr Asn Ala Cys Asn Gly Thr Asn
1235 1240 1245

Gly Ala Tyr Ala Ala Arg Trp Ser Asn Met Gly Asn Thr Gly Gly
1250 1255 1260

Cys Ala Arg Cys Ala Arg Gly Gly Asn Ala Ala Tyr Gly Thr Asn
1265 1270 1275

Thr Thr Tyr Trp Ser Asn Thr Gly Tyr Trp Ser Asn Gly Thr Asn
1280 1285 1290

Ala Thr Gly Cys Ala Tyr Gly Ala Arg Gly Cys Asn Met Thr Asn
1295 1300 1305

Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr Thr Ala Tyr Ala Cys Asn
1310 1315 1320

Cys Ala Arg Ala Ala Arg Trp Ser Asn Met Thr Asn Trp Ser Asn
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Met Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn Ala Ala Arg
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Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Met Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr
50 55 60

Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
85 90 95

Gly Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Ala Ala Tyr Thr
100 105 110

Gly Gly Gly Thr Asn Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Met Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Thr
145 150 155 160

Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Gly Gly Asn Ala Cys
165 170 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
180 185 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Ala
195 200 205

Cys Asn Ala Thr His Trp Ser Asn Gly Thr Asn Gly Ala Tyr Ala Cys
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225 230 235 240

Trp Ser Asn Met Thr Asn Ala Ala Arg Met Thr Asn Thr Thr Tyr Trp
245 250 255

Ser Asn Gly Thr Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala
260 265 270

Tyr Ala Cys Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Thr Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Ala Cys Asn Thr Ala Tyr Thr
290 295 300

Ala Tyr Gly Ala Tyr Ala Thr His Met Thr Asn Ala Cys Asn Gly Gly
305 310 315 320

Asn Thr Ala Tyr Cys Cys Asn Thr Thr Tyr Thr Ala Tyr Thr Thr Tyr
325 330 335

Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly
340 345 350

Gly Asn Ala Cys Asn Met Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr
355 360 365

Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn
370 375 380

Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr
385 390 395 400

Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly
405 410 415

Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn
420 425 430

Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met
435 440 445

Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala
450 455 460

Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg
465 470 475 480

Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr
485 490 495

Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr
500 505 510

Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr
515 520 525

Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met
530 535 540

Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr
545 550 555 560

Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
565 570 575

Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp
580 585 590

Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys
595 600 605

Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr
610 615 620

Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys
625 630 635 640

Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr
645 650 655

Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg
660 665 670

Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly
675 680 685

2410.

Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys
690 695 700

Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn
705 710 715 720

Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met
725 730 735

Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys
740 745 750

Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly
755 760 765

Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly
770 775 780

Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr
785 790 795 800

Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr
805 810 815

Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys
820 825 830

Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr
835 840 845

Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn
850 855 860

Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala
865 870 875 880

Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala
885 890 895

Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr
900 905 910

Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met
915 920 925

Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala
930 935 940

Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn
945 950 955 960

Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala
965 970 975

2411

Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly
980 985 990

Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His
995 1000 1005

Gly Ala Arg Ala Ala Arg Ala Cys Asn Ala Thr His Trp Ser Asn
1010 1015 1020

Ala Ala Arg Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Ala Arg
1025 1030 1035

Cys Cys Asn Met Gly Asn Gly Ala Arg Cys Cys Asn Cys Ala Arg
1040 1045 1050

Gly Thr Asn Thr Ala Tyr Ala Cys Asn Met Thr Asn Cys Cys Asn
1055 1060 1065

Cys Cys Asn Trp Ser Asn Met Gly Asn Gly Ala Arg Gly Ala Arg
1070 1075 1080

Ala Thr Gly Ala Cys Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg
1085 1090 1095

Gly Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr Gly Tyr
1100 1105 1110

Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Gly Asn Thr Thr Tyr
1115 1120 1125

Thr Ala Tyr Cys Cys Asn Trp Ser Asn Gly Ala Tyr Ala Thr His
1130 1135 1140

Gly Cys Asn Gly Thr Asn Gly Ala Arg Thr Gly Gly Gly Ala Arg
1145 1150 1155

Trp Ser Asn Ala Ala Tyr Gly Gly Asn Cys Ala Arg Cys Cys Asn
1160 1165 1170

Gly Ala Arg Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr Ala Ala Arg
1175 1180 1185

Ala Cys Asn Ala Cys Asn Cys Cys Asn Cys Cys Asn Ala Thr Gly
1190 1195 1200

Met Thr Asn Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Gly Asn
1205 1210 1215

Trp Ser Asn Thr Thr Tyr Thr Thr Tyr Met Thr Asn Thr Ala Tyr
1220 1225 1230

Trp Ser Asn Ala Ala Arg Met Thr Asn Ala Cys Asn Gly Thr Asn
1235 1240 1245

2412

Gly Ala Tyr Ala Ala Arg Trp Ser Asn Met Gly Asn Thr Gly Gly
1250 1255 1260

Cys Ala Arg Cys Ala Arg Gly Gly Asn Ala Ala Tyr Gly Thr Asn
1265 1270 1275

Thr Thr Tyr Trp Ser Asn Thr Gly Tyr Trp Ser Asn Gly Thr Asn
1280 1285 1290

Ala Thr Gly Cys Ala Tyr Gly Ala Arg Gly Cys Asn Met Thr Asn
1295 1300 1305

Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr Thr Ala Tyr Ala Cys Asn
1310 1315 1320

Cys Ala Arg Ala Ala Arg Trp Ser Asn Met Thr Asn Trp Ser Asn
1325 1330 1335

Met Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn Ala Ala Arg
1340 1345 1350

<210> 602
<211> 1338
<212> PRT
<213> Homo Sapiens

<400> 602

Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Cys Ala Arg Cys
1 5 10 15

Ala Arg Thr Gly Gly Gly Gly Asn Gly Cys Asn Gly Gly Asn Met Thr
20 25 30

Asn Met Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Gly Ala Arg
35 40 45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Thr Asn Thr Ala Tyr Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Ala Tyr
85 90 95

Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr Gly Gly Ala Thr His Met
100 105 110

Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

```
Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr His
    130                 135                 140

Gly Gly Asn Gly Ala Arg Ala Thr His Ala Ala Tyr Cys Ala Tyr Trp
145                 150                 155                 160

Ser Asn Gly Gly Asn Trp Ser Asn Ala Cys Asn Ala Ala Tyr Thr Ala
                165                 170                 175

Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn Met Thr Asn Ala Ala Arg
            180                 185                 190

Trp Ser Asn Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Trp
        195                 200                 205

Ser Asn Gly Thr Asn Gly Ala Tyr Ala Cys Asn Trp Ser Asn Ala Ala
    210                 215                 220

Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Met Thr Asn
225                 230                 235                 240

Ala Ala Arg Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Ala
                245                 250                 255

Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala Tyr Ala Cys Asn Gly Cys
            260                 265                 270

Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn
        275                 280                 285

Met Gly Asn Gly Gly Asn Gly Gly Asn Thr Ala Tyr Trp Ser Asn Trp
    290                 295                 300

Ser Asn Trp Ser Asn Thr Gly Gly Thr Ala Tyr Thr Gly Gly Thr Thr
305                 310                 315                 320

Tyr Gly Ala Tyr Cys Cys Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg
                325                 330                 335

Gly Gly Asn Ala Cys Asn Met Thr Asn Gly Thr Asn Ala Cys Asn Gly
            340                 345                 350

Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys
        355                 360                 365

Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn
    370                 375                 380

Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr
385                 390                 395                 400

Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser
                405                 410                 415
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Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn
            420                 425                 430

Met Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala
        435                 440                 445

Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala
    450                 455                 460

Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn
465                 470                 475                 480

Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met
                485                 490                 495

Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala
            500                 505                 510

Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn
        515                 520                 525

Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met
    530                 535                 540

Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser
545                 550                 555                 560

Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn
                565                 570                 575

Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala
            580                 585                 590

Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly
        595                 600                 605

Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg
    610                 615                 620

Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly
625                 630                 635                 640

Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala
                645                 650                 655

Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn
            660                 665                 670

Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys
        675                 680                 685

Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys
    690                 695                 700
```

2415

Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr
705 710 715 720

Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys
725 730 735

Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr
740 745 750

Gly Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn
755 760 765

Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly
770 775 780

Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala
785 790 795 800

Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn
805 810 815

Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly
820 825 830

Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr
835 840 845

Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn
850 855 860

Ala Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys
865 870 875 880

Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr
885 890 895

Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn
900 905 910

Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys
915 920 925

Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly
930 935 940

Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr
945 950 955 960

Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly
965 970 975

Gly Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr
980 985 990

His Gly Ala Arg Ala Ala Arg Ala Cys Asn Ala Thr His Trp Ser Asn
995 1000 1005

Ala Ala Arg Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Ala Arg
1010 1015 1020

Cys Cys Asn Met Gly Asn Gly Ala Arg Cys Cys Asn Cys Ala Arg
1025 1030 1035

Gly Thr Asn Thr Ala Tyr Ala Cys Asn Met Thr Asn Cys Cys Asn
1040 1045 1050

Cys Cys Asn Trp Ser Asn Met Gly Asn Gly Ala Arg Gly Ala Arg
1055 1060 1065

Ala Thr Gly Ala Cys Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg
1070 1075 1080

Gly Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr Gly Tyr
1085 1090 1095

Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Gly Asn Thr Thr Tyr
1100 1105 1110

Thr Ala Tyr Cys Cys Asn Trp Ser Asn Gly Ala Tyr Ala Thr His
1115 1120 1125

Gly Cys Asn Gly Thr Asn Gly Ala Arg Thr Gly Gly Gly Ala Arg
1130 1135 1140

Trp Ser Asn Ala Ala Tyr Gly Gly Asn Cys Ala Arg Cys Cys Asn
1145 1150 1155

Gly Ala Arg Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr Ala Ala Arg
1160 1165 1170

Ala Cys Asn Ala Cys Asn Cys Cys Asn Cys Cys Asn Ala Thr Gly
1175 1180 1185

Met Thr Asn Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Gly Asn
1190 1195 1200

Trp Ser Asn Thr Thr Tyr Thr Thr Tyr Met Thr Asn Thr Ala Tyr
1205 1210 1215

Trp Ser Asn Ala Ala Arg Met Thr Asn Ala Cys Asn Gly Thr Asn
1220 1225 1230

Gly Ala Tyr Ala Ala Arg Trp Ser Asn Met Gly Asn Thr Gly Gly
1235 1240 1245

Cys Ala Arg Cys Ala Arg Gly Gly Asn Ala Ala Tyr Gly Thr Asn
1250 1255 1260

2417

```
Thr Thr  Tyr Trp Ser Asn Thr  Gly Tyr Trp Ser Asn  Gly Thr Asn
    1265                 1270                 1275

Ala Thr  Gly Cys Ala Tyr Gly  Ala Arg Gly Cys Asn  Met Thr Asn
    1280                 1285                 1290

Cys Ala  Tyr Ala Ala Tyr Cys  Ala Tyr Thr Ala Tyr  Ala Cys Asn
    1295                 1300                 1305

Cys Ala  Arg Ala Ala Arg Trp  Ser Asn Met Thr Asn  Trp Ser Asn
    1310                 1315                 1320

Met Thr  Asn Trp Ser Asn Cys  Cys Asn Gly Gly Asn  Ala Ala Arg
    1325                 1330                 1335
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<210> 603
<211> 1338
<212> PRT
<213> Homo Sapiens

<400> 603

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Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Cys Ala Arg Cys
1               5                  10                  15

Ala Arg Thr Gly Gly Gly Gly Asn Gly Cys Asn Gly Gly Asn Met Thr
            20                  25                  30

Asn Met Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Gly Ala Arg
        35                  40                  45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr
    50                  55                  60

Gly Tyr Gly Cys Asn Gly Thr Asn Thr Ala Tyr Gly Gly Asn Gly Gly
65                  70                  75                  80

Asn Trp Ser Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Ala Tyr
                85                  90                  95

Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr Gly Gly Ala Thr His Met
            100                 105                 110

Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
        115                 120                 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr His
    130                 135                 140

Gly Gly Asn Gly Ala Arg Ala Thr His Ala Ala Tyr Cys Ala Tyr Trp
145                 150                 155                 160
```

Ser Asn Gly Gly Asn Trp Ser Asn Ala Cys Asn Ala Ala Tyr Thr Ala
165 170 175

Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn Met Thr Asn Ala Ala Arg
180 185 190

Trp Ser Asn Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr His Trp
195 200 205

Ser Asn Gly Thr Asn Gly Ala Tyr Ala Cys Asn Trp Ser Asn Ala Ala
210 215 220

Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Met Thr Asn
225 230 235 240

Ala Ala Arg Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Ala
245 250 255

Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala Tyr Ala Cys Asn Gly Cys
260 265 270

Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn
275 280 285

Met Gly Asn Gly Gly Asn Gly Gly Asn Thr Ala Tyr Trp Ser Asn Trp
290 295 300

Ser Asn Trp Ser Asn Thr Gly Gly Thr Thr Tyr Thr Gly Gly Thr Thr
305 310 315 320

Tyr Gly Ala Tyr Cys Cys Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg
325 330 335

Gly Gly Asn Ala Cys Asn Met Thr Asn Gly Thr Asn Ala Cys Asn Gly
340 345 350

Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys
355 360 365

Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn
370 375 380

Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr
385 390 395 400

Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser
405 410 415

Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn
420 425 430

Met Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala
435 440 445

2419

```
Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala
    450                 455                 460

Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn
465                 470                 475                 480

Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met
                485                 490                 495

Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala
            500                 505                 510

Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn
        515                 520                 525

Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met
    530                 535                 540

Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser
545                 550                 555                 560

Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn
                565                 570                 575

Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala
            580                 585                 590

Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly
        595                 600                 605

Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg
    610                 615                 620

Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly
625                 630                 635                 640

Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala
                645                 650                 655

Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn
            660                 665                 670

Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys
        675                 680                 685

Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys
    690                 695                 700

Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr
705                 710                 715                 720

Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys
                725                 730                 735
```

```
Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr
            740                 745                 750

Gly Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn
        755                 760                 765

Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly
    770                 775                 780

Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala
785                 790                 795                 800

Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn
                805                 810                 815

Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly
            820                 825                 830

Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr
        835                 840                 845

Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn
    850                 855                 860

Ala Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys
865                 870                 875                 880

Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr
                885                 890                 895

Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn
            900                 905                 910

Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys
        915                 920                 925

Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly
    930                 935                 940

Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr
945                 950                 955                 960

Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly
                965                 970                 975

Gly Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr
            980                 985                 990

His Gly Ala Arg Ala Ala Arg Ala  Cys Asn Ala Thr His  Trp Ser Asn
        995                 1000                1005

Ala Ala  Arg Ala Cys Asn Ala  Ala Arg Gly Gly Asn  Cys Ala Arg
    1010                1015                1020
```

Cys Cys Asn Met Gly Asn Gly Ala Arg Cys Cys Asn Cys Ala Arg
1025 1030 1035

Gly Thr Asn Thr Ala Tyr Ala Cys Asn Met Thr Asn Cys Cys Asn
1040 1045 1050

Cys Cys Asn Trp Ser Asn Met Gly Asn Gly Ala Arg Gly Ala Arg
1055 1060 1065

Ala Thr Gly Ala Cys Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg
1070 1075 1080

Gly Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr Gly Tyr
1085 1090 1095

Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Gly Asn Thr Thr Tyr
1100 1105 1110

Thr Ala Tyr Cys Cys Asn Trp Ser Asn Gly Ala Tyr Ala Thr His
1115 1120 1125

Gly Cys Asn Gly Thr Asn Gly Ala Arg Thr Gly Gly Gly Ala Arg
1130 1135 1140

Trp Ser Asn Ala Ala Tyr Gly Gly Asn Cys Ala Arg Cys Cys Asn
1145 1150 1155

Gly Ala Arg Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr Ala Ala Arg
1160 1165 1170

Ala Cys Asn Ala Cys Asn Cys Cys Asn Cys Cys Asn Ala Thr Gly
1175 1180 1185

Met Thr Asn Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Gly Asn
1190 1195 1200

Trp Ser Asn Thr Thr Tyr Thr Thr Tyr Met Thr Asn Thr Ala Tyr
1205 1210 1215

Trp Ser Asn Ala Ala Arg Met Thr Asn Ala Cys Asn Gly Thr Asn
1220 1225 1230

Gly Ala Tyr Ala Ala Arg Trp Ser Asn Met Gly Asn Thr Gly Gly
1235 1240 1245

Cys Ala Arg Cys Ala Arg Gly Gly Asn Ala Ala Tyr Gly Thr Asn
1250 1255 1260

Thr Thr Tyr Trp Ser Asn Thr Gly Tyr Trp Ser Asn Gly Thr Asn
1265 1270 1275

Ala Thr Gly Cys Ala Tyr Gly Ala Arg Gly Cys Asn Met Thr Asn
1280 1285 1290

2422

Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr Thr Ala Tyr Ala Cys Asn
1295 1300 1305

Cys Ala Arg Ala Ala Arg Trp Ser Asn Met Thr Asn Trp Ser Asn
1310 1315 1320

Met Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn Ala Ala Arg
1325 1330 1335

<210> 604
<211> 1347
<212> PRT
<213> Homo Sapiens

<400> 604

Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Met Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Gly Ala Arg
35 40 45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr
50 55 60

Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr Gly Gly Ala Thr His Met
100 105 110

Gly Asn Cys Ala Arg Cys Cys Asn Gly Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr His
130 135 140

Gly Gly Asn Met Gly Asn Ala Thr His Thr Ala Tyr Ala Cys Asn Trp
145 150 155 160

Ser Asn Gly Gly Asn Ala Cys Asn Ala Cys Asn Ala Ala Tyr Thr Ala
165 170 175

Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn Met Thr Asn Ala Ala Arg
180 185 190

2423

```
Trp Ser Asn Met Gly Asn Gly Thr Asn Ala Cys Asn Ala Thr Gly Trp
        195                 200                 205

Ser Asn Gly Thr Asn Gly Ala Tyr Ala Cys Asn Trp Ser Asn Ala Ala
    210                 215                 220

Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Met Thr Asn
225                 230                 235                 240

Ala Ala Arg Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Ala
                245                 250                 255

Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala Tyr Ala Cys Asn Gly Cys
            260                 265                 270

Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn
        275                 280                 285

Met Gly Asn Gly Ala Tyr Gly Gly Asn Thr Ala Tyr Trp Ser Asn Thr
    290                 295                 300

Ala Tyr Gly Gly Asn Cys Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala
305                 310                 315                 320

Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn
                325                 330                 335

Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Ala
            340                 345                 350

Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser
        355                 360                 365

Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn
    370                 375                 380

Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met
385                 390                 395                 400

Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly
                405                 410                 415

Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn
            420                 425                 430

Ala Cys Asn Gly Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr
        435                 440                 445

Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala
    450                 455                 460

Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn
465                 470                 475                 480
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2424

Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp
485 490 495

Ser Asn Gly Gly Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser
500 505 510

Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr
515 520 525

Cys Cys Asn Gly Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp
530 535 540

Ser Asn Trp Ser Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser
545 550 555 560

Asn Met Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn
565 570 575

Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala
580 585 590

Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys
595 600 605

Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn
610 615 620

Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala
625 630 635 640

Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala
645 650 655

Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg
660 665 670

Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys
675 680 685

Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys
690 695 700

Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn
705 710 715 720

Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys
725 730 735

Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala
740 745 750

Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn
755 760 765

1428

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Met Gly Asn Ala Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala
    770                 775                 780

Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala
785                 790                 795                 800

Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr
                805                 810                 815

Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala
            820                 825                 830

Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly
        835                 840                 845

Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr
    850                 855                 860

Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met
865                 870                 875                 880

Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala
                885                 890                 895

Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn
            900                 905                 910

Gly Thr Asn Trp Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly
        915                 920                 925

Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly
    930                 935                 940

Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg
945                 950                 955                 960

Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp
                965                 970                 975

Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys Cys
            980                 985                 990

Asn Gly Cys Asn Cys Cys Asn Ala  Thr His Gly Ala Arg  Ala Ala Arg
        995                 1000                1005

Ala Cys  Asn Ala Thr His Trp  Ser Asn Ala Ala Arg  Ala Cys Asn
    1010                1015                1020

Ala Ala  Arg Gly Gly Asn Cys  Ala Arg Cys Cys Asn  Met Gly Asn
    1025                1030                1035

Gly Ala  Arg Cys Cys Asn Cys  Ala Arg Gly Thr Asn  Thr Ala Tyr
    1040                1045                1050
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2426

Ala Cys Asn Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn
1055 1060 1065

Met Gly Asn Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn
1070 1075 1080

Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn
1085 1090 1095

Met Thr Asn Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn
1100 1105 1110

Ala Ala Arg Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn
1115 1120 1125

Trp Ser Asn Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn
1130 1135 1140

Gly Ala Arg Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr
1145 1150 1155

Gly Gly Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr
1160 1165 1170

Ala Ala Tyr Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn
1175 1180 1185

Cys Cys Asn Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr
1190 1195 1200

Trp Ser Asn Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr
1205 1210 1215

Thr Thr Tyr Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg
1220 1225 1230

Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg
1235 1240 1245

Trp Ser Asn Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg
1250 1255 1260

Gly Gly Asn Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn
1265 1270 1275

Thr Gly Tyr Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr
1280 1285 1290

Gly Ala Arg Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr
1295 1300 1305

Cys Ala Tyr Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg
1310 1315 1320

2427

Trp Ser Asn Met Thr Asn Trp Ser Asn Met Thr Asn Trp Ser Asn
1325 1330 1335

Cys Cys Asn Gly Gly Asn Ala Ala Arg
1340 1345

<210> 605
<211> 1356
<212> PRT
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<400> 605

Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Met Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Gly Ala Arg
35 40 45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr
50 55 60

Gly Tyr Ala Cys Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Gly Asn
85 90 95

Gly Gly Asn Trp Ser Asn Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Met Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Thr
145 150 155 160

Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Ala Cys
165 170 175

Asn Ala Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
180 185 190

Met Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Ala
195 200 205

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Cys Asn Ala Thr His Trp Ser Asn Ala Thr His Gly Thr Asn Ala Cys
    210                 215                 220

Asn Trp Ser Asn Met Gly Asn Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225                 230                 235                 240

Trp Ser Asn Met Thr Asn Ala Ala Arg Met Thr Asn Trp Ser Asn Trp
                245                 250                 255

Ser Asn Gly Thr Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Gly Ala
            260                 265                 270

Tyr Ala Cys Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Trp Ser Asn Gly Cys Asn Met
    290                 295                 300

Thr Asn Met Gly Asn Thr Ala Tyr Thr Thr Tyr Gly Ala Tyr Thr Gly
305                 310                 315                 320

Gly Met Thr Asn Thr Thr Tyr Trp Ser Asn Gly Ala Tyr Gly Thr Asn
                325                 330                 335

Trp Ser Asn Gly Ala Tyr Ala Thr His Thr Gly Gly Gly Gly Asn Cys
            340                 345                 350

Ala Arg Gly Gly Asn Ala Cys Asn Ala Thr Gly Gly Thr Asn Ala Cys
        355                 360                 365

Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn
    370                 375                 380

Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly
385                 390                 395                 400

Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys
                405                 410                 415

Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn
            420                 425                 430

Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly
        435                 440                 445

Cys Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr
    450                 455                 460

Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn
465                 470                 475                 480

Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp
                485                 490                 495
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2429

Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys
500 505 510

Asn Met Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn
515 520 525

Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly
530 535 540

Thr Asn Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly
545 550 555 560

Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn
565 570 575

Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys
580 585 590

Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly
595 600 605

Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn
610 615 620

Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala
625 630 635 640

Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala
645 650 655

Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn
660 665 670

Gly Ala Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly
675 680 685

Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly
690 695 700

Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn
705 710 715 720

Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr
725 730 735

Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala
740 745 750

Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn
755 760 765

Ala Thr Gly Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys
770 775 780

2430.

Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr
785 790 795 800

Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn
805 810 815

Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly
820 825 830

Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala
835 840 845

Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg
850 855 860

Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala
865 870 875 880

Cys Asn Ala Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala
885 890 895

Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn
900 905 910

Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly
915 920 925

Thr Asn Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala
930 935 940

Tyr Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr
945 950 955 960

Gly Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr
965 970 975

Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala
980 985 990

Arg Gly Gly Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn
995 1000 1005

Ala Thr His Gly Ala Arg Ala Ala Arg Ala Cys Asn Ala Thr His
1010 1015 1020

Trp Ser Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg Gly Gly Asn
1025 1030 1035

Cys Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Cys Cys Asn
1040 1045 1050

Cys Ala Arg Gly Thr Asn Thr Ala Tyr Ala Cys Asn Met Thr Asn
1055 1060 1065

Cys Cys Asn Cys Cys Asn Trp Ser Asn Met Gly Asn Gly Ala Arg
1070 1075 1080

Gly Ala Arg Ala Thr Gly Ala Cys Asn Ala Ala Arg Ala Ala Tyr
1085 1090 1095

Cys Ala Arg Gly Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn
1100 1105 1110

Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Gly Asn
1115 1120 1125

Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Trp Ser Asn Gly Ala Tyr
1130 1135 1140

Ala Thr His Gly Cys Asn Gly Thr Asn Gly Ala Arg Thr Gly Gly
1145 1150 1155

Gly Ala Arg Trp Ser Asn Ala Ala Tyr Gly Gly Asn Cys Ala Arg
1160 1165 1170

Cys Cys Asn Gly Ala Arg Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr
1175 1180 1185

Ala Ala Arg Ala Cys Asn Ala Cys Asn Cys Cys Asn Cys Cys Asn
1190 1195 1200

Ala Thr Gly Met Thr Asn Gly Ala Tyr Trp Ser Asn Gly Ala Tyr
1205 1210 1215

Gly Gly Asn Trp Ser Asn Thr Thr Tyr Thr Thr Tyr Met Thr Asn
1220 1225 1230

Thr Ala Tyr Trp Ser Asn Ala Ala Arg Met Thr Asn Ala Cys Asn
1235 1240 1245

Gly Thr Asn Gly Ala Tyr Ala Ala Arg Trp Ser Asn Met Gly Asn
1250 1255 1260

Thr Gly Gly Cys Ala Arg Cys Ala Arg Gly Gly Asn Ala Ala Tyr
1265 1270 1275

Gly Thr Asn Thr Thr Tyr Trp Ser Asn Thr Gly Tyr Trp Ser Asn
1280 1285 1290

Gly Thr Asn Ala Thr Gly Cys Ala Tyr Gly Ala Arg Gly Cys Asn
1295 1300 1305

Met Thr Asn Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr Thr Ala Tyr
1310 1315 1320

Ala Cys Asn Cys Ala Arg Ala Ala Arg Trp Ser Asn Met Thr Asn
1325 1330 1335

2432

Trp Ser Asn Met Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn
1340 1345 1350

Ala Ala Arg
1355

<210> 606
<211> 1338
<212> PRT
<213> Homo Sapiens

<400> 606

Gly Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Met Thr
20 25 30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Ala Arg
35 40 45

Trp Ser Asn Met Thr Asn Ala Ala Arg Ala Thr His Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Gly Asn Trp Ser Asn Gly Gly Asn Thr Ala
65 70 75 80

Tyr Met Gly Asn Thr Thr Tyr Ala Cys Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Ala Thr Gly Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
130 135 140

Gly Gly Asn Ala Thr His Ala Thr His Thr Ala Tyr Cys Cys Asn Gly
145 150 155 160

Ala Tyr Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Ala Cys Asn Met Gly
165 170 175

Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn Thr Thr Tyr
180 185 190

Cys Ala Arg Gly Gly Asn Cys Ala Arg Gly Thr Asn Ala Cys Asn Ala
195 200 205

Thr His Trp Ser Asn Gly Cys Asn Gly Ala Tyr Ala Ala Arg Trp Ser
210 215 220

Asn Ala Thr His Trp Ser Asn Ala Cys Asn Gly Cys Asn Thr Ala Tyr
225 230 235 240

Met Thr Asn Cys Ala Arg Thr Gly Gly Trp Ser Asn Trp Ser Asn Met
245 250 255

Thr Asn Ala Ala Arg Gly Cys Asn Trp Ser Asn Gly Ala Tyr Ala Cys
260 265 270

Asn Gly Cys Asn Ala Thr Gly Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Cys Ala Arg Ala Ala Arg Trp Ser Asn Thr
290 295 300

Ala Tyr Gly Gly Asn Thr Ala Tyr Trp Ser Asn Thr Ala Tyr Thr Thr
305 310 315 320

Tyr Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg
325 330 335

Gly Gly Asn Ala Cys Asn Met Thr Asn Gly Thr Asn Ala Cys Asn Gly
340 345 350

Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys
355 360 365

Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn
370 375 380

Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr
385 390 395 400

Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser
405 410 415

Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn
420 425 430

Met Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala
435 440 445

Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala
450 455 460

Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn
465 470 475 480

Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met
485 490 495

Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala
500 505 510

Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn
515 520 525

Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met
530 535 540

Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser
545 550 555 560

Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn
565 570 575

Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala
580 585 590

Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly
595 600 605

Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg
610 615 620

Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly
625 630 635 640

Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala
645 650 655

Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn
660 665 670

Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys
675 680 685

Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys
690 695 700

Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr
705 710 715 720

Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys
725 730 735

Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr
740 745 750

Gly Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn
755 760 765

Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly
770 775 780

Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala
785 790 795 800

Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn
805 810 815

Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly
820 825 830

Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr
835 840 845

Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn
850 855 860

Ala Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys
865 870 875 880

Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr
885 890 895

Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn
900 905 910

Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys
915 920 925

Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly
930 935 940

Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr
945 950 955 960

Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly
965 970 975

Gly Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr
980 985 990

His Gly Ala Arg Ala Ala Arg Ala Cys Asn Ala Thr His Trp Ser Asn
995 1000 1005

Ala Ala Arg Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Ala Arg
1010 1015 1020

Cys Cys Asn Met Gly Asn Gly Ala Arg Cys Cys Asn Cys Ala Arg
1025 1030 1035

Gly Thr Asn Thr Ala Tyr Ala Cys Asn Met Thr Asn Cys Cys Asn
1040 1045 1050

Cys Cys Asn Trp Ser Asn Met Gly Asn Gly Ala Arg Gly Ala Arg
1055 1060 1065

Ala Thr Gly Ala Cys Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg
1070 1075 1080

Gly Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr Gly Tyr
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Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Gly Asn Thr Thr Tyr
1100 1105 1110

Thr Ala Tyr Cys Cys Asn Trp Ser Asn Gly Ala Tyr Ala Thr His
1115 1120 1125

Gly Cys Asn Gly Thr Asn Gly Ala Arg Thr Gly Gly Gly Ala Arg
1130 1135 1140

Trp Ser Asn Ala Ala Tyr Gly Gly Asn Cys Ala Arg Cys Cys Asn
1145 1150 1155

Gly Ala Arg Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr Ala Ala Arg
1160 1165 1170

Ala Cys Asn Ala Cys Asn Cys Cys Asn Cys Cys Asn Ala Thr Gly
1175 1180 1185

Met Thr Asn Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Gly Asn
1190 1195 1200

Trp Ser Asn Thr Thr Tyr Thr Thr Tyr Met Thr Asn Thr Ala Tyr
1205 1210 1215

Trp Ser Asn Ala Ala Arg Met Thr Asn Ala Cys Asn Gly Thr Asn
1220 1225 1230

Gly Ala Tyr Ala Ala Arg Trp Ser Asn Met Gly Asn Thr Gly Gly
1235 1240 1245

Cys Ala Arg Cys Ala Arg Gly Gly Asn Ala Ala Tyr Gly Thr Asn
1250 1255 1260

Thr Thr Tyr Trp Ser Asn Thr Gly Tyr Trp Ser Asn Gly Thr Asn
1265 1270 1275

Ala Thr Gly Cys Ala Tyr Gly Ala Arg Gly Cys Asn Met Thr Asn
1280 1285 1290

Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr Thr Ala Tyr Ala Cys Asn
1295 1300 1305

Cys Ala Arg Ala Ala Arg Trp Ser Asn Met Thr Asn Trp Ser Asn
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Met Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn Ala Ala Arg
1325 1330 1335

<210> 607
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<400> 607

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1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
20 25 30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Ala Arg
35 40 45

Trp Ser Asn Met Thr Asn Ala Ala Arg Ala Thr His Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Gly Asn Trp Ser Asn Gly Gly Asn Thr Ala
65 70 75 80

Tyr Trp Ser Asn Thr Thr Tyr Ala Cys Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Ala Thr Gly Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
130 135 140

Gly Gly Asn Ala Thr His Ala Thr His Thr Ala Tyr Cys Cys Asn Gly
145 150 155 160

Ala Tyr Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Cys Asn Met Gly
165 170 175

Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn Thr Thr Tyr
180 185 190

Cys Ala Arg Gly Gly Asn Cys Ala Arg Gly Thr Asn Ala Cys Asn Ala
195 200 205

Thr His Trp Ser Asn Gly Cys Asn Gly Ala Tyr Ala Ala Arg Trp Ser
210 215 220

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Asn Ala Thr His Ala Ala Tyr Ala Cys Asn Gly Cys Asn Thr Ala Tyr
225                 230                 235                 240

Met Thr Asn Cys Ala Arg Thr Gly Gly Trp Ser Asn Trp Ser Asn Met
                245                 250                 255

Thr Asn Ala Ala Arg Gly Cys Asn Trp Ser Asn Gly Ala Tyr Ala Cys
            260                 265                 270

Asn Gly Cys Asn Ala Thr Gly Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Met Gly Asn Cys Ala Arg Gly Gly Asn Thr Ala Tyr Gly
    290                 295                 300

Gly Asn Trp Ser Asn Gly Gly Asn Thr Gly Gly Gly Gly Asn Thr Ala
305                 310                 315                 320

Tyr Thr Thr Tyr Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn
                325                 330                 335

Cys Ala Arg Gly Gly Asn Ala Cys Asn Met Thr Asn Gly Thr Asn Ala
            340                 345                 350

Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser
        355                 360                 365

Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn
    370                 375                 380

Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys
385                 390                 395                 400

Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys
                405                 410                 415

Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn
            420                 425                 430

Gly Cys Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly
        435                 440                 445

Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys
    450                 455                 460

Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn
465                 470                 475                 480

Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly
                485                 490                 495

Cys Asn Met Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr
            500                 505                 510
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Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn
        515                 520                 525

Gly Thr Asn Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly
    530                 535                 540

Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser
545                 550                 555                 560

Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn
                565                 570                 575

Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly
            580                 585                 590

Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys
        595                 600                 605

Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr
    610                 615                 620

Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala
625                 630                 635                 640

Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr
                645                 650                 655

Asn Gly Ala Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr
            660                 665                 670

Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr
        675                 680                 685

Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr
    690                 695                 700

Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn
705                 710                 715                 720

Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala
                725                 730                 735

Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr
            740                 745                 750

Asn Ala Thr Gly Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn
        755                 760                 765

Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly
    770                 775                 780

Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser
785                 790                 795                 800
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Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg
                805                 810                 815

Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr
            820                 825                 830

Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala
        835                 840                 845

Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg
    850                 855                 860

Ala Cys Asn Ala Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly
865                 870                 875                 880

Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys
                885                 890                 895

Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn
            900                 905                 910

Gly Thr Asn Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys
        915                 920                 925

Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala
    930                 935                 940

Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg
945                 950                 955                 960

Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala
                965                 970                 975

Ala Arg Gly Gly Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys
            980                 985                 990

Asn Ala Thr His Gly Ala Arg Ala  Ala Arg Ala Cys Asn  Ala Thr His
        995                 1000                1005

Trp Ser  Asn Ala Ala Arg Ala  Cys Asn Ala Ala Arg  Gly Gly Asn
    1010                1015                1020

Cys Ala  Arg Cys Cys Asn Met  Gly Asn Gly Ala Arg  Cys Cys Asn
    1025                1030                1035

Cys Ala  Arg Gly Thr Asn Thr  Ala Tyr Ala Cys Asn  Met Thr Asn
    1040                1045                1050

Cys Cys  Asn Cys Cys Asn Trp  Ser Asn Met Gly Asn  Gly Ala Arg
    1055                1060                1065

Gly Ala  Arg Ala Thr Gly Ala  Cys Asn Ala Ala Arg  Ala Ala Tyr
    1070                1075                1080
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Cys Ala  Arg Gly Thr Asn Trp  Ser Asn Met Thr Asn  Ala Cys Asn
    1085                1090                1095

Thr Gly  Tyr Met Thr Asn Gly  Thr Asn Ala Ala Arg  Gly Gly Asn
    1100                1105                1110

Thr Thr  Tyr Thr Ala Tyr Cys  Cys Asn Trp Ser Asn  Gly Ala Tyr
    1115                1120                1125

Ala Thr  His Gly Cys Asn Gly  Thr Asn Gly Ala Arg  Thr Gly Gly
    1130                1135                1140

Gly Ala  Arg Trp Ser Asn Ala  Ala Tyr Gly Gly Asn  Cys Ala Arg
    1145                1150                1155

Cys Cys  Asn Gly Ala Arg Ala  Ala Tyr Ala Ala Tyr  Thr Ala Tyr
    1160                1165                1170

Ala Ala  Arg Ala Cys Asn Ala  Cys Asn Cys Cys Asn  Cys Cys Asn
    1175                1180                1185

Ala Thr  Gly Met Thr Asn Gly  Ala Tyr Trp Ser Asn  Gly Ala Tyr
    1190                1195                1200

Gly Gly  Asn Trp Ser Asn Thr  Thr Tyr Thr Thr Tyr  Met Thr Asn
    1205                1210                1215

Thr Ala  Tyr Trp Ser Asn Ala  Ala Arg Met Thr Asn  Ala Cys Asn
    1220                1225                1230

Gly Thr  Asn Gly Ala Tyr Ala  Ala Arg Trp Ser Asn  Met Gly Asn
    1235                1240                1245

Thr Gly  Gly Cys Ala Arg Cys  Ala Arg Gly Gly Asn  Ala Ala Tyr
    1250                1255                1260

Gly Thr  Asn Thr Thr Tyr Trp  Ser Asn Thr Gly Tyr  Trp Ser Asn
    1265                1270                1275

Gly Thr  Asn Ala Thr Gly Cys  Ala Tyr Gly Ala Arg  Gly Cys Asn
    1280                1285                1290

Met Thr  Asn Cys Ala Tyr Ala  Ala Tyr Cys Ala Tyr  Thr Ala Tyr
    1295                1300                1305

Ala Cys  Asn Cys Ala Arg Ala  Ala Arg Trp Ser Asn  Met Thr Asn
    1310                1315                1320

Trp Ser  Asn Met Thr Asn Trp  Ser Asn Cys Cys Asn  Gly Gly Asn
    1325                1330                1335

Ala Ala  Arg
    1340
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9442

<210> 608
<211> 1359
<212> PRT
<213> Homo Sapiens

<400> 608

Gly Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
20 25 30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Ala Arg
35 40 45

Trp Ser Asn Met Thr Asn Ala Ala Arg Ala Thr His Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Gly Asn Trp Ser Asn Gly Gly Asn Thr Ala
65 70 75 80

Tyr Trp Ser Asn Thr Thr Tyr Ala Cys Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Ala Thr Gly Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Met Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
130 135 140

Gly Gly Asn Ala Thr His Ala Thr His Thr Ala Tyr Cys Cys Asn Gly
145 150 155 160

Gly Asn Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Ala Thr His Met Gly
165 170 175

Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn Thr Thr Tyr
180 185 190

Cys Ala Arg Gly Gly Asn Cys Ala Arg Gly Thr Asn Ala Cys Asn Ala
195 200 205

Thr His Trp Ser Asn Gly Cys Asn Gly Ala Tyr Ala Ala Arg Trp Ser
210 215 220

Asn Ala Thr His Trp Ser Asn Ala Cys Asn Gly Cys Asn Thr Ala Tyr
225 230 235 240

Met Thr Asn Cys Ala Arg Thr Gly Gly Trp Ser Asn Trp Ser Asn Met
245 250 255

Thr Asn Ala Ala Arg Gly Cys Asn Trp Ser Asn Gly Ala Tyr Ala Cys
260 265 270

Asn Gly Cys Asn Ala Thr Gly Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Cys Ala Arg Gly Gly Asn Met Thr Asn Gly
290 295 300

Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Ala Cys Asn Trp Ser
305 310 315 320

Asn Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr
325 330 335

Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr Gly Gly Gly
340 345 350

Gly Asn Cys Ala Arg Gly Gly Asn Ala Cys Asn Ala Cys Asn Gly Thr
355 360 365

Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn
370 375 380

Trp Ser Asn Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp
385 390 395 400

Ser Asn Gly Thr Asn Thr Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys
405 410 415

Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn
420 425 430

Ala Cys Asn Trp Ser Asn Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly
435 440 445

Cys Asn Gly Cys Asn Met Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr
450 455 460

Asn Gly Thr Asn Ala Ala Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr
465 470 475 480

Cys Cys Asn Gly Ala Arg Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly
485 490 495

Thr Asn Trp Ser Asn Thr Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly
500 505 510

Asn Gly Cys Asn Met Thr Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn
515 520 525

Gly Thr Asn Cys Ala Tyr Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly
530 535 540

Cys Asn Gly Thr Asn Met Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser
545 550 555 560

Asn Gly Gly Asn Met Thr Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn
565 570 575

Trp Ser Asn Trp Ser Asn Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly
580 585 590

Thr Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr
595 600 605

Tyr Gly Gly Asn Ala Cys Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr
610 615 620

Ala Cys Asn Thr Gly Tyr Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys
625 630 635 640

Ala Tyr Ala Ala Arg Cys Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys
645 650 655

Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn
660 665 670

Gly Thr Asn Gly Ala Arg Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr
675 680 685

Gly Tyr Gly Thr Asn Gly Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys
690 695 700

Asn Thr Gly Tyr Cys Cys Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn
705 710 715 720

Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly
725 730 735

Thr Asn Thr Thr Tyr Met Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys
740 745 750

Asn Ala Ala Arg Cys Cys Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn
755 760 765

Met Thr Asn Ala Thr Gly Ala Thr His Trp Ser Asn Met Gly Asn Ala
770 775 780

Cys Asn Cys Cys Asn Gly Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly
785 790 795 800

Tyr Gly Thr Asn Gly Thr Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn
805 810 815

J44S

Trp Ser Asn Cys Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly
820 825 830

Ala Arg Gly Thr Asn Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly
835 840 845

Gly Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn
850 855 860

Gly Ala Arg Gly Thr Asn Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala
865 870 875 880

Ala Arg Ala Cys Asn Ala Ala Arg Cys Cys Asn Met Gly Asn Gly Ala
885 890 895

Arg Gly Ala Arg Cys Ala Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn
900 905 910

Ala Cys Asn Thr Thr Tyr Met Gly Asn Gly Thr Asn Gly Thr Asn Trp
915 920 925

Ser Asn Gly Thr Asn Met Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr
930 935 940

Asn Cys Ala Tyr Cys Ala Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn
945 950 955 960

Ala Ala Tyr Gly Gly Asn Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala
965 970 975

Ala Arg Thr Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala
980 985 990

Tyr Ala Ala Arg Gly Gly Asn Met Thr Asn Cys Cys Asn Gly Cys Asn
995 1000 1005

Cys Cys Asn Ala Thr His Gly Ala Arg Ala Ala Arg Ala Cys Asn
1010 1015 1020

Ala Thr His Trp Ser Asn Ala Ala Arg Ala Cys Asn Ala Ala Arg
1025 1030 1035

Gly Gly Asn Cys Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg
1040 1045 1050

Cys Cys Asn Cys Ala Arg Gly Thr Asn Thr Ala Tyr Ala Cys Asn
1055 1060 1065

Met Thr Asn Cys Cys Asn Cys Cys Asn Trp Ser Asn Met Gly Asn
1070 1075 1080

Gly Ala Arg Gly Ala Arg Ala Thr Gly Ala Cys Asn Ala Ala Arg
1085 1090 1095

2446

Ala Ala Tyr Cys Ala Arg Gly Thr Asn Trp Ser Asn Met Thr Asn
1100 1105 1110

Ala Cys Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala Arg
1115 1120 1125

Gly Gly Asn Thr Thr Tyr Thr Ala Tyr Cys Cys Asn Trp Ser Asn
1130 1135 1140

Gly Ala Tyr Ala Thr His Gly Cys Asn Gly Thr Asn Gly Ala Arg
1145 1150 1155

Thr Gly Gly Gly Ala Arg Trp Ser Asn Ala Ala Tyr Gly Gly Asn
1160 1165 1170

Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr Ala Ala Tyr
1175 1180 1185

Thr Ala Tyr Ala Ala Arg Ala Cys Asn Ala Cys Asn Cys Cys Asn
1190 1195 1200

Cys Cys Asn Ala Thr Gly Met Thr Asn Gly Ala Tyr Trp Ser Asn
1205 1210 1215

Gly Ala Tyr Gly Gly Asn Trp Ser Asn Thr Thr Tyr Thr Thr Tyr
1220 1225 1230

Met Thr Asn Thr Ala Tyr Trp Ser Asn Ala Ala Arg Met Thr Asn
1235 1240 1245

Ala Cys Asn Gly Thr Asn Gly Ala Tyr Ala Ala Arg Trp Ser Asn
1250 1255 1260

Met Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg Gly Gly Asn
1265 1270 1275

Ala Ala Tyr Gly Thr Asn Thr Thr Tyr Trp Ser Asn Thr Gly Tyr
1280 1285 1290

Trp Ser Asn Gly Thr Asn Ala Thr Gly Cys Ala Tyr Gly Ala Arg
1295 1300 1305

Gly Cys Asn Met Thr Asn Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr
1310 1315 1320

Thr Ala Tyr Ala Cys Asn Cys Ala Arg Ala Ala Arg Trp Ser Asn
1325 1330 1335

Met Thr Asn Trp Ser Asn Met Thr Asn Trp Ser Asn Cys Cys Asn
1340 1345 1350

Gly Gly Asn Ala Ala Arg
1355

<210> 609
<211> 1353
<212> PRT
<213> Homo Sapiens

<400> 609

Cys Ala Arg Gly Thr Asn Cys Ala Arg Met Thr Asn Cys Ala Arg Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Met Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Ala Cys Asn Met Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Ala Thr His Trp Ser Asn Gly Gly Asn Gly Ala
65 70 75 80

Tyr Trp Ser Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Trp Ser Asn Gly Cys Asn Gly Cys Asn Thr Gly Gly Ala Ala Tyr Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Trp Ser Asn Cys Cys
115 120 125

Asn Trp Ser Asn Met Gly Asn Gly Gly Asn Met Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Met Thr Asn Gly Gly Asn Met Gly Asn Ala Cys Asn Thr
145 150 155 160

Ala Tyr Thr Gly Tyr Met Gly Asn Trp Ser Asn Ala Ala Arg Thr Gly
165 170 175

Gly Thr Ala Tyr Ala Ala Tyr Gly Ala Tyr Thr Ala Tyr Gly Cys Asn
180 185 190

Gly Thr Asn Trp Ser Asn Gly Thr Asn Ala Ala Arg Trp Ser Asn Met
195 200 205

Gly Asn Ala Thr His Ala Cys Asn Ala Thr His Ala Ala Tyr Cys Cys
210 215 220

Asn Gly Ala Tyr Ala Cys Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr
225 230 235 240

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Cys Ala Arg Thr Thr Tyr Trp Ser Asn Met Thr Asn Cys Ala Arg Met
                245                 250                 255

Thr Asn Ala Ala Tyr Trp Ser Asn Gly Thr Asn Ala Cys Asn Cys Cys
            260                 265                 270

Asn Gly Ala Arg Gly Ala Tyr Ala Cys Asn Gly Cys Asn Gly Thr Asn
        275                 280                 285

Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn Gly
    290                 295                 300

Ala Tyr Met Gly Asn Gly Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly
305                 310                 315                 320

Asn Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly
                325                 330                 335

Gly Ala Tyr Gly Thr Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly
            340                 345                 350

Gly Asn Ala Cys Asn Ala Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr
        355                 360                 365

Asn Trp Ser Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala Cys Asn
    370                 375                 380

Ala Ala Arg Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr
385                 390                 395                 400

Thr Tyr Cys Cys Asn Met Thr Asn Gly Cys Asn Cys Cys Asn Thr Gly
                405                 410                 415

Tyr Trp Ser Asn Met Gly Asn Trp Ser Asn Ala Cys Asn Trp Ser Asn
            420                 425                 430

Gly Ala Arg Trp Ser Asn Ala Cys Asn Gly Cys Asn Gly Cys Asn Met
        435                 440                 445

Thr Asn Gly Gly Asn Thr Gly Tyr Met Thr Asn Gly Thr Asn Ala Ala
    450                 455                 460

Arg Gly Ala Tyr Thr Ala Tyr Thr Thr Tyr Cys Cys Asn Gly Ala Arg
465                 470                 475                 480

Cys Cys Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Trp Ser Asn Thr
                485                 490                 495

Gly Gly Ala Ala Tyr Trp Ser Asn Gly Gly Asn Gly Cys Asn Met Thr
            500                 505                 510

Asn Ala Cys Asn Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Ala Tyr
        515                 520                 525
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Ala Cys Asn Thr Thr Tyr Cys Cys Asn Gly Cys Asn Gly Thr Asn Met
    530                 535                 540

Thr Asn Cys Ala Arg Trp Ser Asn Trp Ser Asn Gly Gly Asn Met Thr
545                 550                 555                 560

Asn Thr Ala Tyr Trp Ser Asn Met Thr Asn Trp Ser Asn Trp Ser Asn
                565                 570                 575

Gly Thr Asn Gly Thr Asn Ala Cys Asn Gly Thr Asn Cys Cys Asn Trp
            580                 585                 590

Ser Asn Trp Ser Asn Ala Ala Tyr Thr Thr Tyr Gly Gly Asn Ala Cys
        595                 600                 605

Asn Cys Ala Arg Ala Cys Asn Thr Ala Tyr Ala Cys Asn Thr Gly Tyr
    610                 615                 620

Ala Ala Tyr Gly Thr Asn Gly Ala Tyr Cys Ala Tyr Ala Ala Arg Cys
625                 630                 635                 640

Cys Asn Trp Ser Asn Ala Ala Tyr Ala Cys Asn Ala Ala Arg Gly Thr
                645                 650                 655

Asn Gly Ala Tyr Ala Ala Arg Ala Cys Asn Gly Thr Asn Gly Ala Arg
            660                 665                 670

Met Gly Asn Ala Ala Arg Thr Gly Tyr Thr Gly Tyr Gly Thr Asn Gly
        675                 680                 685

Ala Arg Thr Gly Tyr Cys Cys Asn Cys Cys Asn Thr Gly Tyr Cys Cys
    690                 695                 700

Asn Gly Cys Asn Cys Cys Asn Cys Cys Asn Gly Thr Asn Gly Cys Asn
705                 710                 715                 720

Gly Gly Asn Cys Cys Asn Trp Ser Asn Gly Thr Asn Thr Thr Tyr Met
                725                 730                 735

Thr Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn Ala Ala Arg Cys Cys
            740                 745                 750

Asn Ala Ala Arg Gly Ala Tyr Ala Cys Asn Met Thr Asn Ala Thr Gly
        755                 760                 765

Ala Thr His Trp Ser Asn Met Gly Asn Ala Cys Asn Cys Cys Asn Gly
    770                 775                 780

Ala Arg Gly Thr Asn Ala Cys Asn Thr Gly Tyr Gly Thr Asn Gly Thr
785                 790                 795                 800

Asn Gly Thr Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Cys Ala Tyr
                805                 810                 815
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Gly Ala Arg Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly Thr Asn Cys
820 825 830

Ala Arg Thr Thr Tyr Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Gly Thr
835 840 845

Asn Gly Ala Tyr Gly Gly Asn Gly Thr Asn Gly Ala Arg Gly Thr Asn
850 855 860

Cys Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Cys Asn Ala
865 870 875 880

Ala Arg Cys Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Arg Cys Ala
885 890 895

Arg Thr Thr Tyr Ala Ala Tyr Trp Ser Asn Ala Cys Asn Thr Thr Tyr
900 905 910

Met Gly Asn Gly Thr Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn Met
915 920 925

Thr Asn Ala Cys Asn Gly Thr Asn Gly Thr Asn Cys Ala Tyr Cys Ala
930 935 940

Arg Gly Ala Tyr Thr Gly Gly Met Thr Asn Ala Ala Tyr Gly Gly Asn
945 950 955 960

Ala Ala Arg Gly Ala Arg Thr Ala Tyr Ala Ala Arg Thr Gly Tyr Ala
965 970 975

Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Gly Gly
980 985 990

Asn Met Thr Asn Cys Cys Asn Gly Cys Asn Cys Cys Asn Ala Thr His
995 1000 1005

Gly Ala Arg Ala Ala Arg Ala Cys Asn Ala Thr His Trp Ser Asn
1010 1015 1020

Ala Ala Arg Ala Cys Asn Ala Ala Arg Gly Gly Asn Cys Ala Arg
1025 1030 1035

Cys Cys Asn Met Gly Asn Gly Ala Arg Cys Cys Asn Cys Ala Arg
1040 1045 1050

Gly Thr Asn Thr Ala Tyr Ala Cys Asn Met Thr Asn Cys Cys Asn
1055 1060 1065

Cys Cys Asn Trp Ser Asn Met Gly Asn Gly Ala Arg Gly Ala Arg
1070 1075 1080

Ala Thr Gly Ala Cys Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg
1085 1090 1095

Gly Thr Asn Trp Ser Asn Met Thr Asn Ala Cys Asn Thr Gly Tyr
1100 1105 1110

Met Thr Asn Gly Thr Asn Ala Ala Arg Gly Gly Asn Thr Thr Tyr
1115 1120 1125

Thr Ala Tyr Cys Cys Asn Trp Ser Asn Gly Ala Tyr Ala Thr His
1130 1135 1140

Gly Cys Asn Gly Thr Asn Gly Ala Arg Thr Gly Gly Gly Ala Arg
1145 1150 1155

Trp Ser Asn Ala Ala Tyr Gly Gly Asn Cys Ala Arg Cys Cys Asn
1160 1165 1170

Gly Ala Arg Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr Ala Ala Arg
1175 1180 1185

Ala Cys Asn Ala Cys Asn Cys Cys Asn Cys Cys Asn Ala Thr Gly
1190 1195 1200

Met Thr Asn Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Gly Asn
1205 1210 1215

Trp Ser Asn Thr Thr Tyr Thr Thr Tyr Met Thr Asn Thr Ala Tyr
1220 1225 1230

Trp Ser Asn Ala Ala Arg Met Thr Asn Ala Cys Asn Gly Thr Asn
1235 1240 1245

Gly Ala Tyr Ala Ala Arg Trp Ser Asn Met Gly Asn Thr Gly Gly
1250 1255 1260

Cys Ala Arg Cys Ala Arg Gly Gly Asn Ala Ala Tyr Gly Thr Asn
1265 1270 1275

Thr Thr Tyr Trp Ser Asn Thr Gly Tyr Trp Ser Asn Gly Thr Asn
1280 1285 1290

Ala Thr Gly Cys Ala Tyr Gly Ala Arg Gly Cys Asn Met Thr Asn
1295 1300 1305

Cys Ala Tyr Ala Ala Tyr Cys Ala Tyr Thr Ala Tyr Ala Cys Asn
1310 1315 1320

Cys Ala Arg Ala Ala Arg Trp Ser Asn Met Thr Asn Trp Ser Asn
1325 1330 1335

Met Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn Ala Ala Arg
1340 1345 1350

<210> 610
<211> 336

<212> PRT
<213> Homo Sapiens

<400> 610

Gly Ala Tyr Gly Thr Asn Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Tyr Thr Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Cys Cys Asn Gly Thr Asn Cys Ala Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr Met Gly Asn Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Tyr Thr Asn Gly Thr Asn Thr Ala Tyr Trp Ser Asn
85 90 95

Gly Ala Tyr Gly Gly Asn Ala Ala Tyr Cys Ala Asn Thr Ala Tyr Tyr
100 105 110

Thr Asn Ala Ala Tyr Thr Gly Gly Thr Thr Tyr Cys Ala Arg Cys Ala
115 120 125

Arg Met Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala Arg Trp Ser Asn
130 135 140

Cys Cys Asn Met Gly Asn Met Gly Asn Tyr Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Thr Gly
165 170 175

Gly Gly Ala Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
180 185 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Ala Ala Tyr Gly Gly Asn Trp
195 200 205

Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly Ala
210 215 220

Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Ala Ala Arg Ala Thr His
225 230 235 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
245 250 255

2482

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
260 265 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Trp Ser Asn
275 280 285

Cys Ala Asn Cys Ala Tyr Thr Gly Gly Cys Cys Asn Ala Thr His Cys
290 295 300

Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala
305 310 315 320

Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
325 330 335

<210> 611
<211> 336
<212> PRT
<213> Homo Sapiens

<400> 611

Gly Ala Tyr Gly Thr Asn Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Tyr Thr Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Cys Cys Asn Gly Thr Asn Cys Ala Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr Met Gly Asn Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Tyr Thr Asn Gly Thr Asn Thr Ala Tyr Trp Ser Asn
85 90 95

Gly Ala Tyr Gly Gly Asn Ala Ala Tyr Cys Ala Asn Thr Ala Tyr Tyr
100 105 110

Thr Asn Ala Ala Tyr Thr Gly Gly Thr Thr Tyr Cys Ala Arg Cys Ala
115 120 125

Arg Met Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala Arg Trp Ser Asn
130 135 140

Cys Cys Asn Met Gly Asn Met Gly Asn Tyr Thr Asn Ala Thr His Thr
145 150 155 160

2453

Ala Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Thr Gly
165 170 175

Gly Gly Ala Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
180 185 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp
195 200 205

Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly Ala
210 215 220

Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Ala Ala Arg Ala Thr His
225 230 235 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
245 250 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
260 265 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr His Cys Ala Arg Gly Gly Asn
275 280 285

Cys Ala Asn Cys Ala Tyr Thr Gly Gly Cys Cys Asn Cys Ala Asn Cys
290 295 300

Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala
305 310 315 320

Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
325 330 335

<210> 612
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<400> 612

Gly Ala Tyr Gly Thr Asn Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Tyr Thr Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Cys Cys Asn Gly Thr Asn Cys Ala Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr Met Gly Asn Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Tyr Thr Asn Gly Thr Asn Thr Ala Tyr Trp Ser Asn
85 90 95

Gly Ala Tyr Gly Gly Asn Ala Ala Tyr Cys Ala Asn Thr Ala Tyr Tyr
100 105 110

Thr Asn Ala Ala Tyr Thr Gly Gly Tyr Thr Asn Cys Ala Arg Cys Ala
115 120 125

Arg Met Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala Arg Trp Ser Asn
130 135 140

Cys Cys Asn Met Gly Asn Met Gly Asn Tyr Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Thr Gly
165 170 175

Gly Gly Ala Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
180 185 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp
195 200 205

Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly Ala
210 215 220

Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Ala Ala Arg Ala Thr His
225 230 235 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
245 250 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
260 265 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Gly Gly Asn
275 280 285

Cys Ala Asn Cys Ala Tyr Thr Gly Gly Cys Cys Asn Ala Thr His Cys
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Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala
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35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Tyr Thr Asn Tyr Thr Asn Cys Ala Tyr Trp Ser Asn
85 90 95

Gly Ala Tyr Gly Gly Asn Ala Ala Arg Cys Ala Asn Thr Ala Tyr Tyr
100 105 110

Thr Asn Thr Ala Tyr Thr Gly Gly Thr Ala Tyr Tyr Thr Asn Cys Ala
115 120 125

Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn
130 135 140

Cys Cys Asn Cys Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Gly Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Met Gly
165 170 175

Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
180 185 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp
195 200 205

Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly Ala
210 215 220

Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Ala Ala Arg Ala Thr His
225 230 235 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
245 250 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
260 265 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Gly Gly Asn
275 280 285

Ala Thr His Cys Ala Arg Tyr Thr Asn Cys Cys Asn Thr Gly Tyr Trp
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Ser Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala
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Asn Ala Ala Arg Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
325 330 335

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35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Tyr Thr Asn Tyr Thr Asn Cys Ala Tyr Trp Ser Asn
85 90 95

Gly Ala Tyr Gly Gly Asn Ala Ala Arg Cys Ala Asn Thr Ala Tyr Tyr
100 105 110

Thr Asn Thr Ala Tyr Thr Gly Gly Thr Ala Tyr Tyr Thr Asn Cys Ala
115 120 125

Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn
130 135 140

Cys Cys Asn Cys Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Gly Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Met Gly
165 170 175

Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
180 185 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp
195 200 205

Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly Ala
210 215 220

Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Ala Ala Arg Ala Thr His
225 230 235 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
245 250 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
260 265 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Trp Ser Asn
275 280 285

Ala Thr His Cys Ala Arg Tyr Thr Asn Cys Cys Asn Tyr Thr Asn Cys
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Ala Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Cys Ala
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Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
325 330 335

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Asn Trp Ser Asn Gly Thr Asn Cys Ala Asn Cys Cys Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Tyr Thr Asn Tyr Thr Asn Cys Ala Tyr Trp Ser Asn
85 90 95

Gly Ala Tyr Gly Gly Asn Ala Ala Arg Cys Ala Asn Thr Ala Tyr Tyr
100 105 110

Thr Asn Thr Ala Tyr Thr Gly Gly Thr Thr Tyr Tyr Thr Asn Cys Ala
115 120 125

Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn
130 135 140

Cys Cys Asn Cys Ala Arg Cys Cys Asn Tyr Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Gly Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Met Gly
165 170 175

Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
180 185 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp
195 200 205

Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly Ala
210 215 220

Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Ala Ala Arg Ala Thr His
225 230 235 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
245 250 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
260 265 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Trp Ser Asn
275 280 285

Ala Thr His Cys Ala Arg Tyr Thr Asn Cys Cys Asn Ala Thr His Cys
290 295 300

Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Tyr Gly Gly Asn Cys Ala
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Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
325 330 335

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2459

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Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
    50                  55                  60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Gly Gly Asn Ala Thr His Gly Cys Asn Ala Ala Tyr Thr Ala Tyr
                85                  90                  95

Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Thr
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Thr Asn Gly Cys Asn Trp Ser Asn Cys Ala Asn Tyr
145                 150                 155                 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Cys Ala Asn Thr
                245                 250                 255
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Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Ala Ala Tyr Thr Ala
260 265 270

Tyr Ala Ala Tyr Trp Ser Asn Gly Cys Asn Cys Cys Asn Thr Thr Tyr
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Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Cys
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Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Thr His Ala Ala
305 310 315 320

Arg

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<212> PRT
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Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Ala
50 55 60

Thr His Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Gly Asn Ala Thr His Trp Ser Asn Ala Ala Tyr Gly Ala Tyr
85 90 95

Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Thr
115 120 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Cys Ala Asn Tyr
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Ala Ala Arg Thr Ala
260 265 270

Tyr Ala Ala Tyr Trp Ser Asn Gly Thr Asn Cys Cys Asn Tyr Thr Asn
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Cys
290 295 300

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305 310 315 320

Arg

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<400> 618

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20 25 30

Asn Cys Cys Asn Gly Thr Asn Cys Ala Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr Met Gly Asn Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Tyr Thr Asn Gly Thr Asn Cys Ala Tyr Trp Ser Asn
85 90 95

Gly Ala Tyr Gly Gly Asn Ala Ala Tyr Cys Ala Asn Thr Ala Tyr Tyr
100 105 110

Thr Asn Trp Ser Asn Thr Gly Gly Tyr Thr Asn Cys Ala Arg Cys Ala
115 120 125

Arg Met Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn
130 135 140

Cys Cys Asn Met Gly Asn Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Ala Ala Arg Ala Thr His Trp Ser Asn Ala Ala Tyr Met Gly
165 170 175

Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
180 185 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp
195 200 205

Ser Asn Gly Gly Asn Gly Cys Asn Gly Gly Asn Cys Ala Asn Gly Ala
210 215 220

Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Ala Ala Arg Ala Thr His
225 230 235 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
245 250 255

Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
260 265 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Gly Cys Asn
275 280 285

Cys Ala Asn Cys Ala Arg Thr Thr Tyr Cys Cys Asn Cys Ala Tyr Cys
290 295 300

Ala Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala
305 310 315 320

Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Thr His Ala Ala Arg
325 330 335

<210> 619
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<212> PRT
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            20                  25                  30

Asn Cys Cys Asn Gly Thr Asn Cys Ala Asn Tyr Thr Asn Gly Gly Asn
        35                  40                  45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
    50                  55                  60

Ser Asn Thr Gly Tyr Met Gly Asn Trp Ser Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Trp Ser Asn Tyr Thr Asn Gly Thr Asn Cys Ala Tyr Trp Ser Asn
                85                  90                  95

Gly Ala Tyr Gly Gly Asn Ala Ala Tyr Cys Ala Asn Thr Ala Tyr Tyr
            100                 105                 110

Thr Asn Trp Ser Asn Thr Gly Gly Tyr Thr Asn Cys Ala Arg Cys Ala
        115                 120                 125

Arg Met Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn
    130                 135                 140

Cys Cys Asn Met Gly Asn Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Ala Ala Arg Ala Thr His Trp Ser Asn Ala Ala Tyr Met Gly
                165                 170                 175

Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys Asn
            180                 185                 190

Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Cys
        195                 200                 205

Ala Asn Gly Gly Asn Gly Cys Asn Gly Gly Asn Cys Ala Asn Gly Ala
    210                 215                 220

Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Ala Ala Arg Ala Thr His
225                 230                 235                 240

Trp Ser Asn Met Gly Asn Gly Thr Asn Gly Ala Arg Gly Cys Asn Gly
                245                 250                 255
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Ala Arg Gly Ala Tyr Gly Thr Asn Gly Gly Asn Gly Thr Asn Thr Ala
260 265 270

Tyr Thr Ala Tyr Thr Gly Tyr Ala Thr Gly Cys Ala Arg Gly Cys Asn
275 280 285

Cys Ala Asn Cys Ala Arg Thr Thr Tyr Cys Cys Asn Cys Ala Tyr Cys
290 295 300

Ala Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Cys Ala
305 310 315 320

Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
325 330 335

<210> 620
<211> 324
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<400> 620

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Ala Arg Trp Ser Asn Cys Cys Asn Gly Gly Asn Cys Ala Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Tyr Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Tyr Thr Asn Trp
50 55 60

Ser Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Cys Ala Asn Gly Thr Asn Ala Thr His Trp Ser Asn Trp Ser Asn
85 90 95

Thr Ala Tyr Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys
100 105 110

Ala Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala
115 120 125

Arg Gly Cys Asn Cys Cys Asn Met Gly Asn Tyr Thr Asn Tyr Thr Asn
130 135 140

Ala Thr His Trp Ser Asn Gly Gly Asn Gly Cys Asn Trp Ser Asn Trp
145 150 155 160

Ser Asn Met Gly Asn Gly Cys Asn Cys Ala Asn Gly Gly Asn Ala Thr
165 170 175

His Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn
180 185 190

Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys
195 200 205

Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala
210 215 220

Asn Ala Thr His Trp Ser Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg
225 230 235 240

Cys Cys Asn Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Gly
245 250 255

Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala
260 265 270

Arg Thr Ala Tyr Gly Gly Asn Trp Ser Asn Trp Ser Asn Cys Cys Asn
275 280 285

Met Gly Asn Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly
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Gly Asn Cys Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr
305 310 315 320

His Ala Ala Arg

<210> 621
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<400> 621

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20 25 30

Asn Trp Ser Asn Tyr Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Tyr Thr Asn Trp
50 55 60

2466

Ser Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Gly Thr Asn Trp Ser Asn Met Gly Asn Tyr Thr Asn
85 90 95

Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala
100 105 110

Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys
115 120 125

Asn Met Gly Asn Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
130 135 140

Gly Gly Asn Gly Cys Asn Trp Ser Asn Met Gly Asn Met Gly Asn Gly
145 150 155 160

Cys Asn Cys Ala Asn Gly Gly Asn Ala Thr His Cys Cys Asn Gly Ala
165 170 175

Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn
180 185 190

Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr
195 200 205

Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser
210 215 220

Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Cys Cys Asn Gly Ala Arg
225 230 235 240

Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr
245 250 255

Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala Tyr Gly Gly
260 265 270

Asn Trp Ser Asn Trp Ser Asn Cys Cys Asn Met Gly Asn Trp Ser Asn
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Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Ala
290 295 300

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Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Gly Asn Ala Thr His Met Gly Asn Ala Ala Tyr Gly Ala Tyr
85 90 95

Tyr Thr Asn Gly Gly Asn Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Met Gly Asn Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Arg Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Tyr Thr Asn Cys Ala Arg Cys Ala
260 265 270

Tyr Ala Ala Tyr Trp Ser Asn Thr Ala Tyr Cys Cys Asn Cys Cys Asn
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
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305 310 315 320

Arg

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Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Gly Thr Asn Tyr Thr Asn Thr Ala Tyr Trp Ser Asn
85 90 95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
100 105 110

Ala Tyr Tyr Thr Asn Gly Thr Asn Thr Gly Gly Thr Ala Tyr Cys Ala
115 120 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
130 135 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Thr Thr Tyr Ala
145 150 155 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Cys Ala
165 170 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
180 185 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Cys Ala Asn Gly
195 200 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala
210 215 220

Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn
225 230 235 240

Ala Thr His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Gly
245 250 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
260 265 270

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
275 280 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Thr Thr Tyr Cys Cys Asn Thr
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Asn Cys Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
325 330 335

Ala Ala Arg

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Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
50 55 60

2470

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Gly Thr Asn Tyr Thr Asn Thr Ala Tyr Trp Ser Asn
85 90 95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
100 105 110

Ala Tyr Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
115 120 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
130 135 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala
145 150 155 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Cys Ala
165 170 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
180 185 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
195 200 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala
210 215 220

Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn
225 230 235 240

Ala Thr His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Gly
245 250 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
260 265 270

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
275 280 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Cys Ala Asn Cys Ala Asn Thr
290 295 300

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Asn Cys Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
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Ala Ala Arg

1471

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Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Ala Ala Tyr Gly Thr Asn Tyr Thr Asn Thr Ala Tyr Trp Ser Asn
85 90 95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
100 105 110

Ala Tyr Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
115 120 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
130 135 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala
145 150 155 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Cys Ala
165 170 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
180 185 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
195 200 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala
210 215 220

Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn
225 230 235 240

2472

Ala Thr His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Gly
245 250 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
260 265 270

Asn Thr Ala Tyr Thr Thr Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
275 280 285

Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Cys Ala Asn Cys Cys Asn Met
290 295 300

Gly Asn Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly
305 310 315 320

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<213> Homo Sapiens

<400> 626

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Tyr Thr
20 25 30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Ala Ala Tyr Gly Thr Asn Tyr Thr Asn Thr Ala Tyr Trp Ser Asn
85 90 95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
100 105 110

Ala Tyr Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
115 120 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
130 135 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala
145 150 155 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Cys Ala
165 170 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
180 185 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
195 200 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala
210 215 220

Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn
225 230 235 240

Ala Thr His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Gly
245 250 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
260 265 270

Asn Thr Ala Tyr Thr Thr Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
275 280 285

Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Cys Ala Asn Cys Cys Asn Met
290 295 300

Gly Asn Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly
305 310 315 320

Asn Cys Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
325 330 335

Ala Ala Arg

<210> 627
<211> 339
<212> PRT
<213> Homo Sapiens

<400> 627

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

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Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Tyr Thr
            20                  25                  30

Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
    50                  55                  60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Trp Ser Asn Gly Thr Asn Tyr Thr Asn Thr Ala Tyr Trp Ser Asn
                85                  90                  95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
            100                 105                 110

Ala Tyr Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
        115                 120                 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
    130                 135                 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala
145                 150                 155                 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Cys Ala
                165                 170                 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
            180                 185                 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Gly Gly Asn Gly
        195                 200                 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala
    210                 215                 220

Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn
225                 230                 235                 240

Ala Thr His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Gly
                245                 250                 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
            260                 265                 270

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
        275                 280                 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Ala Thr His Trp Ser Asn Met
    290                 295                 300
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1415

Gly Asn Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly
305 310 315 320

Asn Cys Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
325 330 335

Ala Ala Arg

<210> 628
<211> 339
<212> PRT
<213> Homo Sapiens

<400> 628

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Tyr Thr
20 25 30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Gly Thr Asn Tyr Thr Asn Thr Ala Tyr Ala Ala Tyr
85 90 95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
100 105 110

Ala Tyr Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
115 120 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
130 135 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala
145 150 155 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Cys Ala
165 170 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
180 185 190

2478

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
195 200 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala
210 215 220

Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn
225 230 235 240

Ala Thr His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Gly
245 250 255

Cys Asn Gly Ala Tyr Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
260 265 270

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
275 280 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Cys Ala Asn Cys Ala Asn Thr
290 295 300

Gly Gly Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly
305 310 315 320

Asn Cys Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
325 330 335

Ala Ala Arg

<210> 629
<211> 339
<212> PRT
<213> Homo Sapiens

<400> 629

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Tyr Thr
20 25 30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

```
Arg Trp Ser Asn Gly Thr Asn Tyr Thr Asn Thr Ala Tyr Ala Ala Tyr
                85                  90                  95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
            100                 105                 110

Ala Tyr Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
        115                 120                 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
    130                 135                 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala
145                 150                 155                 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Cys Ala
                165                 170                 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
            180                 185                 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
        195                 200                 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala
    210                 215                 220

Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn
225                 230                 235                 240

Ala Thr His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Gly
                245                 250                 255

Cys Asn Gly Ala Tyr Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
            260                 265                 270

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
        275                 280                 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Cys Ala Asn Cys Ala Asn Thr
    290                 295                 300

Gly Gly Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly
305                 310                 315                 320

Asn Cys Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
                325                 330                 335

Ala Ala Arg
```

<210> 630
<211> 339

<212> PRT
<213> Homo Sapiens

<400> 630

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Tyr Thr
20 25 30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Gly Thr Asn Tyr Thr Asn Thr Ala Tyr Trp Ser Asn
85 90 95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
100 105 110

Ala Tyr Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
115 120 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
130 135 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Gly Thr Asn Tyr Thr Asn Ala
145 150 155 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Cys Ala
165 170 175

Asn Met Gly Asn Ala Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
180 185 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
195 200 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala
210 215 220

Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn
225 230 235 240

Ala Thr His Trp Ser Asn Gly Gly Asn Tyr Thr Asn Cys Ala Arg Gly
245 250 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Tyr Thr
260 265 270

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
275 280 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Cys Ala Asn Ala Thr Gly Thr
290 295 300

Thr Tyr Trp Ser Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly
305 310 315 320

Asn Cys Ala Asn Ala Ala Arg Tyr Thr Asn Gly Ala Arg Ala Thr His
325 330 335

Ala Ala Arg

<210> 631
<211> 339
<212> PRT
<213> Homo Sapiens

<400> 631

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Tyr Thr
20 25 30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Gly Thr Asn Tyr Thr Asn Gly Ala Tyr Trp Ser Asn
85 90 95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
100 105 110

Ala Tyr Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
115 120 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
130 135 140

```
Cys Cys Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala
145                 150                 155                 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Cys Ala
                165                 170                 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
            180                 185                 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
        195                 200                 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala
    210                 215                 220

Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn
225                 230                 235                 240

Ala Thr His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Gly
                245                 250                 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
            260                 265                 270

Asn Thr Thr Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Tyr Cys Ala Arg
        275                 280                 285

Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Cys Ala Asn Cys Cys Asn Tyr
    290                 295                 300

Thr Asn Cys Ala Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly
305                 310                 315                 320

Asn Cys Ala Asn Ala Ala Arg Gly Thr Asn Gly Cys Asn Ala Thr His
                325                 330                 335

Ala Ala Arg
```

<210> 632
<211> 339
<212> PRT
<213> Homo Sapiens

<400> 632

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Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1               5                   10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Tyr Thr
            20                  25                  30
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2481

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Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
    50                  55                  60

Ala Tyr Thr Gly Tyr Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Trp Ser Asn Ala Thr His Tyr Thr Asn Thr Ala Tyr Met Gly Asn
                85                  90                  95

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr
            100                 105                 110

Ala Tyr Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala
        115                 120                 125

Arg Cys Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Cys Ala Arg
    130                 135                 140

Cys Cys Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala
145                 150                 155                 160

Thr His Thr Ala Tyr Thr Gly Gly Gly Cys Asn Trp Ser Asn Gly Cys
                165                 170                 175

Asn Met Gly Asn Gly Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn
            180                 185                 190

Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly
        195                 200                 205

Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala
    210                 215                 220

Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn
225                 230                 235                 240

Ala Thr His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Gly
                245                 250                 255

Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr Asn Gly Cys Asn Gly Thr
            260                 265                 270

Asn Thr Ala Tyr Thr Thr Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg
        275                 280                 285

Thr Ala Tyr Thr Thr Tyr Ala Thr His Cys Ala Asn Cys Cys Asn Tyr
    290                 295                 300

Thr Asn Cys Ala Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly
305                 310                 315                 320
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Asn Cys Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His
325 330 335

Ala Ala Arg

<210> 633
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 633

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Cys Ala Tyr Thr Ala Tyr
85 90 95

Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Thr Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Trp Ser Asn Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Ala Ala Arg Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala
260 265 270

Tyr Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr Cys Cys Asn Thr Thr Tyr
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Cys
290 295 300

Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 634
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 634

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Gly Cys Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Thr Ala Tyr
85 90 95

Tyr Thr Asn Gly Cys Asn Thr Gly Gly Tyr Thr Asn Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Trp Ser Asn Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala
260 265 270

Tyr Ala Ala Tyr Cys Ala Asn Thr Ala Tyr Cys Cys Asn Thr Thr Tyr
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Cys
290 295 300

Ala Asn Ala Ala Arg Ala Thr Gly Gly Ala Tyr Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 635
<211> 324
<212> PRT
<213> Homo Sapiens

<400> 635

Gly Ala Arg Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

2485

Ala Arg Trp Ser Asn Cys Cys Asn Gly Cys Asn Cys Ala Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Tyr Thr Asn Trp
50 55 60

Ser Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr
85 90 95

Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Gly Ala Tyr Cys Cys Asn Gly Gly Asn Cys Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Met Gly Asn Tyr Thr Asn Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Gly Asn Gly Cys Asn Trp Ser Asn Met Gly Asn Met
145 150 155 160

Gly Asn Gly Cys Asn Cys Ala Asn Gly Gly Asn Ala Thr His Cys Cys
165 170 175

Asn Gly Cys Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Arg Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Trp Ser Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Gly Thr Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Cys Ala
260 265 270

Tyr Ala Ala Tyr Ala Ala Tyr Thr Gly Gly Cys Cys Asn Cys Cys Asn
275 280 285

Thr Gly Gly Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly
290 295 300

Gly Asn Cys Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr
305 310 315 320

His Ala Ala Arg

<210> 636
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 636

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Gly Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Met Gly Asn Thr Gly Gly
85 90 95

Tyr Thr Asn Gly Cys Asn Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Gly Cys
260 265 270

Asn Ala Ala Tyr Trp Ser Asn Thr Thr Tyr Cys Cys Asn Cys Cys Asn
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
290 295 300

Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Thr Thr Tyr Ala Ala
305 310 315 320

Arg

<210> 637
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 637

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Ala Thr His Trp Ser Asn Cys Ala Asn Thr Ala Tyr
85 90 95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Thr Thr Tyr Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Gly Cys Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
260 265 270

Asn Cys Ala Tyr Trp Ser Asn Gly Cys Asn Cys Cys Asn Thr Thr Tyr
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Cys
290 295 300

Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 638
<211> 318
<212> PRT
<213> Homo Sapiens

<400> 638

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Cys Ala Asn Ala Thr His Trp Ser Asn Ala Thr His Thr Ala Tyr
85 90 95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
260 265 270

Asn Thr Ala Tyr Trp Ser Asn Cys Ala Asn Tyr Thr Asn Cys Ala Asn
275 280 285

Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Cys Ala Asn Ala
290 295 300

2490.

Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
305 310 315

<210> 639
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 639

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Ala Thr His Met Gly Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Met Gly Asn Cys Cys Asn Gly Gly Asn Ala Ala Tyr Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
210 215 220

His Met Gly Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
260 265 270

Asn Thr Ala Tyr Trp Ser Asn Ala Thr His Cys Cys Asn Tyr Thr Asn
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Cys
290 295 300

Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 640
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 640

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Gly
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Cys Ala Asn Ala Thr His Trp Ser Asn Met Gly Asn Thr Ala Tyr
85 90 95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

1492

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Cys Ala Asn Tyr
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Tyr Thr
210 215 220

Asn Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Ala Thr
260 265 270

His Thr Ala Tyr Trp Ser Asn Cys Ala Asn Trp Ser Asn Ala Thr His
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
290 295 300

Ala Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 641
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 641

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

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Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
    50                  55                  60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Met Gly Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr
                85                  90                  95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Gly Thr Asn Tyr Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Cys Asn Gly Ala Arg Trp Ser Asn Trp Ser Asn Tyr
145                 150                 155                 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Cys Ala Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
            260                 265                 270

Asn Thr Ala Tyr Ala Thr His Cys Ala Asn Cys Cys Asn Ala Thr His
        275                 280                 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
    290                 295                 300

Ala Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Thr
305                 310                 315                 320
```

2494

His

<210> 642
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 642

```
Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1               5                  10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
            20                  25                  30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
    50                  55                  60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Trp Ser Asn Ala Thr His Trp Ser Asn Met Gly Asn Thr Ala Tyr
                85                  90                  95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Cys Ala Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr
145                 150                 155                 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
    210                 215                 220
```

2495

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Ala Ala Tyr Thr Thr Tyr Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
260 265 270

Asn Thr Ala Tyr Thr Thr Tyr Cys Ala Asn Cys Cys Asn Ala Thr His
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
290 295 300

Ala Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 643
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 643

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Cys Ala Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Thr Thr
210 215 220

Tyr Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
260 265 270

Asn Thr Ala Tyr Thr Thr Tyr Trp Ser Asn Cys Cys Asn Ala Thr His
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
290 295 300

Ala Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 644
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 644

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

2497

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Cys Ala Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Tyr Thr
210 215 220

Asn Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Trp Ser Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
260 265 270

Asn Thr Thr Tyr Thr Ala Tyr Cys Ala Asn Cys Cys Asn Ala Thr His
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
290 295 300

Ala Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 645
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 645

```
Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1               5                  10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
            20                  25                  30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
    50                  55                  60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr
                85                  90                  95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Tyr
145                 150                 155                 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
    210                 215                 220
```

2199

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
260 265 270

Asn Thr Ala Tyr Thr Thr Tyr Cys Ala Asn Cys Cys Asn Ala Thr His
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
290 295 300

Ala Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 646
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 646

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

```
Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Cys Ala Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr
145                 150                 155                 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Trp Ser Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
            260                 265                 270

Asn Thr Thr Tyr Thr Ala Tyr Gly Cys Asn Cys Cys Asn Ala Thr His
        275                 280                 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
    290                 295                 300

Ala Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305                 310                 315                 320

Arg
```

<210> 647
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 647

```
Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1               5                   10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
            20                  25                  30
```

2501

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Cys Ala Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr
145 150 155 160

Thr Asn Cys Ala Arg Trp Ser Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Thr Thr Tyr Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Trp Ser
260 265 270

Asn Thr Ala Tyr Thr Thr Tyr Cys Ala Asn Cys Cys Asn Ala Thr His
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
290 295 300

Ala Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

1502

Arg

<210> 648
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 648

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Thr Ala Tyr
85 90 95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Tyr
145 150 155 160

Thr Asn Gly Ala Arg Cys Ala Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala
260 265 270

Tyr Gly Ala Tyr Thr Ala Tyr Tyr Thr Asn Cys Cys Asn Thr Thr Tyr
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Cys
290 295 300

Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Tyr Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 649
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 649

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Trp Ser Asn
85 90 95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

2504

```
Asn Cys Cys Asn Gly Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Tyr
145                 150                 155                 160

Thr Asn Gly Ala Arg Cys Ala Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Cys Ala Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Gly
            260                 265                 270

Tyr Gly Ala Tyr Gly Ala Tyr Tyr Thr Asn Cys Cys Asn Tyr Thr Asn
        275                 280                 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Cys
    290                 295                 300

Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305                 310                 315                 320

Arg
```

<210> 650
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 650

```
Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1               5                   10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
            20                  25                  30
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1505

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Gly Ala Tyr Thr Ala Tyr
85 90 95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Tyr
145 150 155 160

Thr Asn Gly Ala Arg Cys Ala Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Tyr Thr Ala
260 265 270

Tyr Gly Ala Tyr Ala Ala Tyr Tyr Thr Asn Cys Cys Asn Tyr Thr Asn
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Cys
290 295 300

Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

2506

Arg

<210> 651
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 651

```
Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1               5                  10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
            20                  25                  30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Gly Cys Asn Ala Thr His Cys
    50                  55                  60

Ala Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Thr Ala Tyr
                85                  90                  95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Tyr
145                 150                 155                 160

Thr Asn Gly Ala Arg Cys Ala Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Ala Thr
    210                 215                 220
```

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala
260 265 270

Tyr Gly Ala Tyr Ala Ala Tyr Tyr Thr Asn Cys Cys Asn Tyr Thr Asn
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Cys
290 295 300

Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 652
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 652

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Trp Ser Asn
85 90 95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

```
Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Thr His Tyr
145                 150                 155                 160

Thr Asn Gly Ala Arg Cys Ala Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Ala Arg Cys Ala Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Cys Ala Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Gly
            260                 265                 270

Tyr Gly Ala Tyr Ala Thr His Tyr Thr Asn Cys Cys Asn Tyr Thr Asn
        275                 280                 285

Trp Ser Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Cys
    290                 295                 300

Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305                 310                 315                 320

Arg
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<210> 653
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 653

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Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1               5                   10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
            20                  25                  30
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1509

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Trp Ser Asn
85 90 95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Tyr
145 150 155 160

Thr Asn Gly Ala Arg Cys Ala Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala
260 265 270

Tyr Gly Ala Tyr Ala Ala Tyr Tyr Thr Asn Cys Cys Asn Tyr Thr Asn
275 280 285

Gly Cys Asn Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Cys
290 295 300

Ala Asn Ala Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Met Gly
305 310 315 320

JS10

Asn

<210> 654
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 654

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Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1               5                  10                  15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
            20                  25                  30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Tyr Gly Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
    50                  55                  60

Ala Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Gly Ala Tyr Ala Thr His Cys Ala Asn Ala Ala Tyr Thr Ala Tyr
                85                  90                  95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Tyr
145                 150                 155                 160

Thr Asn Gly Ala Arg Cys Ala Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Ala Thr
    210                 215                 220
```

2811

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala
260 265 270

Tyr Gly Ala Tyr Trp Ser Asn Tyr Thr Asn Cys Cys Asn Ala Thr His
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
290 295 300

Ala Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 655
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 655

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Thr Ala Tyr
85 90 95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Tyr Thr Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

2312

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
130 135 140

Cys Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Tyr
145 150 155 160

Thr Asn Gly Ala Arg Cys Ala Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Ala Thr
210 215 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Arg Thr Ala
260 265 270

Tyr Gly Ala Tyr Ala Ala Tyr Tyr Thr Asn Cys Cys Asn Ala Thr His
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
290 295 300

Ala Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 656
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 656

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

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Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
        35                  40                  45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
    50                  55                  60

Ala Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65                  70                  75                  80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Gly Ala Tyr Thr Ala Tyr
                85                  90                  95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
            100                 105                 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
        115                 120                 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
    130                 135                 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Tyr
145                 150                 155                 160

Thr Asn Gly Ala Arg Cys Ala Asn Gly Gly Asn Gly Thr Asn Cys Cys
                165                 170                 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
            180                 185                 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
        195                 200                 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Ala Thr
    210                 215                 220

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225                 230                 235                 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Cys Ala Asn Thr
                245                 250                 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Tyr Thr Ala
            260                 265                 270

Tyr Gly Ala Tyr Ala Ala Tyr Tyr Thr Asn Cys Cys Asn Ala Thr His
        275                 280                 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
    290                 295                 300

Ala Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305                 310                 315                 320
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Arg

<210> 657
<211> 321
<212> PRT
<213> Homo Sapiens

<400> 657

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala
65 70 75 80

Arg Gly Ala Tyr Ala Thr His Trp Ser Asn Ala Ala Tyr Trp Ser Asn
85 90 95

Tyr Thr Asn Ala Ala Tyr Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys
100 105 110

Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys
115 120 125

Asn Cys Cys Asn Ala Ala Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His
130 135 140

Thr Ala Tyr Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Tyr
145 150 155 160

Thr Asn Gly Ala Arg Cys Ala Asn Gly Gly Asn Gly Thr Asn Cys Cys
165 170 175

Asn Trp Ser Asn Met Gly Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn
180 185 190

Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly
195 200 205

Ala Tyr Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Ala Thr
210 215 220

JSIS

His Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys Ala Arg Cys Cys Asn
225 230 235 240

Gly Ala Arg Gly Ala Tyr Ala Thr His Gly Cys Asn Cys Ala Asn Thr
245 250 255

Ala Tyr Thr Ala Tyr Thr Gly Tyr Cys Ala Arg Cys Ala Tyr Thr Ala
260 265 270

Tyr Gly Ala Tyr Ala Ala Tyr Tyr Thr Asn Cys Cys Asn Ala Thr His
275 280 285

Cys Ala Asn Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys
290 295 300

Ala Asn Met Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala
305 310 315 320

Arg

<210> 658
<211> 360
<212> PRT
<213> Homo Sapiens

<400> 658

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
20 25 30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Cys Asn
35 40 45

Trp Ser Asn Gly Thr Asn Ala Ala Arg Gly Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Ala
65 70 75 80

Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Gly Asn Ala Thr His Trp Ser Asn Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Cys Ala
115 120 125

```
Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
    130                 135                 140

Gly Gly Asn Thr Gly Gly Ala Thr His Trp Ser Asn Gly Cys Asn Trp
145                 150                 155                 160

Ser Asn Ala Ala Tyr Gly Gly Asn Ala Ala Tyr Cys Ala Asn Ala Ala
                165                 170                 175

Tyr Thr Ala Tyr Gly Cys Asn Cys Ala Arg Ala Ala Arg Tyr Thr Asn
            180                 185                 190

Cys Ala Arg Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala
        195                 200                 205

Thr Gly Cys Ala Asn Cys Ala Asn Gly Ala Tyr Cys Ala Asn Trp Ser
    210                 215                 220

Asn Cys Ala Asn Trp Ser Asn Cys Ala Asn Gly Cys Asn Thr Ala Tyr
225                 230                 235                 240

Ala Thr Gly Gly Ala Arg Tyr Thr Asn Met Gly Asn Trp Ser Asn Tyr
                245                 250                 255

Thr Asn Met Gly Asn Trp Ser Asn Gly Ala Tyr Gly Ala Tyr Cys Ala
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Met Gly Asn Gly Ala Arg Gly Ala Tyr Ala Ala Tyr Thr
    290                 295                 300

Gly Gly Ala Ala Tyr Thr Ala Tyr Gly Gly Asn Thr Thr Tyr Thr Thr
305                 310                 315                 320

Tyr Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg
                325                 330                 335

Gly Gly Asn Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly
            340                 345                 350

Thr Asn Trp Ser Asn Trp Ser Asn
        355                 360
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<210> 659
<211> 351
<212> PRT
<213> Homo Sapiens

<400> 659

Cys Ala Arg Gly Thr Asn Cys Ala Tyr Tyr Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
20 25 30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Cys Asn
35 40 45

Trp Ser Asn Gly Thr Asn Ala Ala Arg Gly Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Gly Gly Asn Thr Ala
65 70 75 80

Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Gly Gly Asn Cys Ala Tyr
85 90 95

Thr Ala Tyr Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Cys Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
130 135 140

Gly Gly Asn Thr Gly Gly Ala Thr His Ala Ala Tyr Cys Cys Asn Ala
145 150 155 160

Ala Tyr Trp Ser Asn Gly Gly Asn Gly Gly Asn Cys Ala Asn Ala Ala
165 170 175

Tyr Thr Gly Tyr Gly Cys Asn Cys Ala Arg Ala Ala Arg Thr Thr Tyr
180 185 190

Cys Ala Arg Gly Gly Asn Met Gly Asn Gly Thr Asn Cys Ala Asn Ala
195 200 205

Thr Gly Cys Ala Asn Met Gly Asn Gly Ala Tyr Cys Ala Asn Trp Ser
210 215 220

Asn Ala Thr His Trp Ser Asn Cys Ala Asn Gly Cys Asn Thr Ala Tyr
225 230 235 240

Ala Thr Gly Gly Ala Arg Tyr Thr Asn Trp Ser Asn Met Gly Asn Tyr
245 250 255

Thr Asn Met Gly Asn Trp Ser Asn Gly Ala Tyr Gly Ala Tyr Cys Ala
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Trp Ser Asn Ala Thr His Gly Cys Asn Gly
290 295 300

Thr Asn Gly Cys Asn Tyr Thr Asn Gly Ala Tyr Thr Ala Tyr Thr Gly
305 310 315 320

Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Tyr Thr Asn
325 330 335

Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
340 345 350

<210> 660
<211> 351
<212> PRT
<213> Homo Sapiens

<400> 660

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
20 25 30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Cys Asn
35 40 45

Trp Ser Asn Gly Thr Asn Ala Ala Arg Gly Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Ala
65 70 75 80

Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Gly Gly Asn Thr Ala Tyr
85 90 95

Thr Ala Tyr Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Cys Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
130 135 140

Gly Gly Asn Thr Gly Gly Ala Thr His Ala Ala Tyr Cys Cys Asn Ala
145 150 155 160

Ala Tyr Trp Ser Asn Gly Gly Asn Gly Gly Asn Cys Ala Asn Ala Ala
165 170 175

Tyr Cys Ala Tyr Cys Ala Asn Cys Ala Arg Ala Ala Arg Thr Thr Tyr
180 185 190

Cys Ala Arg Gly Gly Asn Met Gly Asn Gly Thr Asn Cys Ala Asn Ala
195 200 205

Thr Gly Cys Ala Asn Met Gly Asn Gly Ala Tyr Cys Ala Asn Trp Ser
210 215 220

Asn Ala Thr His Trp Ser Asn Cys Ala Asn Gly Cys Asn Thr Ala Tyr
225 230 235 240

Ala Thr Gly Gly Ala Arg Tyr Thr Asn Trp Ser Asn Met Gly Asn Tyr
245 250 255

Thr Asn Met Gly Asn Trp Ser Asn Gly Ala Tyr Gly Ala Tyr Cys Ala
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Trp Ser Asn Ala Thr His Gly Cys Asn Gly
290 295 300

Thr Asn Gly Cys Asn Tyr Thr Asn Gly Ala Tyr Thr Ala Tyr Thr Gly
305 310 315 320

Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Tyr Thr Asn
325 330 335

Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
340 345 350

<210> 661
<211> 366
<212> PRT
<213> Homo Sapiens

<400> 661

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
20 25 30

Asn Met Gly Asn Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Cys Asn
35 40 45

Trp Ser Asn Gly Thr Asn Ala Ala Arg Gly Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn Gly Gly Asn Thr Ala
65 70 75 80

Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Gly Ala Arg Tyr Thr Asn
85 90 95

Trp Ser Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
130 135 140

Gly Gly Asn Trp Ser Asn Thr Thr Tyr Gly Ala Tyr Cys Cys Asn Gly
145 150 155 160

Ala Arg Gly Ala Tyr Gly Gly Asn Gly Ala Arg Cys Ala Asn Ala Thr
165 170 175

His Thr Ala Tyr Gly Cys Asn Cys Ala Arg Ala Ala Arg Thr Thr Tyr
180 185 190

Cys Ala Arg Gly Gly Asn Met Gly Asn Gly Thr Asn Cys Ala Asn Ala
195 200 205

Thr Gly Tyr Thr Asn Gly Ala Arg Gly Ala Tyr Cys Ala Asn Trp Ser
210 215 220

Asn Cys Ala Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Thr Ala Tyr
225 230 235 240

Ala Thr Gly Gly Ala Arg Tyr Thr Asn Trp Ser Asn Trp Ser Asn Tyr
245 250 255

Thr Asn Met Gly Asn Trp Ser Asn Gly Ala Arg Gly Ala Tyr Cys Ala
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Cys Ala Asn Gly Ala Arg Gly Gly Asn Gly Ala Tyr Gly
290 295 300

Gly Asn Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala
305 310 315 320

Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr Gly Gly
325 330 335

Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Cys Ala Asn Gly
340 345 350

2321

Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
355 360 365

<210> 662
<211> 366
<212> PRT
<213> Homo Sapiens

<400> 662

Cys Ala Arg Gly Thr Asn Cys Ala Asn Tyr Thr Asn Ala Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Thr Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Cys Ala Asn Gly Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Cys Ala Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Trp Ser Asn Tyr Thr Asn Trp Ser Asn Ala Ala Tyr Gly Cys Asn
85 90 95

Met Gly Asn Ala Thr Gly Gly Gly Asn Gly Thr Asn Trp Ser Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Tyr Thr Asn Gly Cys Asn Cys Ala Tyr Ala Thr His Thr
145 150 155 160

Thr Tyr Trp Ser Asn Ala Ala Tyr Gly Ala Tyr Gly Ala Arg Ala Ala
165 170 175

Arg Trp Ser Asn Thr Ala Tyr Trp Ser Asn Cys Ala Asn Trp Ser Asn
180 185 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Tyr Thr Asn Cys
195 200 205

Ala Asn Ala Thr His Trp Ser Asn Ala Ala Arg Gly Ala Tyr Cys Ala
210 215 220

Asn Trp Ser Asn Ala Ala Arg Trp Ser Asn Cys Ala Arg Gly Thr Asn
225 230 235 240

Gly Thr Asn Tyr Thr Asn Cys Ala Asn Ala Thr Gly Cys Ala Asn Ala
245 250 255

Ala Tyr Ala Thr Gly Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
260 265 270

Tyr Cys Ala Asn Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Ala Thr Gly Thr Ala Tyr Trp
290 295 300

Ser Asn Trp Ser Asn Gly Gly Asn Thr Gly Gly Thr Ala Tyr Gly Gly
305 310 315 320

Asn Gly Thr Asn Thr Thr Tyr Gly Ala Tyr Thr Ala Tyr Thr Gly Gly
325 330 335

Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Tyr Thr Asn Gly
340 345 350

Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
355 360 365

<210> 663
<211> 369
<212> PRT
<213> Homo Sapiens

<400> 663

Cys Ala Arg Gly Thr Asn Cys Ala Asn Tyr Thr Asn Ala Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Thr Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Cys Ala Asn Gly Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Cys Ala Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Trp Ser Asn Tyr Thr Asn Trp Ser Asn Ala Ala Tyr Gly Cys Asn
85 90 95

2323

Met Gly Asn Ala Thr Gly Gly Gly Asn Gly Thr Asn Trp Ser Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Tyr Thr Asn Gly Thr Asn Tyr Thr Asn Ala Thr His Thr
145 150 155 160

Thr Tyr Trp Ser Asn Ala Ala Tyr Gly Ala Tyr Gly Ala Arg Ala Ala
165 170 175

Arg Trp Ser Asn Thr Ala Tyr Trp Ser Asn Cys Ala Asn Trp Ser Asn
180 185 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Tyr Thr Asn Cys
195 200 205

Ala Asn Ala Thr His Trp Ser Asn Ala Ala Arg Gly Ala Tyr Cys Ala
210 215 220

Asn Trp Ser Asn Ala Ala Arg Trp Ser Asn Cys Ala Arg Gly Thr Asn
225 230 235 240

Gly Thr Asn Tyr Thr Asn Cys Ala Asn Ala Thr Gly Cys Ala Asn Ala
245 250 255

Ala Tyr Ala Thr Gly Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
260 265 270

Tyr Cys Ala Asn Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Gly Thr Asn Thr Ala Tyr Trp
290 295 300

Ser Asn Trp Ser Asn Gly Gly Asn Thr Gly Gly Trp Ser Asn Thr Thr
305 310 315 320

Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn
325 330 335

Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Cys
340 345 350

Ala Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser
355 360 365

Asn

<210> 664
<211> 354
<212> PRT
<213> Homo Sapiens

<400> 664

Cys Ala Arg Ala Thr His Cys Ala Asn Tyr Thr Asn Ala Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Cys Ala Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Cys Ala Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Cys Ala Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Trp Ser Asn Tyr Thr Asn Trp Ser Asn Cys Ala Asn Gly Gly Asn
85 90 95

Gly Gly Asn Gly Thr Asn Gly Gly Asn Gly Thr Asn Gly Gly Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Tyr Thr Asn Gly Cys Asn Tyr Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Thr Gly Gly Ala Ala Tyr Gly Ala Tyr Gly Ala Tyr Ala Ala
165 170 175

Arg Met Gly Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn
180 185 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Tyr Thr Asn Cys
195 200 205

Ala Asn Ala Thr His Cys Ala Asn Ala Ala Arg Gly Ala Tyr Cys Ala
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn
225 230 235 240

Gly Thr Asn Tyr Thr Asn Cys Ala Asn Ala Thr Gly Cys Ala Asn Ala
245 250 255

Ala Tyr Ala Thr Gly Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
260 265 270

Tyr Cys Ala Asn Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Cys Ala Tyr Met Gly Asn Met Gly Asn Gly
290 295 300

Ala Arg Tyr Thr Asn Cys Cys Asn Thr Thr Tyr Gly Ala Tyr Thr Ala
305 310 315 320

Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn
325 330 335

Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp
340 345 350

Ser Asn

<210> 665
<211> 354
<212> PRT
<213> Homo Sapiens

<400> 665

Cys Ala Arg Ala Thr His Cys Ala Asn Tyr Thr Asn Ala Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Cys Ala Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Cys Ala Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Cys Ala Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Trp Ser Asn Tyr Thr Asn Trp Ser Asn Cys Ala Asn Gly Gly Asn
85 90 95

Gly Gly Asn Gly Thr Asn Gly Gly Asn Gly Thr Asn Gly Gly Asn Thr
100 105 110

```
Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Tyr Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Tyr Thr Asn Gly Cys Asn Tyr Thr Asn Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Thr Gly Gly Ala Ala Tyr Gly Ala Tyr Gly Ala Tyr Ala Ala
                165                 170                 175

Arg Met Gly Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn
            180                 185                 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Tyr Thr Asn Cys
        195                 200                 205

Ala Asn Ala Thr His Cys Ala Asn Ala Ala Arg Gly Ala Tyr Cys Ala
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Cys Ala Asn Cys Ala Arg Gly Thr Asn
225                 230                 235                 240

Gly Thr Asn Tyr Thr Asn Cys Ala Asn Gly Thr Asn Cys Ala Asn Gly
                245                 250                 255

Ala Tyr Ala Thr Gly Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
            260                 265                 270

Tyr Cys Ala Asn Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Cys Ala Tyr Met Gly Asn Ala Ala Tyr Thr
    290                 295                 300

Gly Gly Cys Ala Asn Cys Cys Asn Thr Thr Tyr Gly Ala Tyr Thr Ala
305                 310                 315                 320

Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn
                325                 330                 335

Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp
            340                 345                 350

Ser Asn
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<210> 666
<211> 354
<212> PRT
<213> Homo Sapiens

<400> 666

Cys Ala Arg Ala Thr His Cys Ala Asn Tyr Thr Asn Ala Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Cys Ala Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Cys Ala Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Cys Ala Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Trp Ser Asn Tyr Thr Asn Ala Ala Tyr Cys Ala Asn Gly Gly Asn
85 90 95

Gly Gly Asn Gly Thr Asn Gly Gly Asn Gly Thr Asn Gly Gly Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Tyr Thr Asn Gly Cys Asn Tyr Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Thr Gly Gly Ala Ala Tyr Gly Ala Tyr Gly Ala Tyr Ala Ala
165 170 175

Arg Met Gly Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn
180 185 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Tyr Thr Asn Cys
195 200 205

Ala Asn Ala Thr His Cys Ala Asn Ala Ala Arg Gly Ala Tyr Cys Ala
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn
225 230 235 240

Gly Thr Asn Tyr Thr Asn Cys Ala Asn Ala Thr Gly Cys Ala Asn Ala
245 250 255

Ala Tyr Ala Thr Gly Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
260 265 270

1528

Tyr Cys Ala Asn Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Cys Ala Tyr Met Gly Asn Tyr Thr Asn Gly
290 295 300

Ala Arg Tyr Thr Asn Cys Cys Asn Thr Thr Tyr Gly Ala Tyr Thr Ala
305 310 315 320

Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn
325 330 335

Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp
340 345 350

Ser Asn

<210> 667
<211> 354
<212> PRT
<213> Homo Sapiens

<400> 667

Cys Ala Arg Ala Thr His Cys Ala Asn Tyr Thr Asn Ala Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Cys Ala Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Cys Ala Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Cys Ala Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Trp Ser Asn Tyr Thr Asn Trp Ser Asn Cys Ala Asn Gly Gly Asn
85 90 95

Gly Gly Asn Gly Thr Asn Gly Gly Asn Gly Thr Asn Gly Gly Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Tyr Thr Asn Gly Ala Arg
130 135 140

```
Thr Gly Gly Tyr Thr Asn Gly Cys Asn Tyr Thr Asn Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Thr Gly Gly Ala Ala Tyr Gly Ala Tyr Gly Ala Tyr Ala Ala
                165                 170                 175

Arg Met Gly Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn
            180                 185                 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Tyr Thr Asn Cys
        195                 200                 205

Ala Asn Ala Thr His Cys Ala Asn Ala Ala Arg Gly Ala Tyr Cys Ala
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn
225                 230                 235                 240

Gly Thr Asn Tyr Thr Asn Cys Ala Asn Ala Thr Gly Cys Ala Asn Ala
                245                 250                 255

Ala Tyr Tyr Thr Asn Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
            260                 265                 270

Tyr Cys Ala Asn Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Cys Ala Tyr Met Gly Asn Met Gly Asn Gly
    290                 295                 300

Ala Arg Gly Thr Asn Cys Cys Asn Thr Thr Tyr Gly Ala Tyr Thr Ala
305                 310                 315                 320

Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn
                325                 330                 335

Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp
            340                 345                 350

Ser Asn
```

<210> 668
<211> 354
<212> PRT
<213> Homo Sapiens

<400> 668

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Cys Ala Arg Ala Thr His Cys Ala Asn Tyr Thr Asn Ala Ala Arg Gly
1               5                   10                  15
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Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Cys Ala Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Cys Ala Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Cys Ala Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Trp Ser Asn Tyr Thr Asn Trp Ser Asn Cys Ala Asn Gly Gly Asn
85 90 95

Gly Gly Asn Gly Thr Asn Gly Gly Asn Gly Thr Asn Gly Gly Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Tyr Thr Asn Gly Cys Asn Tyr Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Thr Gly Gly Ala Ala Tyr Gly Thr Asn Gly Ala Arg Ala Ala
165 170 175

Arg Met Gly Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn
180 185 190

Tyr Thr Asn Met Gly Asn Trp Ser Asn Met Gly Asn Tyr Thr Asn Cys
195 200 205

Ala Asn Ala Thr His Cys Ala Asn Ala Ala Arg Gly Cys Asn Cys Ala
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn
225 230 235 240

Gly Thr Asn Tyr Thr Asn Cys Ala Asn Ala Thr Gly Cys Ala Asn Ala
245 250 255

Ala Tyr Ala Thr Gly Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
260 265 270

Tyr Cys Ala Asn Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Cys Ala Tyr Met Gly Asn Cys Ala Tyr Cys
290 295 300

Ala Asn Ala Ala Tyr Cys Cys Asn Thr Thr Tyr Gly Ala Arg Thr Ala
305 310 315 320

Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn
325 330 335

Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp
340 345 350

Ser Asn

<210> 669
<211> 354
<212> PRT
<213> Homo Sapiens

<400> 669

Cys Ala Arg Ala Thr His Cys Ala Asn Tyr Thr Asn Ala Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Cys Ala Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Cys Ala Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Cys Ala Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Trp Ser Asn Tyr Thr Asn Trp Ser Asn Cys Ala Asn Gly Gly Asn
85 90 95

Gly Gly Asn Gly Thr Asn Gly Gly Asn Gly Thr Asn Gly Gly Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Tyr Thr Asn Gly Cys Asn Tyr Thr Asn Ala Thr His Thr
145 150 155 160

Ala Tyr Thr Gly Gly Ala Ala Tyr Gly Ala Tyr Gly Ala Tyr Ala Ala
165 170 175

Arg Met Gly Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn
180 185 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Tyr Thr Asn Cys
195 200 205

Ala Asn Ala Thr His Cys Ala Asn Ala Ala Arg Gly Ala Tyr Cys Ala
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Gly Thr Asn
225 230 235 240

Gly Thr Asn Tyr Thr Asn Cys Ala Asn Ala Thr Gly Cys Ala Asn Ala
245 250 255

Ala Tyr Ala Thr Gly Gly Ala Tyr Cys Cys Asn Gly Thr Asn Gly Ala
260 265 270

Tyr Cys Ala Asn Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Cys Ala Tyr Met Gly Asn Gly Gly Asn Gly
290 295 300

Ala Arg Tyr Thr Asn Cys Cys Asn Thr Thr Tyr Gly Ala Tyr Thr Ala
305 310 315 320

Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn
325 330 335

Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp
340 345 350

Ser Asn

<210> 670
<211> 363
<212> PRT
<213> Homo Sapiens

<400> 670

Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
35 40 45

```
Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
    50                  55                  60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65                  70                  75                  80

Tyr Cys Cys Asn Thr Thr Tyr Trp Ser Asn Met Gly Asn Thr Ala Tyr
                85                  90                  95

Trp Ser Asn Ala Thr Gly Ala Ala Tyr Thr Gly Gly Gly Thr Asn Met
            100                 105                 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
        115                 120                 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
    130                 135                 140

Trp Ser Asn Gly Cys Asn Ala Thr His Trp Ser Asn Trp Ser Asn Trp
145                 150                 155                 160

Ser Asn Trp Ser Asn Trp Ser Asn Thr Ala Tyr Ala Thr His Thr Ala
                165                 170                 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
            180                 185                 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
        195                 200                 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Gly Cys
    210                 215                 220

Asn Ala Ala Arg Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Thr Ala Tyr
225                 230                 235                 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
                245                 250                 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Met Gly Asn Gly Ala Tyr Met Gly Asn Gly Thr Asn Gly
    290                 295                 300

Gly Asn Gly Cys Asn Cys Ala Asn Cys Cys Asn Gly Ala Tyr Gly Cys
305                 310                 315                 320

Asn Thr Thr Tyr Gly Ala Tyr Ala Thr His Thr Gly Gly Gly Gly Asn
                325                 330                 335
```

2534

Cys Ala Arg Gly Gly Asn Cys Ala Asn Ala Thr Gly Gly Thr Asn Cys
340 345 350

Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
355 360

<210> 671
<211> 384
<212> PRT
<213> Homo Sapiens

<400> 671

Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Tyr Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Cys Asn Ala Thr Gly Ala Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Trp Ser Asn Gly Cys Asn Ala Thr His Trp Ser Asn Gly Gly Asn Trp
145 150 155 160

Ser Asn Gly Gly Asn Gly Gly Asn Trp Ser Asn Cys Ala Asn Thr Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
195 200 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
210 215 220

Asn Ala Ala Arg Ala Ala Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr
225 230 235 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
245 250 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Ala Ala Arg Gly Ala Arg Gly Gly Asn Ala Thr His Gly
290 295 300

Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Ala Asn Gly Cys
305 310 315 320

Asn Gly Ala Arg Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr
325 330 335

Thr Ala Tyr Gly Cys Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr
340 345 350

Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Cys Ala
355 360 365

Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
370 375 380

<210> 672
<211> 375
<212> PRT
<213> Homo Sapiens

<400> 672

Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Tyr Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

2536

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Cys Asn Ala Thr Gly Trp Ser Asn Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Trp Ser Asn Gly Cys Asn Ala Thr His Trp Ser Asn Gly Gly Asn Trp
145 150 155 160

Ser Asn Gly Gly Asn Gly Gly Asn Trp Ser Asn Cys Ala Asn Thr Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
195 200 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
210 215 220

Asn Ala Ala Arg Ala Ala Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr
225 230 235 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
245 250 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Ala Ala Arg Gly Ala Arg Gly Gly Asn Ala Thr His Gly
290 295 300

Cys Asn Gly Cys Asn Met Gly Asn Gly Ala Tyr Trp Ser Asn Thr Ala
305 310 315 320

Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Cys Asn Ala Thr Gly
325 330 335

Gly Ala Tyr Gly Thr Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly
340 345 350

2337

Gly Asn Cys Ala Asn Cys Ala Asn Gly Thr Asn Cys Ala Asn Gly Thr
355 360 365

Asn Trp Ser Asn Trp Ser Asn
370 375

<210> 673
<211> 375
<212> PRT
<213> Homo Sapiens

<400> 673

Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Tyr Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Cys Asn Ala Thr Gly Trp Ser Asn Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Trp Ser Asn Gly Cys Asn Ala Thr His Trp Ser Asn Gly Gly Asn Trp
145 150 155 160

Ser Asn Gly Gly Asn Gly Gly Asn Trp Ser Asn Cys Ala Asn Thr Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
195 200 205

2538

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
210 215 220

Asn Ala Ala Arg Ala Ala Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr
225 230 235 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
245 250 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala
260 265 270

Asn Gly Cys Asn Gly Ala Arg Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Ala Ala Arg Gly Ala Arg Gly Gly Asn Ala Thr His Gly
290 295 300

Cys Asn Gly Gly Asn Met Gly Asn Gly Ala Tyr Trp Ser Asn Thr Ala
305 310 315 320

Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly
325 330 335

Gly Ala Tyr Gly Thr Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly
340 345 350

Gly Asn Cys Ala Asn Cys Ala Asn Gly Thr Asn Cys Ala Asn Gly Thr
355 360 365

Asn Trp Ser Asn Trp Ser Asn
370 375

<210> 674
<211> 369
<212> PRT
<213> Homo Sapiens

<400> 674

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

```
Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65                  70                  75                  80

Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
                85                  90                  95

Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
            100                 105                 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
        115                 120                 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
    130                 135                 140

Gly Cys Asn Thr Thr Tyr Ala Thr His Trp Ser Asn Gly Ala Tyr Gly
145                 150                 155                 160

Ala Tyr Gly Gly Asn Trp Ser Asn Cys Ala Asn Ala Ala Arg Thr Ala
                165                 170                 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
            180                 185                 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
        195                 200                 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
    210                 215                 220

Asn Ala Thr Gly Ala Ala Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr
225                 230                 235                 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
                245                 250                 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Met Gly Asn Trp Ser Asn Thr Ala Tyr Thr Ala Tyr Gly
    290                 295                 300

Ala Tyr Trp Ser Asn Trp Ser Asn Gly Gly Asn Thr Ala Tyr Thr Ala
305                 310                 315                 320

Tyr Thr Ala Tyr Gly Gly Asn Thr Thr Tyr Gly Ala Tyr Thr Ala Tyr
                325                 330                 335

Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Tyr
            340                 345                 350
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2540

Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser
355 360 365

Asn

<210> 675
<211> 342
<212> PRT
<213> Homo Sapiens

<400> 675

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly
145 150 155 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Thr Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
195 200 205

2841

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
210 215 220

Asn Ala Ala Arg Ala Ala Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr
225 230 235 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
245 250 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Ala Ala Tyr Gly Thr Asn Ala Thr His Gly
290 295 300

Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly
305 310 315 320

Asn Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn
325 330 335

Trp Ser Asn Trp Ser Asn
340

<210> 676
<211> 360
<212> PRT
<213> Homo Sapiens

<400> 676

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

```
Gly Ala Tyr Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
            100                 105                 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
        115                 120                 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
    130                 135                 140

Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly
145                 150                 155                 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Thr His Ala Ala Arg Thr Ala
                165                 170                 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
            180                 185                 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
        195                 200                 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
    210                 215                 220

Asn Ala Ala Arg Ala Ala Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr
225                 230                 235                 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
                245                 250                 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala
            260                 265                 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Met Gly Asn Gly Gly Asn Gly Gly Asn Gly Cys Asn Cys
    290                 295                 300

Ala Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Thr Ala Tyr Thr Thr
305                 310                 315                 320

Tyr Cys Ala Arg Cys Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg
                325                 330                 335

Gly Gly Asn Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly
            340                 345                 350

Thr Asn Trp Ser Asn Trp Ser Asn
        355                 360
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<210> 677
<211> 354

<212> PRT
<213> Homo Sapiens

<400> 677

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly
145 150 155 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Thr Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
195 200 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
210 215 220

Asn Ala Ala Arg Ala Ala Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr
225 230 235 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
245 250 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Thr Asn Tyr Thr Asn Tyr Thr Asn Thr Gly Gly Thr Thr Tyr Gly
290 295 300

Gly Asn Gly Ala Arg Cys Ala Asn Thr Thr Tyr Gly Ala Tyr Thr Ala
305 310 315 320

Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Trp Ser Asn
325 330 335

Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Cys
340 345 350

Cys Asn

<210> 678
<211> 345
<212> PRT
<213> Homo Sapiens

<400> 678

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Trp Ser Asn Gly
145 150 155 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Thr Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
195 200 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
210 215 220

Asn Ala Ala Arg Ala Ala Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr
225 230 235 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
245 250 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Ala Ala Tyr Tyr Thr Asn Cys Cys Asn Thr
290 295 300

Thr Tyr Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala
305 310 315 320

Arg Gly Gly Asn Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys Ala Asn
325 330 335

Gly Thr Asn Trp Ser Asn Trp Ser Asn
340 345

<210> 679
<211> 369
<212> PRT
<213> Homo Sapiens

<400> 679

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Gly Ala Tyr Gly
145 150 155 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Ala Tyr Cys Ala Arg Thr Ala
165 170 175

Tyr Thr Ala Tyr Cys Ala Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Gly
195 200 205

Thr Asn Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
210 215 220

Asn Ala Ala Arg Ala Ala Tyr Cys Ala Asn Tyr Thr Asn Thr Thr Tyr
225 230 235 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
245 250 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Trp Ser Asn Cys Ala Tyr Thr Ala Tyr Gly
290 295 300

Gly Asn Gly Gly Asn Gly Ala Tyr Thr Ala Tyr Gly Ala Tyr Thr Ala
305 310 315 320

Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn
325 330 335

Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Cys
340 345 350

Ala Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser
355 360 365

Asn

<210> 680
<211> 360
<212> PRT
<213> Homo Sapiens

<400> 680

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly
145 150 155 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Met Gly
165 170 175

Asn Thr Ala Tyr Gly Thr Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
195 200 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
210 215 220

Asn Ala Ala Arg Ala Ala Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr
225 230 235 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
245 250 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Gly Ala Tyr Gly Gly Asn Thr Gly Gly Cys
290 295 300

Ala Arg Cys Ala Arg Cys Ala Arg Gly Cys Asn Cys Cys Asn Thr Thr
305 310 315 320

Tyr Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg
325 330 335

Gly Gly Asn Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly
340 345 350

Thr Asn Trp Ser Asn Trp Ser Asn
355 360

<210> 681
<211> 354
<212> PRT
<213> Homo Sapiens

<400> 681

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
20 25 30

2549

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Cys Ala Asn Thr Thr Tyr Met Gly Asn Trp Ser Asn Cys Ala Tyr
85 90 95

Gly Gly Asn Ala Thr Gly Cys Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Gly Cys Asn Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly
145 150 155 160

Ala Tyr Gly Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Ala Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Met Gly Asn Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
195 200 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser
210 215 220

Asn Ala Ala Arg Ala Ala Tyr Cys Ala Asn Tyr Thr Asn Gly Ala Tyr
225 230 235 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
245 250 255

Thr Asn Met Gly Asn Gly Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Thr Gly Gly Gly Gly Asn Ala Thr His Trp
290 295 300

Ser Asn Gly Cys Asn Cys Cys Asn Thr Thr Tyr Gly Ala Tyr Thr Gly
305 310 315 320

Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn
325 330 335

Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp
340 345 350

Ser Asn

<210> 682
<211> 345
<212> PRT
<213> Homo Sapiens

<400> 682

Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Gly Cys Asn Thr Ala Tyr
85 90 95

Trp Ser Asn Ala Thr Gly Ala Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Trp Ser Asn Thr Ala Tyr Ala Thr His Trp Ser Asn Trp Ser Asn Trp
145 150 155 160

Ser Asn Gly Gly Asn Met Gly Asn Cys Ala Asn Ala Thr His Thr Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

1551

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
195 200 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Gly Cys
210 215 220

Asn Ala Ala Arg Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Thr Thr Tyr
225 230 235 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
245 250 255

Thr Asn Met Gly Asn Gly Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Ala
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Tyr Thr Asn Thr Gly Gly Gly Cys Asn Cys Cys Asn Thr
290 295 300

Thr Tyr Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala
305 310 315 320

Arg Gly Gly Asn Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys Ala Asn
325 330 335

Gly Thr Asn Trp Ser Asn Trp Ser Asn
340 345

<210> 683
<211> 375
<212> PRT
<213> Homo Sapiens

<400> 683

Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Trp Ser Asn Ala Thr Gly Ala Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Trp Ser Asn Cys Ala Tyr Ala Thr His Trp Ser Asn Trp Ser Asn Trp
145 150 155 160

Ser Asn Trp Ser Asn Met Gly Asn Cys Ala Asn Ala Thr His Thr Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
195 200 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Gly Cys
210 215 220

Asn Ala Ala Arg Ala Ala Tyr Trp Ser Asn Gly Thr Asn Thr Ala Tyr
225 230 235 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
245 250 255

Thr Asn Met Gly Asn Gly Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Ala
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Gly Ala Tyr Gly Gly Asn Thr Ala Tyr Ala
290 295 300

Ala Tyr Thr Gly Gly Ala Ala Tyr Gly Gly Asn Gly Gly Asn Gly Gly
305 310 315 320

Asn Ala Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly
325 330 335

Gly Ala Tyr Gly Thr Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly
340 345 350

Gly Asn Cys Ala Asn Cys Ala Asn Gly Thr Asn Cys Ala Asn Gly Thr
355 360 365

2583

Asn Trp Ser Asn Trp Ser Asn
370 375

<210> 684
<211> 375
<212> PRT
<213> Homo Sapiens

<400> 684

Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Thr
65 70 75 80

Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Trp Ser Asn Ala Thr Gly Ala Ala Tyr Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Gly Thr Asn
130 135 140

Trp Ser Asn Cys Ala Tyr Ala Thr His Trp Ser Asn Met Gly Asn Trp
145 150 155 160

Ser Asn Trp Ser Asn Met Gly Asn Cys Ala Asn Ala Thr His Thr Ala
165 170 175

Tyr Thr Ala Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn
180 185 190

Ala Ala Arg Gly Gly Asn Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala
195 200 205

Thr His Trp Ser Asn Met Gly Asn Gly Ala Tyr Ala Ala Tyr Gly Cys
210 215 220

Asn Ala Ala Arg Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Thr Ala Tyr
225 230 235 240

Tyr Thr Asn Cys Ala Arg Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr
245 250 255

Thr Asn Met Gly Asn Gly Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Ala
260 265 270

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Gly Ala Tyr Gly Gly Asn Thr Ala Tyr Ala
290 295 300

Ala Tyr Thr Gly Gly Ala Ala Tyr Ala Ala Tyr Gly Gly Asn Gly Gly
305 310 315 320

Asn Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly
325 330 335

Gly Ala Tyr Gly Thr Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly
340 345 350

Gly Asn Cys Ala Asn Cys Ala Asn Gly Thr Asn Cys Ala Asn Gly Thr
355 360 365

Asn Trp Ser Asn Trp Ser Asn
370 375

<210> 685
<211> 354
<212> PRT
<213> Homo Sapiens

<400> 685

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

1555

Asn Trp Ser Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Gly Asn
85 90 95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Cys
145 150 155 160

Ala Tyr Trp Ser Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Cys Ala
165 170 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
180 185 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Cys
195 200 205

Ala Asn Ala Thr His Trp Ser Asn Gly Thr Asn Gly Ala Tyr Cys Ala
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225 230 235 240

Trp Ser Asn Tyr Thr Asn Ala Ala Tyr Tyr Thr Asn Trp Ser Asn Trp
245 250 255

Ser Asn Gly Thr Asn Cys Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala
260 265 270

Tyr Cys Ala Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Gly Gly Asn Cys Cys Asn Thr
290 295 300

Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr
305 310 315 320

Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn
325 330 335

Cys Ala Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp
340 345 350

Ser Asn

2556

<210> 686
<211> 381
<212> PRT
<213> Homo Sapiens

<400> 686

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Met Gly Asn Gly Gly Asn
85 90 95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Thr
145 150 155 160

Ala Tyr Cys Ala Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Cys Ala
165 170 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
180 185 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Ala
195 200 205

Ala Tyr Ala Thr Gly Trp Ser Asn Gly Thr Asn Gly Ala Tyr Cys Ala
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225 230 235 240

2554

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Tyr Thr Asn Trp Ser Asn Trp
245 250 255

Ser Asn Gly Thr Asn Cys Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala
260 265 270

Tyr Cys Ala Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Gly Cys Asn Tyr Thr Asn Met
290 295 300

Gly Asn Gly Gly Asn Ala Thr His Gly Thr Asn Tyr Thr Asn Ala Thr
305 310 315 320

Gly Gly Thr Asn Thr Ala Tyr Gly Thr Asn Tyr Thr Asn Gly Gly Asn
325 330 335

Gly Cys Asn Tyr Thr Asn Gly Ala Tyr Ala Thr His Thr Gly Gly Gly
340 345 350

Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Ala Ala Arg Gly Thr
355 360 365

Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
370 375 380

<210> 687
<211> 381
<212> PRT
<213> Homo Sapiens

<400> 687

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
85 90 95

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Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
            100                 105                 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Cys Ala
                165                 170                 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
            180                 185                 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Cys
        195                 200                 205

Ala Asn Ala Thr His Trp Ser Asn Gly Thr Asn Gly Ala Tyr Cys Ala
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225                 230                 235                 240

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Tyr Thr Asn Trp Ser Asn Trp
                245                 250                 255

Ser Asn Gly Thr Asn Cys Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala
            260                 265                 270

Tyr Cys Ala Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Gly Ala Tyr Gly Ala Arg Cys
    290                 295                 300

Ala Asn Gly Thr Asn Gly Thr Asn Met Gly Asn Gly Gly Asn Tyr Thr
305                 310                 315                 320

Asn Ala Thr His Met Gly Asn Thr Ala Tyr Thr Gly Tyr Thr Ala Tyr
                325                 330                 335

Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr Gly Gly Gly
            340                 345                 350

Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Cys Ala Asn Gly Thr
        355                 360                 365

Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
    370                 375                 380
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<210> 688
<211> 366
<212> PRT
<213> Homo Sapiens

<400> 688

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Ala Ala Tyr Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
85 90 95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Cys
145 150 155 160

Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Cys Ala
165 170 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
180 185 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Ala Thr His Cys
195 200 205

Ala Asn Ala Thr His Trp Ser Asn Gly Cys Asn Gly Ala Tyr Cys Ala
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225 230 235 240

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Tyr Thr Asn Ala Ala Tyr Trp
245 250 255

Ser Asn Gly Thr Asn Cys Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala
260 265 270

Tyr Cys Ala Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Gly Ala Tyr Met Gly Asn Gly
290 295 300

Gly Asn Gly Gly Asn Gly Gly Asn Gly Ala Tyr Thr Ala Tyr Gly Gly
305 310 315 320

Asn Met Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr Gly Gly
325 330 335

Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Cys Ala Asn Gly
340 345 350

Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
355 360 365

<210> 689
<211> 366
<212> PRT
<213> Homo Sapiens

<400> 689

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Ala Ala Tyr Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
85 90 95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
100 105 110

2361

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Cys
145 150 155 160

Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Cys Ala
165 170 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
180 185 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Ala Thr His Cys
195 200 205

Ala Asn Ala Thr His Trp Ser Asn Gly Cys Asn Gly Ala Tyr Cys Ala
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225 230 235 240

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Tyr Thr Asn Ala Ala Tyr Trp
245 250 255

Ser Asn Gly Thr Asn Cys Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala
260 265 270

Tyr Cys Ala Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Gly Ala Tyr Met Gly Asn Gly
290 295 300

Gly Asn Gly Gly Asn Gly Gly Asn Gly Ala Tyr Thr Ala Tyr Gly Gly
305 310 315 320

Asn Met Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr Gly Gly
325 330 335

Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Cys Ala Asn Gly
340 345 350

Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
355 360 365

<210> 690
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<400> 690

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Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
85 90 95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Cys
145 150 155 160

Ala Tyr Trp Ser Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Cys Ala
165 170 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
180 185 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Ala Thr His Cys
195 200 205

Ala Asn Ala Ala Arg Trp Ser Asn Gly Thr Asn Gly Ala Tyr Cys Ala
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225 230 235 240

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Tyr Thr Asn Trp Ser Asn Trp
245 250 255

Ser Asn Gly Thr Asn Cys Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala
260 265 270

Tyr Cys Ala Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Trp Ser Asn Ala Ala Tyr Ala
290 295 300

Ala Tyr Thr Ala Tyr Gly Gly Asn Thr Gly Tyr Thr Thr Tyr Gly Cys
305 310 315 320

Asn Tyr Thr Asn Thr Gly Gly Gly Gly Asn Met Gly Asn Gly Gly Asn
325 330 335

Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp
340 345 350

Ser Asn Trp Ser Asn
355

<210> 691
<211> 357
<212> PRT
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<400> 691

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
85 90 95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Cys
145 150 155 160

Ala Tyr Trp Ser Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Cys Ala
165 170 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
180 185 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Ala Thr His Cys
195 200 205

Ala Asn Ala Ala Arg Trp Ser Asn Gly Thr Asn Gly Ala Tyr Cys Ala
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225 230 235 240

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Tyr Thr Asn Trp Ser Asn Trp
245 250 255

Ser Asn Gly Thr Asn Cys Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala
260 265 270

Tyr Cys Ala Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Trp Ser Asn Ala Ala Tyr Ala
290 295 300

Ala Tyr Thr Ala Tyr Gly Gly Asn Thr Gly Tyr Thr Thr Tyr Gly Cys
305 310 315 320

Asn Tyr Thr Asn Thr Gly Gly Gly Gly Asn Met Gly Asn Gly Gly Asn
325 330 335

Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp
340 345 350

Ser Asn Trp Ser Asn
355

<210> 692
<211> 399
<212> PRT
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<400> 692

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
85 90 95

Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Cys
145 150 155 160

Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Cys Ala
165 170 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
180 185 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Cys
195 200 205

Ala Asn Ala Thr His Trp Ser Asn Gly Thr Asn Gly Ala Tyr Cys Ala
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225 230 235 240

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Tyr Thr Asn Trp Ser Asn Trp
245 250 255

Ser Asn Gly Thr Asn Cys Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala
260 265 270

Tyr Cys Ala Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Trp Ser Asn Gly Gly Asn Thr Ala Tyr Ala
290 295 300

2566

Ala Tyr Thr Ala Tyr Gly Gly Asn Tyr Thr Asn Thr Ala Tyr Thr Ala
305 310 315 320

Tyr Thr Ala Tyr Gly Ala Tyr Trp Ser Asn Trp Ser Asn Gly Gly Asn
325 330 335

Thr Ala Tyr Cys Cys Asn Trp Ser Asn Thr Ala Tyr Thr Ala Tyr Thr
340 345 350

Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr Gly
355 360 365

Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Cys Ala Asn
370 375 380

Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
385 390 395

<210> 693
<211> 375
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<213> Homo Sapiens

<400> 693

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
85 90 95

Gly Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Ala Ala Tyr Thr
100 105 110

Gly Gly Gly Thr Asn Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
115 120 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Thr
145 150 155 160

Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Gly Gly Asn Cys Ala
165 170 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
180 185 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Cys
195 200 205

Ala Asn Ala Thr His Trp Ser Asn Gly Thr Asn Gly Ala Tyr Cys Ala
210 215 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225 230 235 240

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Tyr Thr Asn Thr Thr Tyr Trp
245 250 255

Ser Asn Gly Thr Asn Cys Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala
260 265 270

Tyr Cys Ala Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Thr Tyr
275 280 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Cys Ala Asn Thr Ala Tyr Thr
290 295 300

Ala Tyr Gly Ala Tyr Ala Thr His Tyr Thr Asn Cys Ala Asn Gly Gly
305 310 315 320

Asn Thr Ala Tyr Cys Cys Asn Thr Thr Tyr Thr Ala Tyr Thr Thr Tyr
325 330 335

Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly
340 345 350

Gly Asn Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr
355 360 365

Asn Trp Ser Asn Trp Ser Asn
370 375

<210> 694
<211> 375
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<213> Homo Sapiens

<400> 694

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Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
            20                  25                  30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
        35                  40                  45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
    50                  55                  60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65                  70                  75                  80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Gly Gly Asn
                85                  90                  95

Gly Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Ala Ala Tyr Thr
            100                 105                 110

Gly Gly Gly Thr Asn Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Gly Gly Asn Cys Ala
                165                 170                 175

Asn Thr Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
            180                 185                 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Cys
        195                 200                 205

Ala Asn Ala Thr His Trp Ser Asn Gly Thr Asn Gly Ala Tyr Cys Ala
    210                 215                 220

Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225                 230                 235                 240

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Tyr Thr Asn Thr Thr Tyr Trp
                245                 250                 255

Ser Asn Gly Thr Asn Cys Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala
            260                 265                 270

Tyr Cys Ala Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Thr Tyr
        275                 280                 285
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Thr Gly Tyr Gly Cys Asn Met Gly Asn Cys Ala Asn Thr Ala Tyr Thr
290 295 300

Ala Tyr Gly Ala Tyr Ala Thr His Tyr Thr Asn Cys Ala Asn Gly Gly
305 310 315 320

Asn Thr Ala Tyr Cys Cys Asn Thr Thr Tyr Thr Ala Tyr Thr Thr Tyr
325 330 335

Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly
340 345 350

Gly Asn Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr
355 360 365

Asn Trp Ser Asn Trp Ser Asn
370 375

<210> 695
<211> 360
<212> PRT
<213> Homo Sapiens

<400> 695

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Cys
1 5 10 15

Ala Arg Thr Gly Gly Gly Gly Asn Gly Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Tyr Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Gly Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Thr Asn Thr Ala Tyr Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Ala Tyr
85 90 95

Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr Gly Gly Ala Thr His Met
100 105 110

Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr His
130 135 140

Gly Gly Asn Gly Ala Arg Ala Thr His Ala Ala Tyr Cys Ala Tyr Trp
145 150 155 160

Ser Asn Gly Gly Asn Trp Ser Asn Cys Ala Asn Ala Ala Tyr Thr Ala
165 170 175

Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg
180 185 190

Trp Ser Asn Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Trp
195 200 205

Ser Asn Gly Thr Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala
210 215 220

Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn
225 230 235 240

Ala Ala Arg Tyr Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Cys
245 250 255

Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala Tyr Cys Ala Asn Gly Cys
260 265 270

Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn
275 280 285

Met Gly Asn Gly Gly Asn Gly Gly Asn Thr Ala Tyr Trp Ser Asn Trp
290 295 300

Ser Asn Trp Ser Asn Thr Gly Gly Thr Ala Tyr Thr Gly Gly Thr Thr
305 310 315 320

Tyr Gly Ala Tyr Cys Cys Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg
325 330 335

Gly Gly Asn Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly
340 345 350

Thr Asn Trp Ser Asn Trp Ser Asn
355 360

<210> 696
<211> 360
<212> PRT
<213> Homo Sapiens

<400> 696

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Cys
1 5 10 15

Ala Arg Thr Gly Gly Gly Gly Asn Gly Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Tyr Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Gly Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Thr Asn Thr Ala Tyr Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Thr Thr Tyr Trp Ser Asn Gly Gly Asn Thr Ala Tyr
85 90 95

Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr Gly Gly Ala Thr His Met
100 105 110

Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr His
130 135 140

Gly Gly Asn Gly Ala Arg Ala Thr His Ala Ala Tyr Cys Ala Tyr Trp
145 150 155 160

Ser Asn Gly Gly Asn Trp Ser Asn Cys Ala Asn Ala Ala Tyr Thr Ala
165 170 175

Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg
180 185 190

Trp Ser Asn Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Trp
195 200 205

Ser Asn Gly Thr Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala
210 215 220

Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn
225 230 235 240

Ala Ala Arg Tyr Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Cys
245 250 255

Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala Tyr Cys Ala Asn Gly Cys
260 265 270

Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn
275 280 285

Met Gly Asn Gly Gly Asn Gly Gly Asn Thr Ala Tyr Trp Ser Asn Trp
290 295 300

2542

Ser Asn Trp Ser Asn Thr Gly Gly Thr Thr Tyr Thr Gly Gly Thr Thr
305 310 315 320

Tyr Gly Ala Tyr Cys Cys Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg
325 330 335

Gly Gly Asn Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly
340 345 350

Thr Asn Trp Ser Asn Trp Ser Asn
355 360

<210> 697
<211> 369
<212> PRT
<213> Homo Sapiens

<400> 697

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Gly Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65 70 75 80

Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr Gly Gly Ala Thr His Met
100 105 110

Gly Asn Cys Ala Arg Cys Cys Asn Gly Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr His
130 135 140

Gly Gly Asn Met Gly Asn Ala Thr His Thr Ala Tyr Cys Ala Asn Trp
145 150 155 160

Ser Asn Gly Gly Asn Cys Ala Asn Cys Ala Asn Ala Ala Tyr Thr Ala
165 170 175

Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg
180 185 190

Trp Ser Asn Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr Gly Trp
195 200 205

Ser Asn Gly Thr Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala
210 215 220

Arg Ala Ala Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn
225 230 235 240

Ala Ala Arg Tyr Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Cys
245 250 255

Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala Tyr Cys Ala Asn Gly Cys
260 265 270

Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn
275 280 285

Met Gly Asn Gly Ala Tyr Gly Gly Asn Thr Ala Tyr Trp Ser Asn Thr
290 295 300

Ala Tyr Gly Gly Asn Cys Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala
305 310 315 320

Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn
325 330 335

Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Cys
340 345 350

Ala Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser
355 360 365

Asn

<210> 698
<211> 378
<212> PRT
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<400> 698

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

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Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Gly Ala Arg
        35                  40                  45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
    50                  55                  60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Gly Gly Asn Gly Gly
65                  70                  75                  80

Asn Trp Ser Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Gly Gly Asn
                85                  90                  95

Gly Gly Asn Trp Ser Asn Thr Ala Tyr Thr Gly Gly Trp Ser Asn Thr
            100                 105                 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys
        115                 120                 125

Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg
    130                 135                 140

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Ala Tyr Ala Thr His Thr
145                 150                 155                 160

Ala Tyr Thr Ala Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Cys Ala
                165                 170                 175

Asn Ala Ala Tyr Thr Ala Tyr Ala Ala Tyr Cys Cys Asn Trp Ser Asn
            180                 185                 190

Tyr Thr Asn Ala Ala Arg Trp Ser Asn Met Gly Asn Gly Thr Asn Cys
        195                 200                 205

Ala Asn Ala Thr His Trp Ser Asn Ala Thr His Gly Thr Asn Cys Ala
    210                 215                 220

Asn Trp Ser Asn Met Gly Asn Ala Ala Tyr Cys Ala Arg Thr Thr Tyr
225                 230                 235                 240

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Tyr Thr Asn Trp Ser Asn Trp
                245                 250                 255

Ser Asn Gly Thr Asn Cys Ala Asn Gly Cys Asn Gly Cys Asn Gly Ala
            260                 265                 270

Tyr Cys Ala Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr
        275                 280                 285

Thr Gly Tyr Gly Cys Asn Met Gly Asn Trp Ser Asn Gly Cys Asn Tyr
    290                 295                 300

Thr Asn Met Gly Asn Thr Ala Tyr Thr Thr Tyr Gly Ala Tyr Thr Gly
305                 310                 315                 320
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Gly Tyr Thr Asn Thr Thr Tyr Trp Ser Asn Gly Ala Tyr Gly Thr Asn
325 330 335

Trp Ser Asn Gly Ala Tyr Ala Thr His Thr Gly Gly Gly Gly Asn Cys
340 345 350

Ala Arg Gly Gly Asn Cys Ala Asn Ala Thr Gly Gly Thr Asn Cys Ala
355 360 365

Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
370 375

<210> 699
<211> 360
<212> PRT
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<400> 699

Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Tyr Thr
20 25 30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Ala Arg
35 40 45

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Ala Thr His Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Gly Asn Trp Ser Asn Gly Gly Asn Thr Ala
65 70 75 80

Tyr Met Gly Asn Thr Thr Tyr Cys Ala Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Ala Thr Gly Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
130 135 140

Gly Gly Asn Ala Thr His Ala Thr His Thr Ala Tyr Cys Cys Asn Gly
145 150 155 160

Ala Tyr Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Cys Ala Asn Met Gly
165 170 175

2376

Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn Thr Thr Tyr
180 185 190

Cys Ala Arg Gly Gly Asn Cys Ala Arg Gly Thr Asn Cys Ala Asn Ala
195 200 205

Thr His Trp Ser Asn Gly Cys Asn Gly Ala Tyr Ala Ala Arg Trp Ser
210 215 220

Asn Ala Thr His Trp Ser Asn Cys Ala Asn Gly Cys Asn Thr Ala Tyr
225 230 235 240

Tyr Thr Asn Cys Ala Arg Thr Gly Gly Trp Ser Asn Trp Ser Asn Tyr
245 250 255

Thr Asn Ala Ala Arg Gly Cys Asn Trp Ser Asn Gly Ala Tyr Cys Ala
260 265 270

Asn Gly Cys Asn Ala Thr Gly Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Cys Ala Arg Ala Ala Arg Trp Ser Asn Thr
290 295 300

Ala Tyr Gly Gly Asn Thr Ala Tyr Trp Ser Asn Thr Ala Tyr Thr Thr
305 310 315 320

Tyr Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn Cys Ala Arg
325 330 335

Gly Gly Asn Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys Ala Asn Gly
340 345 350

Thr Asn Trp Ser Asn Trp Ser Asn
355 360

<210> 700
<211> 363
<212> PRT
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<400> 700

Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
20 25 30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Ala Arg
35 40 45

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Trp Ser Asn Tyr Thr Asn Ala Ala Arg Ala Thr His Trp Ser Asn Thr
    50                  55                  60

Gly Tyr Ala Ala Arg Gly Gly Asn Trp Ser Asn Gly Gly Asn Thr Ala
65                  70                  75                  80

Tyr Trp Ser Asn Thr Thr Tyr Cys Ala Asn Trp Ser Asn Thr Ala Tyr
                85                  90                  95

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Gly Gly Gly Thr Asn Met
            100                 105                 110

Gly Asn Cys Ala Arg Ala Thr Gly Cys Cys Asn Gly Gly Asn Ala Ala
        115                 120                 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
    130                 135                 140

Gly Gly Asn Ala Thr His Ala Thr His Thr Ala Tyr Cys Cys Asn Gly
145                 150                 155                 160

Ala Tyr Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Cys Asn Met Gly
                165                 170                 175

Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn Thr Thr Tyr
            180                 185                 190

Cys Ala Arg Gly Gly Asn Cys Ala Arg Gly Thr Asn Cys Ala Asn Ala
        195                 200                 205

Thr His Trp Ser Asn Gly Cys Asn Gly Ala Tyr Ala Ala Arg Trp Ser
    210                 215                 220

Asn Ala Thr His Ala Ala Tyr Cys Ala Asn Gly Cys Asn Thr Ala Tyr
225                 230                 235                 240

Tyr Thr Asn Cys Ala Arg Thr Gly Gly Trp Ser Asn Trp Ser Asn Tyr
                245                 250                 255

Thr Asn Ala Ala Arg Gly Cys Asn Trp Ser Asn Gly Ala Tyr Cys Ala
            260                 265                 270

Asn Gly Cys Asn Ala Thr Gly Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
        275                 280                 285

Gly Cys Asn Met Gly Asn Cys Ala Arg Gly Gly Asn Thr Ala Tyr Gly
    290                 295                 300

Gly Asn Trp Ser Asn Gly Gly Asn Thr Gly Gly Gly Gly Asn Thr Ala
305                 310                 315                 320

Tyr Thr Thr Tyr Gly Ala Tyr Thr Ala Tyr Thr Gly Gly Gly Gly Asn
                325                 330                 335
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Cys Ala Arg Gly Gly Asn Cys Ala Asn Tyr Thr Asn Gly Thr Asn Cys
340 345 350

Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
355 360

<210> 701
<211> 381
<212> PRT
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<400> 701

Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
20 25 30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Ala Arg
35 40 45

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Ala Thr His Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Gly Asn Trp Ser Asn Gly Gly Asn Thr Ala
65 70 75 80

Tyr Trp Ser Asn Thr Thr Tyr Cys Ala Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Thr Gly Gly Ala Thr His Gly Gly Asn Thr Gly Gly Gly Thr Asn Met
100 105 110

Gly Asn Cys Ala Arg Ala Thr Gly Cys Cys Asn Gly Gly Asn Ala Ala
115 120 125

Arg Gly Gly Asn Tyr Thr Asn Gly Ala Arg Thr Gly Gly Ala Thr Gly
130 135 140

Gly Gly Asn Ala Thr His Ala Thr His Thr Ala Tyr Cys Cys Asn Gly
145 150 155 160

Gly Asn Gly Ala Tyr Trp Ser Asn Gly Ala Tyr Ala Thr His Met Gly
165 170 175

Asn Thr Ala Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn Thr Thr Tyr
180 185 190

Cys Ala Arg Gly Gly Asn Cys Ala Arg Gly Thr Asn Cys Ala Asn Ala
195 200 205

2579

Thr His Trp Ser Asn Gly Cys Asn Gly Ala Tyr Ala Ala Arg Trp Ser
210 215 220

Asn Ala Thr His Trp Ser Asn Cys Ala Asn Gly Cys Asn Thr Ala Tyr
225 230 235 240

Tyr Thr Asn Cys Ala Arg Thr Gly Gly Trp Ser Asn Trp Ser Asn Tyr
245 250 255

Thr Asn Ala Ala Arg Gly Cys Asn Trp Ser Asn Gly Ala Tyr Cys Ala
260 265 270

Asn Gly Cys Asn Ala Thr Gly Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
275 280 285

Gly Cys Asn Met Gly Asn Cys Ala Arg Gly Gly Asn Tyr Thr Asn Gly
290 295 300

Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly Asn Cys Ala Asn Trp Ser
305 310 315 320

Asn Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr
325 330 335

Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn Thr Gly Gly Gly
340 345 350

Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Cys Ala Asn Gly Thr
355 360 365

Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn
370 375 380

<210> 702
<211> 375
<212> PRT
<213> Homo Sapiens

<400> 702

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

1580

Gly Tyr Gly Cys Asn Ala Thr His Trp Ser Asn Gly Gly Asn Gly Ala
65 70 75 80

Tyr Trp Ser Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Thr Ala Tyr
85 90 95

Trp Ser Asn Gly Cys Asn Gly Cys Asn Thr Gly Gly Ala Ala Tyr Thr
100 105 110

Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Trp Ser Asn Cys Cys
115 120 125

Asn Trp Ser Asn Met Gly Asn Gly Gly Asn Tyr Thr Asn Gly Ala Arg
130 135 140

Thr Gly Gly Tyr Thr Asn Gly Gly Asn Met Gly Asn Cys Ala Asn Thr
145 150 155 160

Ala Tyr Thr Gly Tyr Met Gly Asn Trp Ser Asn Ala Ala Arg Thr Gly
165 170 175

Gly Thr Ala Tyr Ala Ala Tyr Gly Ala Tyr Thr Ala Tyr Gly Cys Asn
180 185 190

Gly Thr Asn Trp Ser Asn Gly Thr Asn Ala Ala Arg Trp Ser Asn Met
195 200 205

Gly Asn Ala Thr His Cys Ala Asn Ala Thr His Ala Ala Tyr Cys Cys
210 215 220

Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Ala Ala Tyr
225 230 235 240

Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Cys Ala Arg Tyr
245 250 255

Thr Asn Ala Ala Tyr Trp Ser Asn Gly Thr Asn Cys Ala Asn Cys Cys
260 265 270

Asn Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr Asn
275 280 285

Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn Gly
290 295 300

Ala Tyr Met Gly Asn Gly Cys Asn Gly Thr Asn Gly Cys Asn Gly Gly
305 310 315 320

Asn Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly
325 330 335

Gly Ala Tyr Gly Thr Asn Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly
340 345 350

Gly Asn Cys Ala Asn Cys Ala Asn Gly Thr Asn Cys Ala Asn Gly Thr
355 360 365

Asn Trp Ser Asn Trp Ser Asn
370 375

<210> 703
<211> 324
<212> ADN
<213> Homo Sapiens

<400> 703
cgaactgtgg ctgcaccatc tgtcttcatc ttcccgccat ctgatgagca gttgaaatct 60

ggaactgcta gcgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag 120

tggaaggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac 180

agcaaggaca gcacctacag cctcagcagc accctgacgc tgagcaaagc agactacgag 240

aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag 300

agcttcaaca ggggagagtg ttag 324

<210> 704
<211> 981
<212> ADN
<213> Homo Sapiens

<400> 704
gcctccacca agggcccatc ggtcttcccc ctggcgccct gctctagaag cacctccgag 60

agcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 120

tggaactcag gcgctctgac cagcggcgtg cacaccttcc cagctgtcct acagtcctca 180

ggactctact ccctcagcag cgtggtgacc gtgccctcca gcaacttcgg cacccagacc 240

tacacatgca acgtagatca caagcccagc aacaccaagg tggacaagac agttgagcgc 300

aaatgttgtg tcgagtgccc accgtgccca gcaccacctg tggcaggacc gtcagtcttc 360

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacgtgc 420

gtggtggtgg acgtgagcca cgaagacccc gaggtccagt tcaactggta cgtggacggc 480

gtggaggtgc ataatgccaa gacaaagcca cgggaggagc agttcaacag cacgttccgt 540

gtggtcagcg tcctcaccgt tgtgcaccag gactggctga acggcaagga gtacaagtgc 600

aaggtctcca acaaaggcct cccagccccc atcgagaaaa ccatctccaa aaccaaaggg 660

cagccccgag aaccacaggt gtacaccctg cccccatccc gggaggagat gaccaagaac 720

caggtcagcc tgacctgcct ggtcaaaggc ttctacccca gcgacatcgc cgtggagtgg 780

gagagcaatg ggcagccgga gaacaactac aagaccacac ctcccatgct ggactccgac 840

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 900

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 960

tccctgtctc cgggtaaatg a 981

<210> 705
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 705

Met Gly Asn Trp Ser Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Tyr
1 5 10 15

Thr Asn Gly Thr Asn Thr Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Gly
20 25 30

Asn Ala Ala Tyr Cys Ala Asn Thr Ala Tyr Tyr Thr Asn Ala Ala Tyr
35 40 45

<210> 706
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 706

Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Tyr
1 5 10 15

Thr Asn Tyr Thr Asn Cys Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Gly
20 25 30

Asn Ala Ala Arg Cys Ala Asn Thr Ala Tyr Tyr Thr Asn Thr Ala Tyr
35 40 45

<210> 707
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 707

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Gly Gly Asn Ala
1 5 10 15

1583

Thr His Gly Cys Asn Ala Ala Tyr Thr Ala Tyr Tyr Thr Asn Gly Cys
20 25 30

Asn

<210> 708
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 708

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Gly Gly Asn Ala
1 5 10 15

Thr His Trp Ser Asn Ala Ala Tyr Gly Ala Tyr Tyr Thr Asn Gly Cys
20 25 30

Asn

<210> 709
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 709

Met Gly Asn Trp Ser Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Tyr
1 5 10 15

Thr Asn Gly Thr Asn Cys Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Gly
20 25 30

Asn Ala Ala Tyr Cys Ala Asn Thr Ala Tyr Tyr Thr Asn Trp Ser Asn
35 40 45

<210> 710
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 710

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Cys Ala Asn Gly
1 5 10 15

Thr Asn Ala Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr Tyr Thr
20 25 30

Asn Gly Cys Asn
35

2384

<210> 711
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 711

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Gly
1 5 10 15

Thr Asn Trp Ser Asn Met Gly Asn Tyr Thr Asn Gly Cys Asn
20 25 30

<210> 712
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 712

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Gly Gly Asn Ala
1 5 10 15

Thr His Met Gly Asn Ala Ala Tyr Gly Ala Tyr Tyr Thr Asn Gly Gly
20 25 30

Asn

<210> 713
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 713

Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Gly
1 5 10 15

Thr Asn Tyr Thr Asn Thr Ala Tyr Trp Ser Asn Trp Ser Asn Ala Ala
20 25 30

Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr Ala Tyr Tyr Thr Asn
35 40 45

Gly Thr Asn
50

<210> 714
<211> 51
<212> PRT
<213> Homo Sapiens

1585

<400> 714

Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Gly
1 5 10 15

Thr Asn Tyr Thr Asn Thr Ala Tyr Trp Ser Asn Trp Ser Asn Ala Ala
20 25 30

Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr Ala Tyr Tyr Thr Asn
35 40 45

Gly Cys Asn
50

<210> 715
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 715

Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala Arg Ala Ala Tyr Gly
1 5 10 15

Thr Asn Tyr Thr Asn Thr Ala Tyr Trp Ser Asn Trp Ser Asn Ala Ala
20 25 30

Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr Ala Tyr Tyr Thr Asn
35 40 45

Gly Cys Asn
50

<210> 716
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 716

Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Gly
1 5 10 15

Thr Asn Tyr Thr Asn Thr Ala Tyr Ala Ala Tyr Trp Ser Asn Ala Ala
20 25 30

Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr Ala Tyr Tyr Thr Asn
35 40 45

Gly Cys Asn
50

<210> 717

1386

<211> 51
<212> PRT
<213> Homo Sapiens

<400> 717

Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Gly
1 5 10 15

Thr Asn Tyr Thr Asn Gly Ala Tyr Trp Ser Asn Trp Ser Asn Ala Ala
20 25 30

Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr Ala Tyr Tyr Thr Asn
35 40 45

Gly Cys Asn
50

<210> 718
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 718

Ala Ala Arg Trp Ser Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Ala
1 5 10 15

Thr His Tyr Thr Asn Thr Ala Tyr Met Gly Asn Trp Ser Asn Ala Ala
20 25 30

Tyr Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr Ala Tyr Tyr Thr Asn
35 40 45

Gly Cys Asn
50

<210> 719
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 719

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Gly Ala Tyr Ala
1 5 10 15

Thr His Trp Ser Asn Cys Ala Tyr Thr Ala Tyr Tyr Thr Asn Gly Cys
20 25 30

Asn

<210> 720
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 720

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Gly Ala Tyr Ala
1 5 10 15

Thr His Trp Ser Asn Ala Ala Tyr Thr Ala Tyr Tyr Thr Asn Gly Cys
20 25 30

Asn

<210> 721
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 721

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Gly
1 5 10 15

Thr Asn Trp Ser Asn Trp Ser Asn Ala Ala Tyr Tyr Thr Asn Gly Cys
20 25 30

Asn

<210> 722
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 722

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Gly Ala Tyr Ala
1 5 10 15

Thr His Trp Ser Asn Met Gly Asn Thr Gly Gly Tyr Thr Asn Gly Cys
20 25 30

Asn

<210> 723
<211> 33
<212> PRT
<213> Homo Sapiens

2388

<400> 723

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Ala
1 5 10 15

Thr His Trp Ser Asn Cys Ala Asn Thr Ala Tyr Tyr Thr Asn Ala Ala
20 25 30

Tyr

<210> 724
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 724

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Cys Ala Asn Ala
1 5 10 15

Thr His Trp Ser Asn Ala Thr His Thr Ala Tyr Tyr Thr Asn Ala Ala
20 25 30

Tyr

<210> 725
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 725

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Ala
1 5 10 15

Thr His Met Gly Asn Trp Ser Asn Thr Ala Tyr Tyr Thr Asn Ala Ala
20 25 30

Tyr

<210> 726
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 726

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Cys Ala Asn Ala
1 5 10 15

2589

Thr His Trp Ser Asn Met Gly Asn Thr Ala Tyr Tyr Thr Asn Ala Ala
20 25 30

Tyr

<210> 727
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 727

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Met Gly Asn Ala
1 5 10 15

Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr Tyr Thr Asn Ala Ala
20 25 30

Tyr

<210> 728
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 728

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Ala
1 5 10 15

Thr His Trp Ser Asn Met Gly Asn Thr Ala Tyr Tyr Thr Asn Ala Ala
20 25 30

Tyr

<210> 729
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 729

Met Gly Asn Gly Cys Asn Trp Ser Asn Cys Ala Arg Trp Ser Asn Ala
1 5 10 15

Thr His Trp Ser Asn Trp Ser Asn Thr Ala Tyr Tyr Thr Asn Ala Ala
20 25 30

Tyr

<210> 730
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 730

Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala Arg Gly Ala Tyr Ala
1 5 10 15

Thr His Trp Ser Asn Ala Ala Tyr Thr Ala Tyr Tyr Thr Asn Ala Ala
20 25 30

Tyr

<210> 731
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 731

Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala Arg Gly Ala Tyr Ala
1 5 10 15

Thr His Trp Ser Asn Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Ala Ala
20 25 30

Tyr

<210> 732
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 732

Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala Arg Gly Ala Tyr Ala
1 5 10 15

Thr His Trp Ser Asn Gly Ala Tyr Thr Ala Tyr Tyr Thr Asn Ala Ala
20 25 30

Tyr

<210> 733
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 733

Cys Ala Arg Gly Cys Asn Trp Ser Asn Cys Ala Arg Gly Ala Tyr Ala
1 5 10 15

Thr His Cys Ala Asn Ala Ala Tyr Thr Ala Tyr Tyr Thr Asn Ala Ala
20 25 30

Tyr

<210> 734
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 734

Ala Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Thr Gly Gly Gly
1 5 10 15

Ala Tyr Trp Ser Asn
20

<210> 735
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 735

Gly Ala Arg Gly Thr Asn Trp Ser Asn Ala Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn
20

<210> 736
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 736

Gly Thr Asn Gly Cys Asn Trp Ser Asn Cys Ala Asn Tyr Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn
20

<210> 737
<211> 21
<212> PRT

2592

<213> Homo Sapiens

<400> 737

Gly Cys Asn Gly Cys Asn Trp Ser Asn Cys Ala Asn Tyr Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn
20

<210> 738
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 738

Ala Ala Arg Ala Thr His Trp Ser Asn Ala Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn
20

<210> 739
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 739

Gly Gly Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Met Gly Asn Gly
1 5 10 15

Cys Asn Cys Ala Asn
20

<210> 740
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 740

Gly Gly Asn Gly Cys Asn Trp Ser Asn Met Gly Asn Met Gly Asn Gly
1 5 10 15

Cys Asn Cys Ala Asn
20

<210> 741
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 741

Gly Cys Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn
20

<210> 742
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 742

Thr Gly Gly Gly Cys Asn Trp Ser Asn Cys Ala Asn Met Gly Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn
20

<210> 743
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 743

Thr Gly Gly Gly Cys Asn Trp Ser Asn Cys Ala Asn Met Gly Asn Ala
1 5 10 15

Ala Arg Trp Ser Asn
20

<210> 744
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 744

Thr Gly Gly Gly Cys Asn Trp Ser Asn Gly Cys Asn Met Gly Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn
20

<210> 745
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 745

Gly Cys Asn Gly Ala Arg Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn
20

<210> 746
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 746

Cys Ala Asn Gly Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn
20

<210> 747
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 747

Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser Asn Tyr Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn
20

<210> 748
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 748

Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Ala Tyr Tyr Thr Asn Gly
1 5 10 15

Ala Arg Cys Ala Asn
20

<210> 749
<211> 21
<212> PRT
<213> Homo Sapiens

<400> 749

2595

Gly Ala Tyr Gly Cys Asn Trp Ser Asn Ala Thr His Tyr Thr Asn Gly
1 5 10 15

Ala Arg Cys Ala Asn
20

<210> 750
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 750

Ala Thr Gly Cys Ala Arg Trp Ser Asn Cys Ala Asn Cys Ala Tyr Thr
1 5 10 15

Gly Gly Cys Cys Asn Ala Thr His Cys Ala Asn
20 25

<210> 751
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 751

Ala Thr His Cys Ala Arg Gly Gly Asn Cys Ala Asn Cys Ala Tyr Thr
1 5 10 15

Gly Gly Cys Cys Asn Cys Ala Asn Cys Ala Asn
20 25

<210> 752
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 752

Ala Thr Gly Cys Ala Arg Gly Gly Asn Cys Ala Asn Cys Ala Tyr Thr
1 5 10 15

Gly Gly Cys Cys Asn Ala Thr His Cys Ala Asn
20 25

<210> 753
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 753

2598

Ala Thr Gly Cys Ala Arg Gly Gly Asn Ala Thr His Cys Ala Arg Tyr
1 5 10 15

Thr Asn Cys Cys Asn Thr Gly Tyr Trp Ser Asn
20 25

<210> 754
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 754

Ala Thr Gly Cys Ala Arg Trp Ser Asn Ala Thr His Cys Ala Arg Tyr
1 5 10 15

Thr Asn Cys Cys Asn Tyr Thr Asn Cys Ala Asn
20 25

<210> 755
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 755

Ala Thr Gly Cys Ala Arg Trp Ser Asn Ala Thr His Cys Ala Arg Tyr
1 5 10 15

Thr Asn Cys Cys Asn Ala Thr His Cys Ala Asn
20 25

<210> 756
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 756

Cys Ala Arg Ala Ala Tyr Thr Ala Tyr Ala Ala Tyr Trp Ser Asn Gly
1 5 10 15

Cys Asn Cys Cys Asn Thr Thr Tyr Cys Ala Asn
20 25

<210> 757
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 757

Cys Ala Arg Ala Ala Arg Thr Ala Tyr Ala Ala Tyr Trp Ser Asn Gly
1 5 10 15

Thr Asn Cys Cys Asn Tyr Thr Asn Cys Ala Asn
20 25

<210> 758
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 758

Ala Thr Gly Cys Ala Arg Gly Cys Asn Cys Ala Asn Cys Ala Arg Thr
1 5 10 15

Thr Tyr Cys Cys Asn Cys Ala Tyr Cys Ala Asn
20 25

<210> 759
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 759

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Gly Gly Asn Trp Ser Asn Trp
1 5 10 15

Ser Asn Cys Cys Asn Met Gly Asn Cys Ala Asn
20 25

<210> 760
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 760

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Gly Gly Asn Trp Ser Asn Trp
1 5 10 15

Ser Asn Cys Cys Asn Met Gly Asn Trp Ser Asn
20 25

<210> 761
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 761

2598

Tyr Thr Asn Cys Ala Arg Cys Ala Tyr Ala Ala Tyr Trp Ser Asn Thr
1 5 10 15

Ala Tyr Cys Cys Asn Cys Cys Asn Cys Ala Asn
20 25

<210> 762
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 762

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Thr
1 5 10 15

Thr Tyr Cys Cys Asn Thr Gly Gly Cys Ala Asn
20 25

<210> 763
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 763

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Cys
1 5 10 15

Ala Asn Cys Ala Asn Thr Gly Gly Cys Ala Asn
20 25

<210> 764
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 764

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Cys
1 5 10 15

Ala Asn Cys Cys Asn Met Gly Asn Cys Ala Asn
20 25

<210> 765
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 765

2599

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Ala
1 5 10 15

Thr His Trp Ser Asn Met Gly Asn Cys Ala Asn
20 25

<210> 766
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 766

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Cys
1 5 10 15

Ala Asn Ala Thr Gly Thr Thr Tyr Trp Ser Asn
20 25

<210> 767
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 767

Cys Ala Tyr Cys Ala Arg Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Cys
1 5 10 15

Ala Asn Cys Cys Asn Tyr Thr Asn Cys Ala Asn
20 25

<210> 768
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 768

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Thr Thr Tyr Ala Thr His Cys
1 5 10 15

Ala Asn Cys Cys Asn Tyr Thr Asn Cys Ala Asn
20 25

<210> 769
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 769

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Ala Ala Tyr Ala Ala Tyr Thr
1 5 10 15

Ala Tyr Cys Cys Asn Thr Thr Tyr Cys Ala Asn
20 25

<210> 770
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 770

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Ala Ala Tyr Cys Ala Asn Thr
1 5 10 15

Ala Tyr Cys Cys Asn Thr Thr Tyr Cys Ala Asn
20 25

<210> 771
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 771

Cys Ala Arg Cys Ala Arg Cys Ala Tyr Ala Ala Tyr Ala Ala Tyr Thr
1 5 10 15

Gly Gly Cys Cys Asn Cys Cys Asn Thr Gly Gly Cys Ala Asn
20 25 30

<210> 772
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 772

Cys Ala Arg Cys Ala Arg Gly Cys Asn Ala Ala Tyr Trp Ser Asn Thr
1 5 10 15

Thr Tyr Cys Cys Asn Cys Cys Asn Cys Ala Asn
20 25

<210> 773
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 773

Cys Ala Arg Cys Ala Arg Trp Ser Asn Cys Ala Tyr Trp Ser Asn Gly
1 5 10 15

Cys Asn Cys Cys Asn Thr Thr Tyr Cys Ala Asn
20 25

<210> 774
<211> 24
<212> PRT
<213> Homo Sapiens

<400> 774

Cys Ala Arg Cys Ala Arg Trp Ser Asn Thr Ala Tyr Trp Ser Asn Cys
1 5 10 15

Ala Asn Tyr Thr Asn Cys Ala Asn
20

<210> 775
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 775

Cys Ala Arg Cys Ala Arg Trp Ser Asn Thr Ala Tyr Trp Ser Asn Ala
1 5 10 15

Thr His Cys Cys Asn Tyr Thr Asn Cys Ala Asn
20 25

<210> 776
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 776

Cys Ala Arg Cys Ala Arg Ala Thr His Thr Ala Tyr Trp Ser Asn Cys
1 5 10 15

Ala Asn Trp Ser Asn Ala Thr His Cys Ala Asn
20 25

<210> 777
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 777

2602

Cys Ala Arg Cys Ala Arg Trp Ser Asn Thr Ala Tyr Ala Thr His Cys
1 5 10 15

Ala Asn Cys Cys Asn Ala Thr His Cys Ala Asn
20 25

<210> 778
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 778

Cys Ala Arg Cys Ala Arg Trp Ser Asn Thr Ala Tyr Thr Thr Tyr Cys
1 5 10 15

Ala Asn Cys Cys Asn Ala Thr His Cys Ala Asn
20 25

<210> 779
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 779

Cys Ala Arg Cys Ala Arg Trp Ser Asn Thr Ala Tyr Thr Thr Tyr Trp
1 5 10 15

Ser Asn Cys Cys Asn Ala Thr His Cys Ala Asn
20 25

<210> 780
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 780

Cys Ala Arg Cys Ala Arg Trp Ser Asn Thr Thr Tyr Thr Ala Tyr Cys
1 5 10 15

Ala Asn Cys Cys Asn Ala Thr His Cys Ala Asn
20 25

<210> 781
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 781

2603

Cys Ala Arg Cys Ala Arg Trp Ser Asn Thr Thr Tyr Thr Ala Tyr Gly
1 5 10 15

Cys Asn Cys Cys Asn Ala Thr His Cys Ala Asn
20 25

<210> 782
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 782

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Gly Ala Tyr Thr Ala Tyr Tyr
1 5 10 15

Thr Asn Cys Cys Asn Thr Thr Tyr Cys Ala Asn
20 25

<210> 783
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 783

Cys Ala Arg Cys Ala Arg Thr Gly Tyr Gly Ala Tyr Gly Ala Tyr Tyr
1 5 10 15

Thr Asn Cys Cys Asn Tyr Thr Asn Cys Ala Asn
20 25

<210> 784
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 784

Cys Ala Arg Cys Ala Tyr Thr Ala Tyr Gly Ala Tyr Ala Ala Tyr Tyr
1 5 10 15

Thr Asn Cys Cys Asn Tyr Thr Asn Cys Ala Asn
20 25

<210> 785
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 785

2694

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Gly Ala Tyr Ala Ala Tyr Tyr
1 5 10 15

Thr Asn Cys Cys Asn Tyr Thr Asn Cys Ala Asn
20 25

<210> 786
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 786

Cys Ala Arg Cys Ala Arg Thr Gly Tyr Gly Ala Tyr Ala Thr His Tyr
1 5 10 15

Thr Asn Cys Cys Asn Tyr Thr Asn Trp Ser Asn
20 25

<210> 787
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 787

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Gly Ala Tyr Ala Ala Tyr Tyr
1 5 10 15

Thr Asn Cys Cys Asn Tyr Thr Asn Gly Cys Asn
20 25

<210> 788
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 788

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Gly Ala Tyr Trp Ser Asn Tyr
1 5 10 15

Thr Asn Cys Cys Asn Ala Thr His Cys Ala Asn
20 25

<210> 789
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 789

2605

Cys Ala Arg Cys Ala Arg Thr Ala Tyr Gly Ala Tyr Ala Ala Tyr Tyr
1 5 10 15

Thr Asn Cys Cys Asn Ala Thr His Cys Ala Asn
20 25

<210> 790
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 790

Cys Ala Arg Cys Ala Tyr Thr Ala Tyr Gly Ala Tyr Ala Ala Tyr Tyr
1 5 10 15

Thr Asn Cys Cys Asn Ala Thr His Cys Ala Asn
20 25

<210> 791
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 791

Gly Gly Asn Thr Ala Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Trp
1 5 10 15

Ser Asn Thr Ala Tyr Gly Gly Asn Ala Thr His Trp Ser Asn
20 25 30

<210> 792
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 792

Gly Gly Asn Thr Ala Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Gly
1 5 10 15

Gly Asn Cys Ala Tyr Thr Ala Tyr Ala Thr Gly Cys Ala Tyr
20 25 30

<210> 793
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 793

2606

Gly Gly Asn Thr Ala Tyr Cys Ala Asn Thr Thr Tyr Cys Ala Asn Gly
1 5 10 15

Gly Asn Thr Ala Tyr Thr Ala Tyr Ala Thr Gly Cys Ala Tyr
20 25 30

<210> 794
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 794

Gly Gly Asn Thr Ala Tyr Cys Ala Asn Tyr Thr Asn Cys Ala Asn Gly
1 5 10 15

Ala Arg Tyr Thr Asn Trp Ser Asn Ala Thr Gly Cys Ala Tyr
20 25 30

<210> 795
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 795

Gly Gly Asn Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Trp Ser Asn Ala
1 5 10 15

Ala Tyr Gly Cys Asn Met Gly Asn Ala Thr Gly Gly Gly Asn Gly Thr
20 25 30

Asn Trp Ser Asn
35

<210> 796
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 796

Gly Gly Asn Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Trp Ser Asn Cys
1 5 10 15

Ala Asn Gly Gly Asn Gly Gly Asn Gly Thr Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Gly Asn
35

<210> 797
<211> 36

2607

<212> PRT
<213> Homo Sapiens

<400> 797

Gly Gly Asn Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Ala Ala Tyr Cys
1 5 10 15

Ala Asn Gly Gly Asn Gly Gly Asn Gly Thr Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Gly Asn
35

<210> 798
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 798

Gly Gly Asn Thr Thr Tyr Cys Cys Asn Thr Thr Tyr Trp Ser Asn Met
1 5 10 15

Gly Asn Thr Ala Tyr Trp Ser Asn Ala Thr Gly Ala Ala Tyr
20 25 30

<210> 799
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 799

Gly Gly Asn Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp
1 5 10 15

Ser Asn Thr Ala Tyr Gly Cys Asn Ala Thr Gly Ala Ala Tyr
20 25 30

<210> 800
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 800

Gly Gly Asn Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp
1 5 10 15

Ser Asn Thr Ala Tyr Gly Cys Asn Ala Thr Gly Trp Ser Asn
20 25 30

2668

<210> 801
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 801

Gly Gly Asn Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp
1 5 10 15

Ser Asn Thr Ala Tyr Gly Gly Asn Ala Thr Gly Cys Ala Tyr
20 25 30

<210> 802
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 802

Gly Gly Asn Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp
1 5 10 15

Ser Asn Thr Ala Tyr Gly Ala Tyr Ala Thr Gly Cys Ala Tyr
20 25 30

<210> 803
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 803

Gly Gly Asn Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Met Gly Asn Trp
1 5 10 15

Ser Asn Cys Ala Tyr Gly Gly Asn Ala Thr Gly Cys Ala Tyr
20 25 30

<210> 804
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 804

Gly Gly Asn Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Gly
1 5 10 15

Cys Asn Thr Ala Tyr Trp Ser Asn Ala Thr Gly Ala Ala Tyr
20 25 30

<210> 805

2669

<211> 30
<212> PRT
<213> Homo Sapiens

<400> 805

Gly Gly Asn Thr Thr Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp
1 5 10 15

Ser Asn Thr Ala Tyr Trp Ser Asn Ala Thr Gly Ala Ala Tyr
20 25 30

<210> 806
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 806

Gly Gly Asn Gly Gly Asn Trp Ser Asn Gly Thr Asn Trp Ser Asn Trp
1 5 10 15

Ser Asn Gly Gly Asn Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly
20 25 30

Gly Trp Ser Asn
35

<210> 807
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 807

Gly Gly Asn Gly Gly Asn Trp Ser Asn Ala Thr His Trp Ser Asn Met
1 5 10 15

Gly Asn Gly Gly Asn Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly
20 25 30

Gly Trp Ser Asn
35

<210> 808
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 808

Gly Gly Asn Gly Gly Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp
1 5 10 15

2610

Ser Asn Gly Gly Asn Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly
20 25 30

Gly Trp Ser Asn
35

<210> 809
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 809

Gly Gly Asn Gly Gly Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp
1 5 10 15

Ser Asn Gly Gly Asn Gly Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Gly
20 25 30

Gly Ala Ala Tyr
35

<210> 810
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 810

Gly Gly Asn Gly Gly Asn Trp Ser Asn Thr Thr Tyr Trp Ser Asn Gly
1 5 10 15

Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn
20 25 30

<210> 811
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 811

Gly Gly Asn Gly Gly Asn Trp Ser Asn Ala Thr His Trp Ser Asn Trp
1 5 10 15

Ser Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Gly Trp Ser Asn
20 25 30

<210> 812
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 812

Gly Gly Asn Gly Gly Asn Trp Ser Asn Gly Thr Asn Trp Ser Asn Trp
1 5 10 15

Ser Asn Gly Gly Asn Gly Gly Asn Trp Ser Asn Thr Ala Tyr Thr Gly
20 25 30

Gly Trp Ser Asn
35

<210> 813
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 813

Gly Gly Asn Thr Ala Tyr Met Gly Asn Thr Thr Tyr Cys Ala Asn Trp
1 5 10 15

Ser Asn Thr Ala Tyr Thr Gly Gly Ala Thr His Gly Gly Asn
20 25 30

<210> 814
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 814

Gly Gly Asn Thr Ala Tyr Trp Ser Asn Thr Thr Tyr Cys Ala Asn Trp
1 5 10 15

Ser Asn Thr Ala Tyr Thr Gly Gly Ala Thr His Gly Gly Asn
20 25 30

<210> 815
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 815

Gly Gly Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn Trp Ser Asn Trp
1 5 10 15

Ser Asn Thr Ala Tyr Trp Ser Asn Gly Cys Asn Gly Cys Asn Thr Gly
20 25 30

Gly Ala Ala Tyr
35

<210> 816
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 816

Thr Gly Gly Ala Thr His Trp Ser Asn Gly Cys Asn Trp Ser Asn Ala
1 5 10 15

Ala Tyr Gly Gly Asn Ala Ala Tyr Cys Ala Asn Ala Ala Tyr Thr Ala
20 25 30

Tyr Gly Cys Asn Cys Ala Arg Ala Ala Arg Tyr Thr Asn Cys Ala Arg
35 40 45

Gly Ala Tyr
50

<210> 817
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 817

Thr Gly Gly Ala Thr His Ala Ala Tyr Cys Cys Asn Ala Ala Tyr Trp
1 5 10 15

Ser Asn Gly Gly Asn Gly Gly Asn Cys Ala Asn Ala Ala Tyr Thr Gly
20 25 30

Tyr Gly Cys Asn Cys Ala Arg Ala Ala Arg Thr Thr Tyr Cys Ala Arg
35 40 45

Gly Gly Asn
50

<210> 818
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 818

Thr Gly Gly Ala Thr His Ala Ala Tyr Cys Cys Asn Ala Ala Tyr Trp
1 5 10 15

Ser Asn Gly Gly Asn Gly Gly Asn Cys Ala Asn Ala Ala Tyr Cys Ala
20 25 30

Tyr Cys Ala Asn Cys Ala Arg Ala Ala Arg Thr Thr Tyr Cys Ala Arg
35 40 45

JG13

Gly Gly Asn
50

<210> 819
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 819

Trp Ser Asn Thr Thr Tyr Gly Ala Tyr Cys Cys Asn Gly Ala Arg Gly
1 5 10 15

Ala Tyr Gly Gly Asn Gly Ala Arg Cys Ala Asn Ala Thr His Thr Ala
20 25 30

Tyr Gly Cys Asn Cys Ala Arg Ala Ala Arg Thr Thr Tyr Cys Ala Arg
35 40 45

Gly Gly Asn
50

<210> 820
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 820

Cys Ala Tyr Ala Thr His Thr Thr Tyr Trp Ser Asn Ala Ala Tyr Gly
1 5 10 15

Ala Tyr Gly Ala Arg Ala Ala Arg Trp Ser Asn Thr Ala Tyr Trp Ser
20 25 30

Asn Cys Ala Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg Trp Ser Asn
35 40 45

<210> 821
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 821

Tyr Thr Asn Ala Thr His Thr Thr Tyr Trp Ser Asn Ala Ala Tyr Gly
1 5 10 15

Ala Tyr Gly Ala Arg Ala Ala Arg Trp Ser Asn Thr Ala Tyr Trp Ser
20 25 30

Asn Cys Ala Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg Trp Ser Asn
35 40 45

2614

<210> 822
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 822

Tyr Thr Asn Ala Thr His Thr Ala Tyr Thr Gly Gly Ala Ala Tyr Gly
1 5 10 15

Ala Tyr Gly Ala Tyr Ala Ala Arg Met Gly Asn Thr Ala Tyr Trp Ser
20 25 30

Asn Cys Cys Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg Trp Ser Asn
35 40 45

<210> 823
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 823

Tyr Thr Asn Ala Thr His Thr Ala Tyr Thr Gly Gly Ala Ala Tyr Gly
1 5 10 15

Thr Asn Gly Ala Arg Ala Ala Arg Met Gly Asn Thr Ala Tyr Trp Ser
20 25 30

Asn Cys Cys Asn Trp Ser Asn Tyr Thr Asn Met Gly Asn Trp Ser Asn
35 40 45

<210> 824
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 824

Gly Cys Asn Ala Thr His Trp Ser Asn Trp Ser Asn Trp Ser Asn Trp
1 5 10 15

Ser Asn Trp Ser Asn Thr Ala Tyr Ala Thr His Thr Ala Tyr Thr Ala
20 25 30

Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn Ala Ala Arg
35 40 45

Gly Gly Asn
50

<210> 825
<211> 51

<212> PRT
<213> Homo Sapiens

<400> 825

Gly Cys Asn Ala Thr His Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly
1 5 10 15

Gly Asn Gly Gly Asn Trp Ser Asn Cys Ala Asn Thr Ala Tyr Thr Ala
20 25 30

Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn Ala Ala Arg
35 40 45

Gly Gly Asn
50

<210> 826
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 826

Thr Thr Tyr Ala Thr His Trp Ser Asn Gly Ala Tyr Gly Ala Tyr Gly
1 5 10 15

Gly Asn Trp Ser Asn Cys Ala Asn Ala Ala Arg Thr Ala Tyr Thr Ala
20 25 30

Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn Ala Ala Arg
35 40 45

Gly Gly Asn
50

<210> 827
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 827

Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly Ala Tyr Gly
1 5 10 15

Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Thr Ala Tyr Thr Ala
20 25 30

Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn Ala Ala Arg
35 40 45

2616

Gly Gly Asn
50

<210> 828
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 828

Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly Ala Tyr Gly
1 5 10 15

Gly Asn Trp Ser Asn Ala Thr His Ala Ala Arg Thr Ala Tyr Thr Ala
20 25 30

Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn Ala Ala Arg
35 40 45

Gly Gly Asn
50

<210> 829
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 829

Gly Thr Asn Ala Thr His Thr Gly Gly Trp Ser Asn Gly Ala Tyr Gly
1 5 10 15

Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Thr Ala Tyr Thr Ala
20 25 30

Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn Ala Ala Arg
35 40 45

Gly Gly Asn
50

<210> 830
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 830

Gly Thr Asn Ala Thr His Thr Gly Gly Gly Ala Tyr Gly Ala Tyr Gly
1 5 10 15

Gly Asn Trp Ser Asn Ala Ala Tyr Cys Ala Arg Thr Ala Tyr Thr Ala
20 25 30

2617

Tyr Cys Ala Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn Ala Ala Arg
35 40 45

Gly Gly Asn
50

<210> 831
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 831

Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly Ala Tyr Gly
1 5 10 15

Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Met Gly Asn Thr Ala
20 25 30

Tyr Gly Thr Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn Ala Ala Arg
35 40 45

Gly Gly Asn
50

<210> 832
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 832

Gly Thr Asn Ala Thr His Thr Gly Gly Thr Ala Tyr Gly Ala Tyr Gly
1 5 10 15

Gly Asn Trp Ser Asn Ala Ala Tyr Ala Ala Arg Ala Ala Tyr Thr Ala
20 25 30

Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn Met Gly Asn
35 40 45

Gly Gly Asn
50

<210> 833
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 833

Thr Ala Tyr Ala Thr His Trp Ser Asn Trp Ser Asn Trp Ser Asn Gly
1 5 10 15

2618

Gly Asn Met Gly Asn Cys Ala Asn Ala Thr His Thr Ala Tyr Thr Ala
20 25 30

Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn Ala Ala Arg
35 40 45

Gly Gly Asn
50

<210> 834
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 834

Cys Ala Tyr Ala Thr His Trp Ser Asn Trp Ser Asn Trp Ser Asn Trp
1 5 10 15

Ser Asn Met Gly Asn Cys Ala Asn Ala Thr His Thr Ala Tyr Thr Ala
20 25 30

Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn Ala Ala Arg
35 40 45

Gly Gly Asn
50

<210> 835
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 835

Cys Ala Tyr Ala Thr His Trp Ser Asn Met Gly Asn Trp Ser Asn Trp
1 5 10 15

Ser Asn Met Gly Asn Cys Ala Asn Ala Thr His Thr Ala Tyr Thr Ala
20 25 30

Tyr Gly Cys Asn Gly Ala Tyr Trp Ser Asn Gly Thr Asn Ala Ala Arg
35 40 45

Gly Gly Asn
50

<210> 836
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 836

2619

Thr Ala Tyr Ala Thr His Cys Ala Tyr Trp Ser Asn Trp Ser Asn Gly
1 5 10 15

Gly Asn Trp Ser Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Ala Ala
20 25 30

Tyr Cys Cys Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg Trp Ser Asn
35 40 45

<210> 837
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 837

Thr Ala Tyr Ala Thr His Thr Ala Tyr Cys Ala Tyr Trp Ser Asn Gly
1 5 10 15

Gly Asn Trp Ser Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Ala Ala
20 25 30

Tyr Cys Cys Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg Trp Ser Asn
35 40 45

<210> 838
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 838

Thr Ala Tyr Ala Thr His Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Gly
1 5 10 15

Gly Asn Trp Ser Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Ala Ala
20 25 30

Tyr Cys Cys Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg Trp Ser Asn
35 40 45

<210> 839
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 839

Thr Ala Tyr Ala Thr His Cys Ala Tyr Thr Ala Tyr Trp Ser Asn Gly
1 5 10 15

Gly Asn Trp Ser Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Ala Ala
20 25 30

2620

Tyr Cys Cys Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg Trp Ser Asn
35 40 45

<210> 840
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 840

Thr Ala Tyr Ala Thr His Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Gly
1 5 10 15

Gly Asn Gly Gly Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Ala Ala
20 25 30

Tyr Cys Cys Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg Trp Ser Asn
35 40 45

<210> 841
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 841

Gly Ala Arg Ala Thr His Ala Ala Tyr Cys Ala Tyr Trp Ser Asn Gly
1 5 10 15

Gly Asn Trp Ser Asn Cys Ala Asn Ala Ala Tyr Thr Ala Tyr Ala Ala
20 25 30

Tyr Cys Cys Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg Trp Ser Asn
35 40 45

<210> 842
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 842

Met Gly Asn Ala Thr His Thr Ala Tyr Cys Ala Asn Trp Ser Asn Gly
1 5 10 15

Gly Asn Cys Ala Asn Cys Ala Asn Ala Ala Tyr Thr Ala Tyr Ala Ala
20 25 30

Tyr Cys Cys Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg Trp Ser Asn
35 40 45

<210> 843
<211> 48

2621

<212> PRT
<213> Homo Sapiens

<400> 843

Thr Ala Tyr Ala Thr His Thr Ala Tyr Thr Ala Tyr Trp Ser Asn Gly
1 5 10 15

Gly Asn Trp Ser Asn Cys Ala Asn Ala Ala Tyr Thr Ala Tyr Ala Ala
20 25 30

Tyr Cys Cys Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg Trp Ser Asn
35 40 45

<210> 844
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 844

Ala Thr His Ala Thr His Thr Ala Tyr Cys Cys Asn Gly Ala Tyr Gly
1 5 10 15

Ala Tyr Trp Ser Asn Gly Ala Tyr Cys Ala Asn Met Gly Asn Thr Ala
20 25 30

Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn Thr Thr Tyr Cys Ala Arg
35 40 45

Gly Gly Asn
50

<210> 845
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 845

Ala Thr His Ala Thr His Thr Ala Tyr Cys Cys Asn Gly Ala Tyr Gly
1 5 10 15

Ala Tyr Trp Ser Asn Gly Ala Tyr Gly Cys Asn Met Gly Asn Thr Ala
20 25 30

Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn Thr Thr Tyr Cys Ala Arg
35 40 45

Gly Gly Asn
50

<210> 846

2622

<211> 51
<212> PRT
<213> Homo Sapiens

<400> 846

Ala Thr His Ala Thr His Thr Ala Tyr Cys Cys Asn Gly Gly Asn Gly
1 5 10 15

Ala Tyr Trp Ser Asn Gly Ala Tyr Ala Thr His Met Gly Asn Thr Ala
20 25 30

Tyr Trp Ser Asn Cys Cys Asn Trp Ser Asn Thr Thr Tyr Cys Ala Arg
35 40 45

Gly Gly Asn
50

<210> 847
<211> 54
<212> PRT
<213> Homo Sapiens

<400> 847

Met Gly Asn Cys Ala Asn Thr Ala Tyr Thr Gly Tyr Met Gly Asn Trp
1 5 10 15

Ser Asn Ala Ala Arg Thr Gly Gly Thr Ala Tyr Ala Ala Tyr Gly Ala
20 25 30

Tyr Thr Ala Tyr Gly Cys Asn Gly Thr Asn Trp Ser Asn Gly Thr Asn
35 40 45

Ala Ala Arg Trp Ser Asn
50

<210> 848
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 848

Gly Ala Arg Gly Ala Tyr Ala Ala Tyr Thr Gly Gly Ala Ala Tyr Thr
1 5 10 15

Ala Tyr Gly Gly Asn Thr Thr Tyr Thr Thr Tyr Gly Ala Tyr Thr Ala
20 25 30

Tyr

<210> 849
<211> 24
<212> PRT
<213> Homo Sapiens

<400> 849

Trp Ser Asn Ala Thr His Gly Cys Asn Gly Thr Asn Gly Cys Asn Tyr
1 5 10 15

Thr Asn Gly Ala Tyr Thr Ala Tyr
20

<210> 850
<211> 39
<212> PRT
<213> Homo Sapiens

<400> 850

Gly Ala Arg Gly Gly Asn Gly Ala Tyr Gly Gly Asn Gly Gly Asn Thr
1 5 10 15

Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Thr
20 25 30

Gly Gly Ala Tyr Gly Thr Asn
35

<210> 851
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 851

Ala Thr Gly Thr Ala Tyr Trp Ser Asn Trp Ser Asn Gly Gly Asn Thr
1 5 10 15

Gly Gly Thr Ala Tyr Gly Gly Asn Gly Thr Asn Thr Thr Tyr Gly Ala
20 25 30

Tyr Thr Ala Tyr
35

<210> 852
<211> 39
<212> PRT
<213> Homo Sapiens

<400> 852

2624

Gly Thr Asn Thr Ala Tyr Trp Ser Asn Trp Ser Asn Gly Gly Asn Thr
1 5 10 15

Gly Gly Trp Ser Asn Thr Thr Tyr Thr Ala Tyr Gly Gly Asn Ala Thr
20 25 30

Gly Gly Ala Tyr Gly Thr Asn
35

<210> 853
<211> 24
<212> PRT
<213> Homo Sapiens

<400> 853

Met Gly Asn Met Gly Asn Gly Ala Arg Tyr Thr Asn Cys Cys Asn Thr
1 5 10 15

Thr Tyr Gly Ala Tyr Thr Ala Tyr
20

<210> 854
<211> 24
<212> PRT
<213> Homo Sapiens

<400> 854

Met Gly Asn Ala Ala Tyr Thr Gly Gly Cys Ala Asn Cys Cys Asn Thr
1 5 10 15

Thr Tyr Gly Ala Tyr Thr Ala Tyr
20

<210> 855
<211> 24
<212> PRT
<213> Homo Sapiens

<400> 855

Met Gly Asn Tyr Thr Asn Gly Ala Arg Tyr Thr Asn Cys Cys Asn Thr
1 5 10 15

Thr Tyr Gly Ala Tyr Thr Ala Tyr
20

<210> 856
<211> 24
<212> PRT
<213> Homo Sapiens

<400> 856

Met Gly Asn Met Gly Asn Gly Ala Arg Gly Thr Asn Cys Cys Asn Thr
1 5 10 15

Thr Tyr Gly Ala Tyr Thr Ala Tyr
20

<210> 857
<211> 24
<212> PRT
<213> Homo Sapiens

<400> 857

Met Gly Asn Cys Ala Tyr Cys Ala Asn Ala Ala Tyr Cys Cys Asn Thr
1 5 10 15

Thr Tyr Gly Ala Arg Thr Ala Tyr
20

<210> 858
<211> 24
<212> PRT
<213> Homo Sapiens

<400> 858

Met Gly Asn Gly Gly Asn Gly Ala Arg Tyr Thr Asn Cys Cys Asn Thr
1 5 10 15

Thr Tyr Gly Ala Tyr Thr Ala Tyr
20

<210> 859
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 859

Gly Ala Tyr Met Gly Asn Gly Thr Asn Gly Gly Asn Gly Cys Asn Cys
1 5 10 15

Ala Asn Cys Cys Asn Gly Ala Tyr Gly Cys Asn Thr Thr Tyr Gly Ala
20 25 30

Tyr Ala Thr His
35

<210> 860
<211> 57
<212> PRT

2626

<213> Homo Sapiens

<400> 860

Gly Ala Arg Gly Gly Asn Ala Thr His Gly Cys Asn Gly Thr Asn Gly
1 5 10 15

Cys Asn Gly Gly Asn Cys Ala Asn Gly Cys Asn Gly Ala Arg Thr Ala
20 25 30

Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Cys Asn
35 40 45

Ala Thr Gly Gly Ala Tyr Gly Thr Asn
50 55

<210> 861
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 861

Gly Ala Arg Gly Gly Asn Ala Thr His Gly Cys Asn Gly Cys Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Trp Ser Asn Thr Ala Tyr Thr Ala Tyr Thr Ala
20 25 30

Tyr Thr Ala Tyr Gly Cys Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn
35 40 45

<210> 862
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 862

Gly Ala Arg Gly Gly Asn Ala Thr His Gly Cys Asn Gly Gly Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Trp Ser Asn Thr Ala Tyr Thr Ala Tyr Thr Ala
20 25 30

Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn
35 40 45

<210> 863
<211> 42
<212> PRT
<213> Homo Sapiens

2621

<400> 863

Trp Ser Asn Thr Ala Tyr Thr Ala Tyr Gly Ala Tyr Trp Ser Asn Trp
1 5 10 15

Ser Asn Gly Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Gly
20 25 30

Asn Thr Thr Tyr Gly Ala Tyr Thr Ala Tyr
35 40

<210> 864
<211> 15
<212> PRT
<213> Homo Sapiens

<400> 864

Ala Ala Tyr Gly Thr Asn Ala Thr His Gly Ala Tyr Thr Ala Tyr
1 5 10 15

<210> 865
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 865

Gly Gly Asn Gly Gly Asn Gly Cys Asn Cys Ala Asn Gly Gly Asn Gly
1 5 10 15

Cys Asn Gly Ala Arg Thr Ala Tyr Thr Thr Tyr Cys Ala Arg Cys Ala
20 25 30

Tyr

<210> 866
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 866

Tyr Thr Asn Thr Gly Gly Thr Thr Tyr Gly Gly Asn Gly Ala Arg Cys
1 5 10 15

Ala Asn Thr Thr Tyr Gly Ala Tyr Thr Ala Tyr
20 25

<210> 867
<211> 18
<212> PRT

<213> Homo Sapiens

<400> 867

Ala Ala Tyr Tyr Thr Asn Cys Cys Asn Thr Thr Tyr Gly Ala Tyr Thr
1 5 10 15

Ala Tyr

<210> 868
<211> 42
<212> PRT
<213> Homo Sapiens

<400> 868

Trp Ser Asn Cys Ala Tyr Thr Ala Tyr Gly Gly Asn Gly Gly Asn Gly
1 5 10 15

Ala Tyr Thr Ala Tyr Gly Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Gly
20 25 30

Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn
35 40

<210> 869
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 869

Gly Ala Tyr Gly Gly Asn Thr Gly Gly Cys Ala Arg Cys Ala Arg Cys
1 5 10 15

Ala Arg Gly Cys Asn Cys Cys Asn Thr Thr Tyr Gly Ala Tyr Thr Ala
20 25 30

Tyr

<210> 870
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 870

Thr Gly Gly Gly Gly Asn Ala Thr His Trp Ser Asn Gly Cys Asn Cys
1 5 10 15

2629

Cys Asn Thr Thr Tyr Gly Ala Tyr Thr Gly Tyr
20 25

<210> 871
<211> 18
<212> PRT
<213> Homo Sapiens

<400> 871

Thr Gly Gly Gly Cys Asn Cys Cys Asn Thr Thr Tyr Gly Ala Tyr Thr
1 5 10 15

Ala Tyr

<210> 872
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 872

Gly Ala Tyr Gly Gly Asn Thr Ala Tyr Ala Ala Tyr Thr Gly Gly Ala
1 5 10 15

Ala Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Ala Ala Tyr Thr Ala
20 25 30

Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn
35 40 45

<210> 873
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 873

Gly Ala Tyr Gly Gly Asn Thr Ala Tyr Ala Ala Tyr Thr Gly Gly Ala
1 5 10 15

Ala Tyr Ala Ala Tyr Gly Gly Asn Gly Gly Asn Thr Ala Tyr Thr Ala
20 25 30

Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn
35 40 45

<210> 874
<211> 24
<212> PRT
<213> Homo Sapiens

<400> 874

Gly Gly Asn Cys Cys Asn Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala
1 5 10 15

Thr Gly Gly Ala Tyr Gly Thr Asn
20

<210> 875
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 875

Gly Cys Asn Tyr Thr Asn Met Gly Asn Gly Gly Asn Ala Thr His Gly
1 5 10 15

Thr Asn Tyr Thr Asn Ala Thr Gly Gly Thr Asn Thr Ala Tyr Gly Thr
20 25 30

Asn Tyr Thr Asn Gly Gly Asn Gly Cys Asn Tyr Thr Asn Gly Ala Tyr
35 40 45

Ala Thr His
50

<210> 876
<211> 51
<212> PRT
<213> Homo Sapiens

<400> 876

Gly Ala Tyr Gly Ala Arg Cys Ala Asn Gly Thr Asn Gly Thr Asn Met
1 5 10 15

Gly Asn Gly Gly Asn Tyr Thr Asn Ala Thr His Met Gly Asn Thr Ala
20 25 30

Tyr Thr Gly Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr
35 40 45

Gly Thr Asn
50

<210> 877
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 877

2631

Gly Ala Tyr Met Gly Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly
1 5 10 15

Ala Tyr Thr Ala Tyr Gly Gly Asn Met Gly Asn Ala Thr Gly Gly Ala
20 25 30

Tyr Gly Thr Asn
35

<210> 878
<211> 27
<212> PRT
<213> Homo Sapiens

<400> 878

Trp Ser Asn Ala Ala Tyr Ala Ala Tyr Thr Ala Tyr Gly Gly Asn Thr
1 5 10 15

Gly Tyr Thr Thr Tyr Gly Cys Asn Tyr Thr Asn
20 25

<210> 879
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 879

Gly Gly Asn Thr Ala Tyr Ala Ala Tyr Thr Ala Tyr Gly Gly Asn Tyr
1 5 10 15

Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Ala Tyr Trp Ser
20 25 30

Asn Trp Ser Asn Gly Gly Asn Thr Ala Tyr Cys Cys Asn Trp Ser Asn
35 40 45

Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly Gly
50 55 60

Ala Tyr Gly Thr Asn
65

<210> 880
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 880

Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Gly Ala Tyr Ala Thr His Tyr
1 5 10 15

Thr Asn Cys Ala Asn Gly Gly Asn Thr Ala Tyr Cys Cys Asn Thr Thr
20 25 30

Tyr Thr Ala Tyr Thr Thr Tyr Gly Ala Tyr Thr Ala Tyr
35 40 45

<210> 881
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 881

Gly Gly Asn Gly Gly Asn Thr Ala Tyr Trp Ser Asn Trp Ser Asn Trp
1 5 10 15

Ser Asn Thr Gly Gly Thr Ala Tyr Thr Gly Gly Thr Thr Tyr Gly Ala
20 25 30

Tyr Cys Cys Asn
35

<210> 882
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 882

Gly Gly Asn Gly Gly Asn Thr Ala Tyr Trp Ser Asn Trp Ser Asn Trp
1 5 10 15

Ser Asn Thr Gly Gly Thr Thr Tyr Thr Gly Gly Thr Thr Tyr Gly Ala
20 25 30

Tyr Cys Cys Asn
35

<210> 883
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 883

Gly Ala Tyr Gly Gly Asn Thr Ala Tyr Trp Ser Asn Thr Ala Tyr Gly
1 5 10 15

Gly Asn Cys Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala
20 25 30

Tyr Gly Gly Asn Ala Thr Gly Gly Ala Tyr Gly Thr Asn
35 40 45

2633

<210> 884
<211> 48
<212> PRT
<213> Homo Sapiens

<400> 884

Trp Ser Asn Gly Cys Asn Tyr Thr Asn Met Gly Asn Thr Ala Tyr Thr
1 5 10 15

Thr Tyr Gly Ala Tyr Thr Gly Gly Tyr Thr Asn Thr Thr Tyr Trp Ser
20 25 30

Asn Gly Ala Tyr Gly Thr Asn Trp Ser Asn Gly Ala Tyr Ala Thr His
35 40 45

<210> 885
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 885

Cys Ala Arg Ala Ala Arg Trp Ser Asn Thr Ala Tyr Gly Gly Asn Thr
1 5 10 15

Ala Tyr Trp Ser Asn Thr Ala Tyr Thr Thr Tyr Gly Ala Tyr Thr Ala
20 25 30

Tyr

<210> 886
<211> 36
<212> PRT
<213> Homo Sapiens

<400> 886

Cys Ala Arg Gly Gly Asn Thr Ala Tyr Gly Gly Asn Trp Ser Asn Gly
1 5 10 15

Gly Asn Thr Gly Gly Gly Gly Asn Thr Ala Tyr Thr Thr Tyr Gly Ala
20 25 30

Tyr Thr Ala Tyr
35

<210> 887
<211> 54
<212> PRT
<213> Homo Sapiens

2634

<400> 887

Cys Ala Arg Gly Gly Asn Tyr Thr Asn Gly Cys Asn Gly Thr Asn Gly
1 5 10 15

Cys Asn Gly Gly Asn Cys Ala Asn Trp Ser Asn Thr Ala Tyr Thr Ala
20 25 30

Tyr Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Thr Gly
35 40 45

Gly Ala Tyr Gly Thr Asn
50

<210> 888
<211> 39
<212> PRT
<213> Homo Sapiens

<400> 888

Gly Ala Tyr Met Gly Asn Gly Cys Asn Gly Thr Asn Gly Cys Asn Gly
1 5 10 15

Gly Asn Thr Ala Tyr Thr Ala Tyr Thr Ala Tyr Gly Gly Asn Ala Thr
20 25 30

Gly Gly Ala Tyr Gly Thr Asn
35

<210> 889
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 889

Gly Ala Tyr Gly Thr Asn Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Tyr Thr Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Cys Cys Asn Gly Thr Asn Cys Ala Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr
65

<210> 890

<211> 69
<212> PRT
<213> Homo Sapiens

<400> 890

Gly Ala Tyr Gly Thr Asn Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Tyr Thr Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Cys Cys Asn Gly Thr Asn Cys Ala Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr
65

<210> 891
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 891

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Cys Ala Asn Cys Cys Asn Tyr Thr Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Thr Asn Cys Ala Asn Cys Cys Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr
65

<210> 892
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 892

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

1626

Ala Arg Cys Ala Asn Cys Cys Asn Tyr Thr Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Thr Asn Cys Ala Asn Cys Cys Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr
65

<210> 893
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 893

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Ala
50 55 60

Thr His Thr Gly Tyr
65

<210> 894
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 894

Ala Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Cys Ala Asn Cys Cys Asn Tyr Thr Asn Trp Ser Asn Trp Ser
20 25 30

Asn Cys Cys Asn Gly Thr Asn Cys Ala Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr
65

<210> 895
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 895

Gly Ala Arg Ala Thr His Gly Thr Asn Tyr Thr Asn Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Gly Asn Cys Ala Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Tyr Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Tyr Thr Asn Trp
50 55 60

Ser Asn Thr Gly Tyr
65

<210> 896
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 896

Gly Ala Arg Ala Thr His Gly Thr Asn Tyr Thr Asn Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Gly Asn Cys Ala Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Tyr Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Tyr Thr Asn Trp
50 55 60

Ser Asn Thr Gly Tyr
65

<210> 897
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 897

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 898
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 898

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Tyr Thr
20 25 30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr
65

<210> 899
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 899

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Tyr Thr
20 25 30

Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr
65

<210> 900
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 900

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Tyr Thr
20 25 30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr
65

<210> 901
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 901

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 902
<211> 69
<212> PRT

2640

<213> Homo Sapiens

<400> 902

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Gly Cys Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 903
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 903

Gly Ala Arg Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Cys Asn Cys Ala Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Thr Asn Trp Ser Asn Cys Cys Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Tyr Thr Asn Trp
50 55 60

Ser Asn Thr Gly Tyr
65

<210> 904
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 904

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Gly Thr
20 25 30

2641

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 905
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 905

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 906
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 906

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

1642

<210> 907
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 907

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 908
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 908

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 909
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 909

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 910
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 910

Thr Gly Gly Tyr Thr Asn Cys Ala Arg Cys Ala Arg Met Gly Asn Cys
1 5 10 15

Cys Asn Gly Gly Asn Cys Ala Arg Trp Ser Asn Cys Cys Asn Met Gly
20 25 30

Asn Met Gly Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 911
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 911

Thr Gly Gly Thr Ala Tyr Tyr Thr Asn Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys Asn Cys Ala
20 25 30

Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 912
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 912

Thr Gly Gly Thr Thr Tyr Tyr Thr Asn Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys Asn Cys Ala
20 25 30

Arg Cys Cys Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 913
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 913

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Thr Asn Cys Cys Asn Ala Ala
20 25 30

Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 914
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 914

Thr Gly Gly Tyr Thr Asn Cys Ala Arg Cys Ala Arg Met Gly Asn Cys
1 5 10 15

Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys Asn Met Gly
20 25 30

Asn Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 915
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 915

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Met Gly
20 25 30

Asn Tyr Thr Asn Tyr Thr Asn Ala Thr His Trp Ser Asn
35 40 45

<210> 916
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 916

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Met Gly
20 25 30

Asn Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 917
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 917

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Cys Cys Asn Ala Ala
20 25 30

Arg Met Gly Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 918
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 918

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys Asn Ala Ala
20 25 30

Arg Tyr Thr Asn Thr Thr Tyr Ala Thr His Thr Ala Tyr
35 40 45

<210> 919
<211> 45
<212> PRT
<213> Homo Sapiens

2646

<400> 919

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys Asn Ala Ala
20 25 30

Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 920
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 920

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Cys Ala Arg Cys Cys Asn Cys Cys Asn Ala Ala
20 25 30

Arg Gly Thr Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 921
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 921

Thr Gly Gly Thr Thr Tyr Cys Ala Arg Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Cys Cys Asn Ala Ala
20 25 30

Arg Trp Ser Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 922
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 922

Thr Gly Gly Tyr Thr Asn Cys Ala Arg Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

2647

Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Cys Cys Asn Ala Ala
20 25 30

Arg Trp Ser Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 923
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 923

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Gly Ala Tyr Cys
1 5 10 15

Cys Asn Gly Gly Asn Cys Ala Arg Gly Cys Asn Cys Cys Asn Met Gly
20 25 30

Asn Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 924
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 924

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Cys Cys Asn Ala Ala
20 25 30

Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 925
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 925

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Cys Cys Asn Ala Ala
20 25 30

Arg Thr Thr Tyr Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 926
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 926

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Met Gly Asn Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Tyr Gly Cys Asn Cys Cys Asn Ala Ala
20 25 30

Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 927
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 927

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Cys Cys Asn Ala Ala
20 25 30

Arg Gly Thr Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 928
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 928

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala Ala Arg Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Cys Cys Asn Gly Ala
20 25 30

Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 929
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 929

Thr Gly Gly Thr Ala Tyr Cys Ala Arg Cys Ala Arg Ala Ala Arg Tyr
1 5 10 15

Thr Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Cys Cys Asn Ala Ala
20 25 30

Arg Tyr Thr Asn Tyr Thr Asn Ala Thr His Cys Ala Tyr
35 40 45

<210> 930
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 930

Gly Gly Asn Gly Thr Asn Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Ala Ala Tyr Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Ala Ala Arg Ala Thr His Trp Ser Asn Met Gly Asn Gly
50 55 60

Thr Asn Gly Ala Arg Gly Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr
65 70 75 80

Asn Gly Gly Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 931
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 931

Gly Gly Asn Gly Thr Asn Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Ala Ala Arg Ala Thr His Trp Ser Asn Met Gly Asn Gly
50 55 60

Thr Asn Gly Ala Arg Gly Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr
65 70 75 80

Asn Gly Gly Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 932
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 932

Gly Gly Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr
65 70 75 80

Asn Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 933
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 933

Gly Gly Asn Gly Thr Asn Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Gly Cys
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Ala Ala Arg Ala Thr His Trp Ser Asn Met Gly Asn Gly
50 55 60

Thr Asn Gly Ala Arg Gly Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr
65 70 75 80

Asn Gly Gly Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 934
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 934

Gly Gly Asn Gly Thr Asn Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Cys Ala Asn Gly Gly Asn Gly Cys
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Ala Ala Arg Ala Thr His Trp Ser Asn Met Gly Asn Gly
50 55 60

Thr Asn Gly Ala Arg Gly Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr
65 70 75 80

Asn Gly Gly Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 935
<211> 96
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<213> Homo Sapiens

<400> 935

Gly Gly Asn Ala Thr His Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Met Gly Asn Tyr
50 55 60

Thr Asn Gly Ala Arg Cys Cys Asn Gly Ala Arg Gly Ala Tyr Thr Thr
65 70 75 80

Tyr Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 936
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 936

Gly Gly Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Arg Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Gly Ala Tyr Thr Thr
65 70 75 80

Tyr Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 937
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 937

Gly Gly Asn Gly Thr Asn Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Cys Ala Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Gly Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr
65 70 75 80

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 938
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 938

Gly Gly Asn Gly Thr Asn Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Gly Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr
65 70 75 80

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 939
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 939

Gly Gly Asn Gly Thr Asn Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Gly Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr
65 70 75 80

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Thr Tyr Thr Gly Tyr
85 90 95

<210> 940
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<213> Homo Sapiens

<400> 940

Gly Gly Asn Gly Thr Asn Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Gly Gly Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Gly Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr
65 70 75 80

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 941
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 941

Gly Gly Asn Gly Thr Asn Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Gly Cys Asn Gly Ala Tyr Gly Ala Tyr Gly Thr
65 70 75 80

Asn Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 942
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 942

Gly Gly Asn Gly Thr Asn Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Gly Gly Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Gly Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr
65 70 75 80

Asn Gly Cys Asn Tyr Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 943
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 943

Gly Gly Asn Gly Thr Asn Cys Cys Asn Gly Ala Tyr Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Gly Cys Asn Gly Ala Arg Gly Ala Tyr Gly Thr
65 70 75 80

Asn Gly Cys Asn Gly Thr Asn Thr Thr Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 944
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 944

Gly Gly Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Ala Ala Arg Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Gly Ala Tyr Thr Thr
65 70 75 80

Tyr Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 945
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 945

Gly Gly Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Gly Ala Tyr Thr Thr
65 70 75 80

Tyr Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 946
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 946

Gly Gly Asn Ala Thr His Cys Cys Asn Gly Cys Asn Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Arg Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Trp Ser Asn Gly Ala Arg Gly Ala Tyr Thr Thr
65 70 75 80

Tyr Gly Cys Asn Gly Thr Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 947
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 947

Gly Gly Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Gly Ala Tyr Thr Thr
65 70 75 80

Tyr Gly Cys Asn Gly Cys Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 948
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 948

Gly Gly Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Met Gly Asn Gly
1 5 10 15

Thr Asn Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Met Gly Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Gly Ala Tyr Thr Thr
65 70 75 80

Tyr Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 949
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 949

Gly Gly Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Tyr Thr Asn Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Gly Ala Tyr Thr Thr
65 70 75 80

Tyr Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 950
<211> 96
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<400> 950

Gly Gly Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Ala Ala Tyr Thr Thr
65 70 75 80

Tyr Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 951
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<400> 951

Gly Gly Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Thr Thr Tyr Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Gly Ala Tyr Thr Thr
65 70 75 80

Tyr Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 952
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<400> 952

Gly Gly Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Tyr Thr Asn Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Gly Ala Tyr Thr Thr
65 70 75 80

Tyr Gly Cys Asn Trp Ser Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 953
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<213> Homo Sapiens

<400> 953

Gly Gly Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Gly Ala Tyr Thr Thr
65 70 75 80

Tyr Gly Cys Asn Trp Ser Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 954
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<400> 954

Gly Gly Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Gly Asn Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Thr Thr Tyr Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Gly Ala Tyr Ala Thr
65 70 75 80

His Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 955
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<400> 955

Gly Gly Asn Gly Thr Asn Cys Cys Asn Trp Ser Asn Met Gly Asn Thr
1 5 10 15

Thr Tyr Trp Ser Asn Gly Gly Asn Trp Ser Asn Gly Gly Asn Trp Ser
20 25 30

Asn Gly Ala Arg Cys Ala Asn Gly Ala Tyr Thr Thr Tyr Cys Ala Asn
35 40 45

Thr Thr Tyr Cys Ala Asn Ala Thr His Trp Ser Asn Trp Ser Asn Tyr
50 55 60

Thr Asn Cys Ala Arg Cys Cys Asn Gly Ala Arg Gly Ala Tyr Ala Thr
65 70 75 80

His Gly Cys Asn Cys Ala Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr
85 90 95

<210> 956
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 956

Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Met
1 5 10 15

Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
20 25 30

<210> 957
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 957

Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Met
1 5 10 15

Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Thr His
20 25 30

<210> 958
<211> 30

<212> PRT
<213> Homo Sapiens

<400> 958

Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Ala
1 5 10 15

Ala Arg Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
20 25 30

<210> 959
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 959

Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Cys Ala Asn Ala
1 5 10 15

Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
20 25 30

<210> 960
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 960

Thr Thr Tyr Gly Gly Asn Cys Ala Tyr Gly Gly Asn Cys Ala Asn Met
1 5 10 15

Gly Asn Tyr Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
20 25 30

<210> 961
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 961

Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala Asn Ala
1 5 10 15

Ala Arg Gly Thr Asn Gly Ala Tyr Ala Thr His Ala Ala Arg
20 25 30

<210> 962
<211> 30
<212> PRT

<213> Homo Sapiens

<400> 962

Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Ala
1 5 10 15

Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
20 25 30

<210> 963
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<212> PRT
<213> Homo Sapiens

<400> 963

Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala Asn Ala
1 5 10 15

Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Ala Ala Arg
20 25 30

<210> 964
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<213> Homo Sapiens

<400> 964

Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Cys Ala Asn Ala
1 5 10 15

Ala Arg Gly Thr Asn Gly Cys Asn Ala Thr His Ala Ala Arg
20 25 30

<210> 965
<211> 30
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<213> Homo Sapiens

<400> 965

Thr Thr Tyr Gly Gly Asn Cys Cys Asn Gly Gly Asn Cys Ala Asn Ala
1 5 10 15

Ala Arg Ala Thr Gly Gly Ala Tyr Ala Thr His Ala Ala Arg
20 25 30

<210> 966
<211> 30
<212> PRT
<213> Homo Sapiens

2669

<400> 966

Thr Thr Tyr Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Ala
1 5 10 15

Ala Arg Gly Thr Asn Gly Ala Arg Thr Thr Tyr Ala Ala Arg
20 25 30

<210> 967
<211> 30
<212> PRT
<213> Homo Sapiens

<400> 967

Thr Thr Tyr Gly Gly Asn Gly Gly Asn Gly Gly Asn Cys Ala Asn Ala
1 5 10 15

Ala Arg Gly Thr Asn Gly Ala Arg Ala Thr His Met Gly Asn
20 25 30

<210> 968
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 968

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
20 25 30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Cys Asn
35 40 45

Trp Ser Asn Gly Thr Asn Ala Ala Arg Gly Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Cys Asn Trp Ser Asn
65 70 75

<210> 969
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 969

Cys Ala Arg Gly Thr Asn Cys Ala Tyr Tyr Thr Asn Gly Thr Asn Cys
1 5 10 15

1665

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
20 25 30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Cys Asn
35 40 45

Trp Ser Asn Gly Thr Asn Ala Ala Arg Gly Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn
65 70 75

<210> 970
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 970

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
20 25 30

Asn Met Gly Asn Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Cys Asn
35 40 45

Trp Ser Asn Gly Thr Asn Ala Ala Arg Gly Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Thr Asn Trp Ser Asn
65 70 75

<210> 971
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 971

Cys Ala Arg Gly Thr Asn Cys Ala Asn Tyr Thr Asn Ala Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Thr Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Cys Ala Asn Gly Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Cys Ala Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn
65 70 75

<210> 972
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 972

Cys Ala Arg Ala Thr His Cys Ala Asn Tyr Thr Asn Ala Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Cys Ala Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Cys Ala Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Cys Ala Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Thr Thr Tyr Trp Ser Asn
65 70 75

<210> 973
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 973

Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn
65 70 75

<210> 974
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 974

Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Tyr Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn
65 70 75

<210> 975
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 975

Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Tyr Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Cys Asn Trp Ser Asn
65 70 75

<210> 976
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 976

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Gly Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Met Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn
65 70 75

<210> 977
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 977

Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Gly Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Cys Ala Arg Cys Cys Asn Gly Gly Asn Gly Gly Asn
35 40 45

Trp Ser Asn Tyr Thr Asn Met Gly Asn Tyr Thr Asn Trp Ser Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Cys Asn Trp Ser Asn
65 70 75

<210> 978
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 978

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn
65 70 75

<210> 979
<211> 75
<212> PRT

<213> Homo Sapiens

<400> 979

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Ala Ala Tyr Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn
65 70 75

<210> 980
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 980

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Cys
1 5 10 15

Ala Arg Thr Gly Gly Gly Gly Asn Gly Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Tyr Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Gly Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Thr Asn Thr Ala Tyr
65 70 75

<210> 981
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 981

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Gly Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn
65 70 75

<210> 982
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 982

Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Tyr Thr
20 25 30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Ala Arg
35 40 45

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Ala Thr His Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Gly Asn Trp Ser Asn
65 70 75

<210> 983
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 983

Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Gly Thr Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Gly Cys Asn Gly Ala Arg Gly Thr
20 25 30

Asn Ala Ala Arg Ala Ala Arg Cys Cys Asn Gly Gly Asn Gly Ala Arg
35 40 45

Trp Ser Asn Tyr Thr Asn Ala Ala Arg Ala Thr His Trp Ser Asn Thr
50 55 60

Gly Tyr Ala Ala Arg Gly Gly Asn Trp Ser Asn
65 70 75

<210> 984
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 984

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Cys
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Ala Thr His Trp Ser Asn
65 70 75

<210> 985
<211> 42
<212> PRT
<213> Homo Sapiens

<400> 985

Thr Gly Gly Gly Thr Asn Met Gly Asn Cys Ala Arg Gly Cys Asn Cys
1 5 10 15

Cys Asn Gly Gly Asn Cys Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala
20 25 30

Arg Thr Gly Gly Ala Thr Gly Gly Gly Asn
35 40

<210> 986
<211> 42
<212> PRT
<213> Homo Sapiens

<400> 986

Thr Gly Gly Gly Thr Asn Met Gly Asn Cys Ala Arg Gly Cys Asn Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala
20 25 30

Arg Thr Gly Gly Ala Thr Gly Gly Gly Asn
35 40

<210> 987
<211> 42
<212> PRT
<213> Homo Sapiens

<400> 987

Thr Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Tyr Thr Asn Gly Ala
20 25 30

Arg Thr Gly Gly Tyr Thr Asn Gly Cys Asn
35 40

<210> 988
<211> 42
<212> PRT
<213> Homo Sapiens

<400> 988

Thr Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Cys Asn Tyr Thr Asn Gly Ala
20 25 30

Arg Thr Gly Gly Tyr Thr Asn Gly Thr Asn
35 40

<210> 989
<211> 42
<212> PRT
<213> Homo Sapiens

<400> 989

Thr Gly Gly Gly Thr Asn Met Gly Asn Cys Ala Arg Gly Cys Asn Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala
20 25 30

Arg Thr Gly Gly Gly Thr Asn Trp Ser Asn
35 40

<210> 990
<211> 42
<212> PRT
<213> Homo Sapiens

<400> 990

Thr Gly Gly Gly Thr Asn Met Gly Asn Cys Ala Arg Gly Cys Asn Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala
20 25 30

Arg Thr Gly Gly Gly Thr Asn Gly Cys Asn
35 40

<210> 991
<211> 42
<212> PRT
<213> Homo Sapiens

<400> 991

Thr Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala
20 25 30

Arg Thr Gly Gly Ala Thr His Gly Gly Asn
35 40

<210> 992
<211> 42
<212> PRT
<213> Homo Sapiens

<400> 992

Thr Gly Gly Gly Thr Asn Met Gly Asn Cys Ala Arg Cys Ala Tyr Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala
20 25 30

Arg Thr Gly Gly Ala Thr His Gly Gly Asn
35 40

<210> 993
<211> 42
<212> PRT
<213> Homo Sapiens

<400> 993

Thr Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala
20 25 30

Arg Thr Gly Gly Ala Thr His Gly Gly Asn
35 40

<210> 994
<211> 42
<212> PRT
<213> Homo Sapiens

<400> 994

Thr Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Cys Cys Asn Gly
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala
20 25 30

Arg Thr Gly Gly Ala Thr His Gly Gly Asn
35 40

<210> 995
<211> 42
<212> PRT
<213> Homo Sapiens

<400> 995

Thr Gly Gly Gly Thr Asn Met Gly Asn Cys Ala Arg Ala Thr Gly Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala
20 25 30

Arg Thr Gly Gly Ala Thr Gly Gly Gly Asn
35 40

<210> 996
<211> 42
<212> PRT
<213> Homo Sapiens

<400> 996

Thr Gly Gly Ala Thr His Met Gly Asn Cys Ala Arg Trp Ser Asn Cys
1 5 10 15

Cys Asn Trp Ser Asn Met Gly Asn Gly Gly Asn Tyr Thr Asn Gly Ala
20 25 30

Arg Thr Gly Gly Tyr Thr Asn Gly Gly Asn
35 40

<210> 997
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 997

Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Cys Ala Asn Trp Ser
20 25 30

Asn Cys Ala Asn Gly Cys Asn Thr Ala Tyr Ala Thr Gly Gly Ala Arg
35 40 45

Tyr Thr Asn Met Gly Asn Trp Ser Asn Tyr Thr Asn Met Gly Asn Trp
50 55 60

Ser Asn Gly Ala Tyr Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 998
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 998

Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr Gly Cys Ala Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Thr His Trp Ser
20 25 30

Asn Cys Ala Asn Gly Cys Asn Thr Ala Tyr Ala Thr Gly Gly Ala Arg
35 40 45

Tyr Thr Asn Trp Ser Asn Met Gly Asn Tyr Thr Asn Met Gly Asn Trp
50 55 60

Ser Asn Gly Ala Tyr Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 999
<211> 96
<212> PRT

<213> Homo Sapiens

<400> 999

Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr Gly Tyr Thr Asn Gly
1 5 10 15

Ala Arg Gly Ala Tyr Cys Ala Asn Trp Ser Asn Cys Ala Asn Gly Ala
20 25 30

Tyr Cys Ala Asn Gly Cys Asn Thr Ala Tyr Ala Thr Gly Gly Ala Arg
35 40 45

Tyr Thr Asn Trp Ser Asn Trp Ser Asn Tyr Thr Asn Met Gly Asn Trp
50 55 60

Ser Asn Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Cys Ala Asn
85 90 95

<210> 1000
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1000

Met Gly Asn Tyr Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Ala
1 5 10 15

Ala Arg Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Trp Ser
20 25 30

Asn Cys Ala Arg Gly Thr Asn Gly Thr Asn Tyr Thr Asn Cys Ala Asn
35 40 45

Ala Thr Gly Cys Ala Asn Ala Ala Tyr Ala Thr Gly Gly Ala Tyr Cys
50 55 60

Cys Asn Gly Thr Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Cys Ala
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1001
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1001

Met Gly Asn Tyr Thr Asn Cys Ala Asn Ala Thr His Cys Ala Asn Ala
1 5 10 15

Ala Arg Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Arg Gly Thr Asn Gly Thr Asn Tyr Thr Asn Cys Ala Asn
35 40 45

Ala Thr Gly Cys Ala Asn Ala Ala Tyr Ala Thr Gly Gly Ala Tyr Cys
50 55 60

Cys Asn Gly Thr Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Cys Ala
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Cys Ala Tyr
85 90 95

<210> 1002
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1002

Met Gly Asn Tyr Thr Asn Cys Ala Asn Ala Thr His Cys Ala Asn Ala
1 5 10 15

Ala Arg Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Cys Ala
20 25 30

Asn Cys Ala Arg Gly Thr Asn Gly Thr Asn Tyr Thr Asn Cys Ala Asn
35 40 45

Gly Thr Asn Cys Ala Asn Gly Ala Tyr Ala Thr Gly Gly Ala Tyr Cys
50 55 60

Cys Asn Gly Thr Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Cys Ala
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Cys Ala Tyr
85 90 95

<210> 1003
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1003

Met Gly Asn Tyr Thr Asn Cys Ala Asn Ala Thr His Cys Ala Asn Ala
1 5 10 15

Ala Arg Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Arg Gly Thr Asn Gly Thr Asn Tyr Thr Asn Cys Ala Asn
35 40 45

Ala Thr Gly Cys Ala Asn Ala Ala Tyr Tyr Thr Asn Gly Ala Tyr Cys
50 55 60

Cys Asn Gly Thr Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Cys Ala
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Cys Ala Tyr
85 90 95

<210> 1004
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1004

Met Gly Asn Tyr Thr Asn Cys Ala Asn Ala Thr His Cys Ala Asn Ala
1 5 10 15

Ala Arg Gly Cys Asn Cys Ala Asn Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Arg Gly Thr Asn Gly Thr Asn Tyr Thr Asn Cys Ala Asn
35 40 45

Ala Thr Gly Cys Ala Asn Ala Ala Tyr Ala Thr Gly Gly Ala Tyr Cys
50 55 60

Cys Asn Gly Thr Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Cys Ala
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Cys Ala Tyr
85 90 95

<210> 1005
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1005

Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala Thr His Trp Ser Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Trp Ser Asn Tyr Thr Asn Thr Ala Tyr Tyr Thr Asn Cys Ala Arg
35 40 45

Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Met Gly Asn Gly
50 55 60

Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1006
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1006

Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala Thr His Trp Ser Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr Tyr Thr Asn Cys Ala Arg
35 40 45

Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Met Gly Asn Gly
50 55 60

Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Ala Ala Arg
85 90 95

<210> 1007
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1007

Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala Thr His Trp Ser Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr Tyr Thr Asn Cys Ala Arg
35 40 45

Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Met Gly Asn Gly
50 55 60

Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Ala
65 70 75 80

Arg Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Ala Ala Arg
85 90 95

<210> 1008
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1008

Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala Thr His Trp Ser Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser Asn Ala Thr Gly Ala Ala
20 25 30

Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr Tyr Thr Asn Cys Ala Arg
35 40 45

Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Met Gly Asn Gly
50 55 60

Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1009
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1009

Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala Thr His Trp Ser Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr Tyr Thr Asn Cys Ala Arg
35 40 45

Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Met Gly Asn Gly
50 55 60

Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1010
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1010

Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala Thr His Trp Ser Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Asn Tyr Thr Asn Thr Ala Tyr Tyr Thr Asn Cys Ala Arg
35 40 45

Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Met Gly Asn Gly
50 55 60

Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Thr Asn Tyr Thr Asn
85 90 95

<210> 1011
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1011

Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala Thr His Trp Ser Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Asn Tyr Thr Asn Gly Ala Tyr Tyr Thr Asn Cys Ala Arg
35 40 45

Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Met Gly Asn Gly
50 55 60

Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1012
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1012

Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala Thr His Trp Ser Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Trp Ser Asn Tyr Thr Asn Thr Thr Tyr Tyr Thr Asn Cys Ala Arg
35 40 45

Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Met Gly Asn Gly
50 55 60

Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Tyr Thr Asn
85 90 95

<210> 1013
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1013

Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala Thr His Trp Ser Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Trp Ser Asn Gly Thr Asn Thr Ala Tyr Tyr Thr Asn Cys Ala Arg
35 40 45

Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Met Gly Asn Gly
50 55 60

Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1014
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1014

Met Gly Asn Thr Thr Tyr Cys Ala Asn Ala Thr His Trp Ser Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Ala Ala Tyr Gly Cys Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Trp Ser Asn Tyr Thr Asn Thr Ala Tyr Tyr Thr Asn Cys Ala Arg
35 40 45

Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Met Gly Asn Gly
50 55 60

Ala Tyr Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1015
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1015

Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Gly
1 5 10 15

Thr Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Ala Ala Tyr
35 40 45

Tyr Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Cys Ala Asn Gly
50 55 60

Cys Asn Gly Cys Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1016
<211> 96
<212> PRT

<213> Homo Sapiens

<400> 1016

Met Gly Asn Gly Thr Asn Ala Ala Tyr Ala Thr Gly Trp Ser Asn Gly
1 5 10 15

Thr Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Ala Ala Arg
35 40 45

Tyr Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Cys Ala Asn Gly
50 55 60

Cys Asn Gly Cys Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1017
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1017

Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Gly
1 5 10 15

Thr Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Ala Ala Arg
35 40 45

Tyr Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Cys Ala Asn Gly
50 55 60

Cys Asn Gly Cys Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1018
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1018

Met Gly Asn Ala Thr His Cys Ala Asn Ala Thr His Trp Ser Asn Gly
1 5 10 15

Cys Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Ala Ala Arg
35 40 45

Tyr Thr Asn Ala Ala Tyr Trp Ser Asn Gly Thr Asn Cys Ala Asn Gly
50 55 60

Cys Asn Gly Cys Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1019
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1019

Met Gly Asn Ala Thr His Cys Ala Asn Ala Ala Arg Trp Ser Asn Gly
1 5 10 15

Thr Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Ala Ala Arg
35 40 45

Tyr Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Cys Ala Asn Gly
50 55 60

Cys Asn Gly Cys Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1020
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1020

Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Gly
1 5 10 15

Thr Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Ala Ala Arg
35 40 45

Tyr Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Cys Ala Asn Gly
50 55 60

Cys Asn Gly Cys Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Trp Ser Asn
85 90 95

<210> 1021
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1021

Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Gly
1 5 10 15

Thr Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Ala Ala Arg
35 40 45

Tyr Thr Asn Thr Thr Tyr Trp Ser Asn Gly Thr Asn Cys Ala Asn Gly
50 55 60

Cys Asn Gly Cys Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Thr Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1022
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1022

Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr Gly Trp Ser Asn Gly
1 5 10 15

Thr Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Ala Ala Arg
35 40 45

Tyr Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Cys Ala Asn Gly
50 55 60

Cys Asn Gly Cys Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1023
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1023

Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Ala
1 5 10 15

Thr His Gly Thr Asn Cys Ala Asn Trp Ser Asn Met Gly Asn Ala Ala
20 25 30

Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Ala Ala Arg
35 40 45

Tyr Thr Asn Trp Ser Asn Trp Ser Asn Gly Thr Asn Cys Ala Asn Gly
50 55 60

Cys Asn Gly Cys Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1024
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1024

Cys Ala Arg Gly Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Gly
1 5 10 15

Cys Asn Gly Ala Tyr Ala Ala Arg Trp Ser Asn Ala Thr His Trp Ser
20 25 30

Asn Cys Ala Asn Gly Cys Asn Thr Ala Tyr Tyr Thr Asn Cys Ala Arg
35 40 45

Thr Gly Gly Trp Ser Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg Gly
50 55 60

Cys Asn Trp Ser Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Ala Thr
65 70 75 80

Gly Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1025
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1025

Cys Ala Arg Gly Thr Asn Cys Ala Asn Ala Thr His Trp Ser Asn Gly
1 5 10 15

Cys Asn Gly Ala Tyr Ala Ala Arg Trp Ser Asn Ala Thr His Ala Ala
20 25 30

Tyr Cys Ala Asn Gly Cys Asn Thr Ala Tyr Tyr Thr Asn Cys Ala Arg
35 40 45

Thr Gly Gly Trp Ser Asn Trp Ser Asn Tyr Thr Asn Ala Ala Arg Gly
50 55 60

Cys Asn Trp Ser Asn Gly Ala Tyr Cys Ala Asn Gly Cys Asn Ala Thr
65 70 75 80

Gly Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1026
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1026

Met Gly Asn Ala Thr His Cys Ala Asn Ala Thr His Ala Ala Tyr Cys
1 5 10 15

Cys Asn Gly Ala Tyr Cys Ala Asn Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Arg Thr Thr Tyr Trp Ser Asn Tyr Thr Asn Cys Ala Arg
35 40 45

Tyr Thr Asn Ala Ala Tyr Trp Ser Asn Gly Thr Asn Cys Ala Asn Cys
50 55 60

Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1027
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 1027

Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Tyr
1 5 10 15

Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser
20 25 30

Asn

<210> 1028
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 1028

Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Cys
1 5 10 15

Ala Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser
20 25 30

Asn

<210> 1029
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 1029

Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Ala
1 5 10 15

Thr Gly Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser
20 25 30

Asn

<210> 1030
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 1030

Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Trp Ser Asn Tyr
1 5 10 15

Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Cys Cys
20 25 30

Asn

<210> 1031
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 1031

Thr Gly Gly Gly Gly Asn Cys Ala Arg Gly Gly Asn Cys Ala Asn Ala
1 5 10 15

Ala Arg Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser
20 25 30

Asn

<210> 1032
<211> 33
<212> PRT
<213> Homo Sapiens

<400> 1032

Thr Gly Gly Gly Gly Asn Met Gly Asn Gly Gly Asn Cys Ala Asn Tyr
1 5 10 15

Thr Asn Gly Thr Asn Cys Ala Asn Gly Thr Asn Trp Ser Asn Trp Ser
20 25 30

Asn

<210> 1033
<211> 16
<212> PRT
<213> Homo sapiens

<220>
<221> CARACTERÍSTICA_MISC
<222> (1)..(1)
<223> X1 se selecciona del grupo que consiste en H y LI

<400> 1033

Xaa Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser Leu Lys Ser
1 5 10 15

<210> 1034
<211> 16
<212> PRT
<213> Homo sapiens

<220>
<221> CARACTERÍSTICA_MISC
<222> (6)..(6)
<223> X1 se selecciona del grupo que consiste en D y V

<220>
<221> CARACTERÍSTICA_MISC
<222> (7)..(7)
<223> X2 se selecciona del grupo que consiste en D y E

<220>
<221> CARACTERÍSTICA_MISC
<222> (15)..(15)
<223> X3 se selecciona del grupo que consiste en K y R

<400> 1034

Leu Ile Tyr Trp Asn Xaa Xaa Lys Arg Tyr Ser Pro Ser Leu Xaa Ser
1 5 10 15

<210> 1035
<211> 13
<212> PRT
<213> Homo sapiens

<220>
<221> CARACTERÍSTICA_MISC
<222> (1)..(1)
<223> X1 se selecciona del grupo que consiste en E y S

<220>
<221> CARACTERÍSTICA_MISC
<222> (2)..(2)
<223> X2 se selecciona del grupo que consiste en D, G y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC

<222> (3)..(3)
<223> X3 se selecciona del grupo que consiste en D, N y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (4)..(4)
<223> X4 se selecciona del grupo que consiste en G y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (5)..(5)
<223> X5 se selecciona del grupo que consiste en G y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (6)..(6)
<223> X6 se selecciona del grupo que consiste en W, Y y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (7)..(7)
<223> X7 se selecciona del grupo que consiste en I, N y Y

<220>
<221> CARACTERÍSTICA_MISC
<222> (8)..(8)
<223> X8 se selecciona del grupo que consiste en A y Y

<220>
<221> CARACTERÍSTICA_MISC
<222> (9)..(9)
<223> X9 se selecciona del grupo que consiste en G, V y Y

<220>
<221> CARACTERÍSTICA_MISC
<222> (10)..(10)
<223> X10 se selecciona del grupo que consiste en A, F y G

<220>
<221> CARACTERÍSTICA_MISC
<222> (11)..(11)
<223> X11 se selecciona del grupo que consiste en F, L y M

<220>
<221> CARACTERÍSTICA_MISC
<222> (13)..(13)
<223> X12 se selecciona del grupo que consiste en V y Y

<400> 1035

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Xaa
1 5 10

<210> 1036
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> CARACTERÍSTICA_MISC
<222> (2)..(2)
<223> X1 se selecciona del grupo que consiste en G y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (3)..(3)
<223> X2 se selecciona del grupo que consiste en K, L y Y

<220>
<221> CARACTERÍSTICA_MISC
<222> (4)..(4)
<223> X3 se selecciona del grupo que consiste en A, G y S

<220>
<221> CARACTERÍSTICA_MISC
<222> (5)..(5)
<223> X4 se selecciona del grupo que consiste en S, V y Y

<220>
<221> CARACTERÍSTICA_MISC
<222> (6)..(6)
<223> X5 se selecciona del grupo que consiste en A y G

<220>
<221> CARACTERÍSTICA_MISC
<222> (7)..(7)
<223> X6 se selecciona del grupo que consiste en G y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (8)..(8)
<223> X7 se selecciona del grupo que consiste en T y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (9)..(9)
<223> X8 se selecciona del grupo que consiste en S y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (10)..(10)
<223> X9 se selecciona del grupo que consiste en Y y ningún aminoácido
<220>

<221> CARACTERÍSTICA_MISC
<222> (11)..(11)
<223> X10 se selecciona del grupo que consiste en W y Y

<220>
<221> CARACTERÍSTICA_MISC
<222> (12)..(12)
<223> X11 se selecciona del grupo que consiste en G, S y Y

<220>
<221> CARACTERÍSTICA_MISC
<222> (14)..(14)
<223> X12 se selecciona del grupo que consiste en F y Y

<220>
<221> CARACTERÍSTICA_MISC
<222> (15)..(15)
<223> X13 se selecciona del grupo que consiste en G y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (16)..(16)
<223> X14 se selecciona del grupo que consiste en M y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (18)..(18)
<223> X15 se selecciona del grupo que consiste en V y Y

<400> 1036

Gln Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Xaa Xaa
1 5 10 15

Asp Xaa

<210> 1037
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> CARACTERÍSTICA_MISC
<222> (1)..(1)
<223> X1 se selecciona del grupo que consiste en D, G, L, S y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (2)..(2)
<223> X2 se selecciona del grupo que consiste en G, H, W, Y y ningún aminoácido
<220>

<221> CARACTERÍSTICA_MISC
<222> (3)..(3)
<223> X3 se selecciona del grupo que consiste en A, F, W, Y y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (4)..(4)
<223> X4 se selecciona del grupo que consiste en D, G, Q, T y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (5)..(5)
<223> X5 se selecciona del grupo que consiste en G, I, Q, S y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (6)..(6)
<223> X6 se selecciona del grupo que consiste en A, D, N, Q, S y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (7)..(7)
<223> X7 se selecciona del grupo que consiste en G, Y y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (8)..(8)
<223> X8 se selecciona del grupo que consiste en D, Y y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (9)..(9)
<223> X9 se selecciona del grupo que consiste en Y y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (10)..(10)
<223> X10 se selecciona del grupo que consiste en A, E, N y Y

<220>
<221> CARACTERÍSTICA_MISC
<222> (11)..(11)
<223> X11 se selecciona del grupo que consiste en G, P, T, V y Y

<220>
<221> CARACTERÍSTICA_MISC
<222> (12)..(12)

<223> X12 se selecciona del grupo que consiste en F y I

<220>
<221> CARACTERÍSTICA_MISC
<222> (13)..(13)
<223> X13 se selecciona del grupo que consiste en D y Q

<220>
<221> CARACTERÍSTICA_MISC
<222> (14)..(14)
<223> X14 se selecciona del grupo que consiste en C, H, V y Y

<400> 1037

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> 1038
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<221> CARACTERÍSTICA_MISC
<222> (1)..(1)
<223> X1 se selecciona del grupo que consiste en E, D y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (2)..(2)
<223> X2 se selecciona del grupo que consiste en G, R y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (3)..(3)
<223> X3 se selecciona del grupo que consiste en I, V, Y y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (4)..(4)
<223> X4 se selecciona del grupo que consiste en A, G, L y N

<220>
<221> CARACTERÍSTICA_MISC
<222> (5)..(5)
<223> X5 se selecciona del grupo que consiste en A, G, V y W

<220>
<221> CARACTERÍSTICA_MISC
<222> (6)..(6)

<223> X6 se selecciona del grupo que consiste en A, N, R y T

<220>
<221> CARACTERÍSTICA_MISC
<222> (7)..(7)
<223> X7 se selecciona del grupo que consiste en G, N, P y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (8)..(8)
<223> X8 se selecciona del grupo que consiste en G, T y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (9)..(9)
<223> X9 se selecciona del grupo que consiste en A y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (10)..(10)
<223> X10 se selecciona del grupo que consiste en D, E y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (11)..(11)
<223> X11 se selecciona del grupo que consiste en S, Y y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (12)..(12)
<223> X12 se selecciona del grupo que consiste en G, Y y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (13)..(13)
<223> X13 se selecciona del grupo que consiste en N, Y y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (14)..(14)
<223> X14 se selecciona del grupo que consiste en Y y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (15)..(15)
<223> X15 se selecciona del grupo que consiste en D, Y y ningún aminoácido

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<220>
<221> CARACTERÍSTICA_MISC
<222> (16)..(16)
<223> X16 se selecciona del grupo que consiste en A, G y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (17)..(17)
<223> X17 se selecciona del grupo que consiste en F y M

<220>
<221> CARACTERÍSTICA_MISC
<222> (19)..(19)
<223> X18 se selecciona del grupo que consiste en I, V y Y

<400> 1038

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Asp Xaa

<210> 1039
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<221> CARACTERÍSTICA_MISC
<222> (1)..(1)
<223> X1 se selecciona del grupo que consiste en A, D, G, S y T

<220>
<221> CARACTERÍSTICA_MISC
<222> (2)..(2)
<223> X2 se selecciona del grupo que consiste en A, E, G, L, N, R, Y y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (3)..(3)
<223> X3 se selecciona del grupo que consiste en A, G, L, N, R, T, Y y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (4)..(4)
<223> X4 se selecciona del grupo que consiste en D, G, R, S, V, Y y ningún aminoácido

<220>

<221> CARACTERÍSTICA_MISC
<222> (5)..(5)
<223> X5 se selecciona del grupo que consiste en A, G, I, S, V, Y y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (6)..(6)
<223> X6 se selecciona del grupo que consiste en F, G, L, R, V y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (7)..(7)
<223> X7 se selecciona del grupo que consiste en L, T, Y y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (8)..(8)
<223> X8 se selecciona del grupo que consiste en Y y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (9)..(9)
<223> X9 se selecciona del grupo que consiste en Y y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (10)..(10)
<223> X10 se selecciona del grupo que consiste en D y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (11)..(11)
<223> X11 se selecciona del grupo que consiste en S y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (12)..(12)
<223> X12 se selecciona del grupo que consiste en S y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (13)..(13)
<223> X13 se selecciona del grupo que consiste en G y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (14)..(14)
<223> X14 se selecciona del grupo que consiste en D, L, M, S, Y y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (15)..(15)
<223> X15 se selecciona del grupo que consiste en H, I, P, V, W y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (16)..(16)
<223> X16 se selecciona del grupo que consiste en F, G, L, R, S, Y y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (17)..(17)
<223> X17 se selecciona del grupo que consiste en D, F, V, W, Y y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (18)..(18)
<223> X18 se selecciona del grupo que consiste en C, F, L, P, S y Y

<220>
<221> CARACTERÍSTICA_MISC
<222> (19)..(19)
<223> X19 se selecciona del grupo que consiste en D, F, G y Y

<220>
<221> CARACTERÍSTICA_MISC
<222> (20)..(20)
<223> X20 se selecciona del grupo que consiste en A, C, G, P, R, V y Y

<220>
<221> CARACTERÍSTICA_MISC
<222> (21)..(21)
<223> X21 se selecciona del grupo que consiste en F, L, M, S y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (22)..(22)
<223> X22 se selecciona del grupo que consiste en A, D y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (23)..(23)
<223> X23 se selecciona del grupo que consiste en I, L, V, Y y ningún aminoácido

<400> 1039

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20

<210> 1040
<211> 14
<212> PRT
<213> Homo sapiens

<220>
<221> CARACTERÍSTICA_MISC
<222> (1)..(1)
<223> X1 se selecciona del grupo que consiste en M y V

<220>
<221> CARACTERÍSTICA_MISC
<222> (7)..(7)
<223> X2 se selecciona del grupo que consiste en S y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (8)..(8)
<223> X3 se selecciona del grupo que consiste en F y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (11)..(11)
<223> X4 se selecciona del grupo que consiste en V y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (12)..(12)
<223> X5 se selecciona del grupo que consiste en F y M

<220>
<221> CARACTERÍSTICA_MISC
<222> (14)..(14)
<223> X6 se selecciona del grupo que consiste en V y Y

<400> 1040

Xaa Tyr Ser Ser Gly Trp Xaa Xaa Tyr Gly Xaa Xaa Asp Xaa
1 5 10

<210> 1041
<211> 8
<212> PRT
<213> Homo sapiens

<220>
<221> CARACTERÍSTICA_MISC
<222> (2)..(2)
<223> X1 se selecciona del grupo que consiste en G, H, L, N y R

<220>
<221> CARACTERÍSTICA_MISC
<222> (3)..(3)
<223> X2 se selecciona del grupo que consiste en E, T y W

<220>
<221> CARACTERÍSTICA_MISC
<222> (4)..(4)
<223> X3 se selecciona del grupo que consiste en L, N, T y V

<220>
<221> CARACTERÍSTICA_MISC
<222> (7)..(7)
<223> X4 se selecciona del grupo que consiste en D y E

<400> 1041

Arg Xaa Xaa Xaa Pro Phe Xaa Tyr
1 5

<210> 1042
<211> 208
<212> PRT
<213> Homo sapiens

<400> 1042

Met Lys Leu Leu Pro Ser Val Val Leu Lys Leu Phe Leu Ala Ala Val
1 5 10 15

Leu Ser Ala Leu Val Thr Gly Glu Ser Leu Glu Arg Leu Arg Arg Gly
20 25 30

Leu Ala Ala Gly Thr Ser Asn Pro Asp Pro Pro Thr Val Ser Thr Asp
35 40 45

Gln Leu Leu Pro Leu Gly Gly Gly Arg Asp Arg Lys Val Arg Asp Leu
50 55 60

Gln Glu Ala Asp Leu Asp Leu Leu Arg Val Thr Leu Ser Ser Lys Pro
65 70 75 80

Gln Ala Leu Ala Thr Pro Asn Lys Glu Glu His Gly Lys Arg Lys Lys
85 90 95

Lys Gly Lys Gly Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr
100 105 110

Lys Asp Phe Cys Ile His Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg
115 120 125

Ala Pro Ser Cys Ile Cys His Pro Gly Tyr His Gly Glu Arg Cys His
130 135 140

Gly Leu Ser Leu Pro Val Glu Asn Arg Leu Tyr Thr Tyr Asp His Thr
145 150 155 160

Thr Ile Leu Ala Val Val Ala Val Val Leu Ser Ser Val Cys Leu Leu
165 170 175

Val Ile Val Gly Leu Leu Met Phe Arg Tyr His Arg Arg Gly Gly Tyr
180 185 190

Asp Val Glu Asn Glu Glu Lys Val Lys Leu Gly Met Thr Asn Ser His
195 200 205

<210> 1043
<211> 19
<212> PRT
<213> Homo sapiens

<400> 1043

Met Lys Leu Leu Pro Ser Val Val Leu Lys Leu Phe Leu Ala Ala Val
1 5 10 15

Leu Ser Ala

<210> 1044
<211> 149
<212> PRT
<213> Homo sapiens

<400> 1044

Met Lys Leu Leu Pro Ser Val Val Leu Lys Leu Phe Leu Ala Ala Val
1 5 10 15

Leu Ser Ala Leu Val Thr Gly Glu Ser Leu Glu Arg Leu Arg Arg Gly
20 25 30

Leu Ala Ala Gly Thr Ser Asn Pro Asp Pro Pro Thr Val Ser Thr Asp
35 40 45

Gln Leu Leu Pro Leu Gly Gly Gly Arg Asp Arg Lys Val Arg Asp Leu
50 55 60

Gln Glu Ala Asp Leu Asp Leu Leu Arg Val Thr Leu Ser Ser Lys Pro
65 70 75 80

Gln Ala Leu Ala Thr Pro Asn Lys Glu Glu His Gly Lys Arg Lys Lys
85 90 95

Lys Gly Lys Gly Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr
100 105 110

Lys Asp Phe Cys Ile His Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg
115 120 125

Ala Pro Ser Cys Ile Cys His Pro Gly Tyr His Gly Glu Arg Cys His
130 135 140

Gly Leu Ser Leu Pro
145

<210> 1045
<211> 87
<212> PRT
<213> Homo sapiens

<400> 1045

Asp Leu Gln Glu Ala Asp Leu Asp Leu Leu Arg Val Thr Leu Ser Ser
1 5 10 15

Lys Pro Gln Ala Leu Ala Thr Pro Asn Lys Glu Glu His Gly Lys Arg
20 25 30

Lys Lys Lys Gly Lys Gly Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg
35 40 45

Lys Tyr Lys Asp Phe Cys Ile His Gly Glu Cys Lys Tyr Val Lys Glu
50 55 60

Leu Arg Ala Pro Ser Cys Ile Cys His Pro Gly Tyr His Gly Glu Arg
65 70 75 80

Cys His Gly Leu Ser Leu Pro
85

<210> 1046
<211> 43
<212> PRT
<213> Homo sapiens

<400> 1046

Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys Ile His Gly Glu Cys Lys
1 5 10 15

Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys Ile Cys His Pro Gly Tyr
20 25 30

His Gly Glu Arg Cys His Gly Leu Ser Leu Pro
35 40

<210> 1047
<211> 149
<212> PRT
<213> Homo sapiens

<400> 1047

Met Lys Leu Leu Pro Ser Val Val Leu Lys Leu Phe Leu Ala Ala Val
1 5 10 15

Leu Ser Ala Leu Val Thr Gly Glu Ser Leu Glu Arg Leu Arg Arg Gly
20 25 30

Leu Ala Ala Gly Thr Ser Asn Pro Asp Pro Pro Thr Val Ser Thr Asp
35 40 45

Gln Leu Leu Pro Leu Gly Gly Gly Arg Asp Arg Lys Val Arg Asp Leu
50 55 60

Gln Glu Ala Asp Leu Asp Leu Leu Arg Val Thr Leu Ser Ser Lys Pro
65 70 75 80

Gln Ala Leu Ala Thr Pro Asn Lys Glu Glu His Gly Lys Arg Lys Lys
85 90 95

Lys Gly Lys Gly Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr
100 105 110

Lys Asp Phe Cys Ile His Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg
115 120 125

Ala Pro Ser Cys Ile Cys His Pro Gly Tyr His Gly Glu Arg Cys His
130 135 140

Gly Leu Ser Leu Pro
145

<210> 1048
<211> 32
<212> ADN
<213> Artificial

<220>
<223> cebador hacia adelante

<400> 1048
gggttaacgc caccatgaag ctgctgccgt cg 32

<210> 1049

<211> 28
<212> ADN
<213> Artificial

<220>
<223> cebador hacia atrás

<400> 1049
ccgctcgagg tgggaattag tcatgccc 28

<210> 1050
<211> 31
<212> ADN
<213> Artificial

<220>
<223> cebador hacia adelante

<400> 1050
ggaattcgcc accatgaagc tgctgccgtc g 31

<210> 1051
<211> 30
<212> ADN
<213> Artificial

<220>
<223> cebador hacia atrás

<400> 1051
ccgctcgagg tgggagctag cagccacgcc 30

<210> 1052
<211> 44
<212> PRT
<213> Homo sapiens

<400> 1052

Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys Ile His Gly Glu Cys
1 5 10 15

Lys Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys Ile Cys His Pro Gly
20 25 30

Tyr His Gly Glu Arg Cys His Gly Leu Ser Leu Pro
35 40

<210> 1053
<211> 49
<212> PRT
<213> Homo sapiens

<400> 1053

Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Tyr Cys
1 5 10 15

Ile His Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys
20 25 30

Ile Cys His Pro Gly Tyr His Gly Glu Arg Cys His Gly Leu Ser Leu
35 40 45

Pro

<210> 1054
<211> 49
<212> PRT
<213> Homo sapiens

<400> 1054

Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys
1 5 10 15

Ile His Gly Glu Cys Lys Tyr Val Lys Glu Phe Arg Ala Pro Ser Cys
20 25 30

Ile Cys His Pro Gly Tyr His Gly Glu Arg Cys His Gly Leu Ser Leu
35 40 45

Pro

<210> 1055
<211> 49
<212> PRT
<213> Homo sapiens

<400> 1055

Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys
1 5 10 15

Ile His Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys
20 25 30

Ile Cys His Pro Gly Tyr His Gly His Arg Cys His Gly Leu Ser Leu
35 40 45

Pro

<210> 1056

2708

<211> 49
<212> PRT
<213> Homo sapiens

<400> 1056

Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys
1 5 10 15

Ile His Gly Glu Cys Arg Tyr Leu Gln Glu Leu Arg Ala Pro Ser Cys
20 25 30

Ile Cys His Pro Gly Tyr His Gly Glu Arg Cys His Gly Leu Ser Leu
35 40 45

Pro

<210> 1057
<211> 49
<212> PRT
<213> Homo sapiens

<400> 1057

Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Tyr Cys
1 5 10 15

Ile His Gly Glu Cys Arg Tyr Leu Gln Glu Leu Arg Ala Pro Ser Cys
20 25 30

Ile Cys His Pro Gly Tyr His Gly Glu Arg Cys His Gly Leu Ser Leu
35 40 45

Pro

<210> 1058
<211> 49
<212> PRT
<213> Homo sapiens

<400> 1058

Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys
1 5 10 15

Ile His Gly Glu Cys Arg Tyr Leu Gln Glu Leu Arg Ala Pro Ser Cys
20 25 30

Ile Cys His Pro Gly Tyr His Gly His Arg Cys His Gly Leu Ser Leu
35 40 45

Pro

<210> 1059
<211> 49
<212> PRT
<213> Homo sapiens

<400> 1059

Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys
1 5 10 15

Ile His Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys
20 25 30

Lys Cys Leu Pro Gly Tyr His Gly Glu Arg Cys His Gly Leu Ser Leu
35 40 45

Pro

<210> 1060
<211> 49
<212> PRT
<213> Homo sapiens

<400> 1060

Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Tyr Cys
1 5 10 15

Ile His Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys
20 25 30

Lys Cys Leu Pro Gly Tyr His Gly Glu Arg Cys His Gly Leu Ser Leu
35 40 45

Pro

<210> 1061
<211> 49
<212> PRT
<213> Homo sapiens

<400> 1061

Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys
1 5 10 15

Ile His Gly Glu Cys Lys Tyr Val Lys Glu Phe Arg Ala Pro Ser Cys
20 25 30

Lys Cys Leu Pro Gly Tyr His Gly Glu Arg Cys His Gly Leu Ser Leu
35 40 45

Pro

<210> 1062
<211> 49
<212> PRT
<213> Homo sapiens

<400> 1062

Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys
1 5 10 15

Ile His Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys
20 25 30

Ile Cys His Pro Gly Tyr His Gly Glu Arg Cys His Gly Leu Ser Thr
35 40 45

Pro

<210> 1063
<211> 49
<212> PRT
<213> Homo sapiens

<400> 1063

Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys
1 5 10 15

Ile His Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys
20 25 30

Ile Cys His Pro Gly Tyr His Gly His Arg Cys His Gly Leu Ser Thr
35 40 45

Pro

<210> 1064
<211> 50
<212> PRT
<213> Homo sapiens

<400> 1064

Leu Gly Lys Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys
1 5 10 15

Leu His Asp Gly Val Cys Lys Tyr Val Lys Glu Leu Arg Ala Pro Ser
20 25 30

Cys Ile Cys His Pro Gly Tyr His Gly Glu Arg Cys His Gly Leu Ser
35 40 45

Leu Pro
50

<210> 1065
<211> 214
<212> PRT
<213> Homo Sapiens

<400> 1065

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Thr Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Leu Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Ser Phe Tyr Thr Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 1066
<211> 23
<212> PRT
<213> Homo Sapiens

<400> 1066

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys
20

<210> 1067
<211> 23
<212> PRT
<213> Homo Sapiens

<400> 1067

Asn Ile Val Met Thr Gln Thr Pro Leu Ser Ser Pro Val Thr Leu Gly
1 5 10 15

Gln Pro Ala Ser Ile Ser Cys
20

<210> 1068
<211> 23
<212> PRT
<213> Homo Sapiens

<400> 1068

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Thr Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys
20

<210> 1069
<211> 23
<212> PRT
<213> Homo Sapiens

<400> 1069

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Gly Val Thr Ile Thr Cys
20

<210> 1070
<211> 23
<212> PRT
<213> Homo Sapiens

<400> 1070

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Ala Ile Thr Cys
20

<210> 1071
<211> 23
<212> PRT
<213> Homo Sapiens

<400> 1071

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys
20

<210> 1072
<211> 23
<212> PRT
<213> Homo Sapiens

<400> 1072

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Arg Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys
20

<210> 1073
<211> 23
<212> PRT
<213> Homo Sapiens

<400> 1073

2714

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys
20

<210> 1074
<211> 15
<212> PRT
<213> Homo Sapiens

<400> 1074

Trp Phe Gln Gln Arg Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr
1 5 10 15

<210> 1075
<211> 32
<212> PRT
<213> Homo Sapiens

<400> 1075

Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 1076
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 1076

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 1077
<211> 69

<212> PRT
<213> Homo Sapiens

<400> 1077

Gly Ala Arg Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Cys Ala Asn Cys Cys Asn Tyr Thr Asn Trp Ser Asn Trp Ser
20 25 30

Asn Cys Cys Asn Gly Thr Asn Cys Ala Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Cys Ala Arg Cys Cys Asn Gly Cys Asn Trp Ser Asn Ala Thr His Trp
50 55 60

Ser Asn Thr Gly Tyr
65

<210> 1078
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 1078

Gly Ala Tyr Ala Thr His Gly Thr Asn Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Gly Ala Tyr Trp Ser Asn Tyr Thr
20 25 30

Asn Gly Cys Asn Gly Thr Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Gly Ala Arg Met Gly Asn Gly Cys Asn Cys Ala Asn Ala Thr His Ala
50 55 60

Ala Tyr Thr Gly Tyr
65

<210> 1079
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 1079

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Met Gly
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 1080
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 1080

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Gly Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 1081
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 1081

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

2717

Ala Asn Thr Gly Tyr
65

<210> 1082
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 1082

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Gly Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Gly Cys Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 1083
<211> 69
<212> PRT
<213> Homo Sapiens

<400> 1083

Gly Ala Tyr Ala Thr His Cys Ala Arg Ala Thr Gly Cys Ala Asn Cys
1 5 10 15

Ala Arg Trp Ser Asn Cys Cys Asn Trp Ser Asn Trp Ser Asn Tyr Thr
20 25 30

Asn Trp Ser Asn Gly Cys Asn Trp Ser Asn Tyr Thr Asn Gly Gly Asn
35 40 45

Gly Ala Tyr Met Gly Asn Gly Thr Asn Cys Ala Asn Ala Thr His Cys
50 55 60

Ala Asn Thr Gly Tyr
65

<210> 1084
<211> 45
<212> PRT
<213> Homo Sapiens

<400> 1084

2718

Thr Gly Gly Thr Thr Tyr Cys Ala Arg Cys Ala Arg Met Gly Asn Cys
1 5 10 15

Cys Asn Gly Gly Asn Cys Ala Arg Trp Ser Asn Cys Cys Asn Met Gly
20 25 30

Asn Met Gly Asn Tyr Thr Asn Ala Thr His Thr Ala Tyr
35 40 45

<210> 1085
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 1085

Cys Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Gly
1 5 10 15

Ala Arg Trp Ser Asn Gly Gly Asn Cys Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Gly Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Cys Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn
65 70 75

<210> 1086
<211> 75
<212> PRT
<213> Homo Sapiens

<400> 1086

Gly Ala Arg Gly Thr Asn Cys Ala Arg Tyr Thr Asn Cys Ala Arg Cys
1 5 10 15

Ala Arg Thr Gly Gly Gly Gly Asn Gly Cys Asn Gly Gly Asn Tyr Thr
20 25 30

Asn Tyr Thr Asn Ala Ala Arg Cys Cys Asn Trp Ser Asn Gly Ala Arg
35 40 45

Cys Ala Asn Tyr Thr Asn Trp Ser Asn Tyr Thr Asn Cys Ala Asn Thr
50 55 60

Gly Tyr Gly Cys Asn Gly Thr Asn Thr Ala Tyr
65 70 75

2719

<210> 1087
<211> 42
<212> PRT
<213> Homo Sapiens

<400> 1087

Thr Gly Gly Gly Thr Asn Met Gly Asn Cys Ala Arg Gly Cys Asn Cys
1 5 10 15

Cys Asn Gly Gly Asn Ala Ala Arg Gly Gly Asn Tyr Thr Asn Gly Ala
20 25 30

Arg Thr Gly Gly Gly Thr Asn Trp Ser Asn
35 40

<210> 1088
<211> 96
<212> PRT
<213> Homo Sapiens

<400> 1088

Met Gly Asn Thr Thr Tyr Cys Ala Asn Gly Thr Asn Trp Ser Asn Met
1 5 10 15

Gly Asn Gly Ala Tyr Ala Ala Tyr Trp Ser Asn Ala Ala Arg Ala Ala
20 25 30

Tyr Cys Ala Asn Tyr Thr Asn Thr Thr Tyr Tyr Thr Asn Cys Ala Arg
35 40 45

Ala Thr Gly Ala Ala Tyr Trp Ser Asn Tyr Thr Asn Met Gly Asn Gly
50 55 60

Cys Asn Gly Ala Arg Gly Ala Tyr Cys Ala Asn Gly Cys Asn Gly Thr
65 70 75 80

Asn Thr Ala Tyr Thr Ala Tyr Thr Gly Tyr Gly Cys Asn Met Gly Asn
85 90 95

<210> 1089
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<221> CARACTERÍSTICA_MISC
<222> (1)..(1)
<223> X1 se selecciona del grupo que consiste en I y M

<220>
<221> CARACTERÍSTICA_MISC

<222> (3)..(3)
<223> X2 se selecciona del grupo que consiste en A, G y S

<220>
<221> CARACTERÍSTICA_MISC
<222> (4)..(4)
<223> X3 se selecciona del grupo que consiste en I y T

<220>
<221> CARACTERÍSTICA_MISC
<222> (5)..(5)
<223> X4 se selecciona del grupo que consiste en H y Q

<220>
<221> CARACTERÍSTICA_MISC
<222> (6)..(6)
<223> X5 se selecciona del grupo que consiste en F, L y W

<220>
<221> CARACTERÍSTICA_MISC
<222> (8)..(8)
<223> X6 se selecciona del grupo que consiste en C, I, H, L y T

<220>
<221> CARACTERÍSTICA_MISC
<222> (9)..(9)
<223> X7 se selecciona del grupo que consiste en S y T

<400> 1089

Xaa Gln Xaa Xaa Xaa Xaa Pro Xaa Xaa
1 5

<210> 1090
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<221> CARACTERÍSTICA_MISC
<222> (3)..(3)
<223> X1 se selecciona del grupo que consiste en I y S

<220>
<221> CARACTERÍSTICA_MISC
<222> (4)..(4)
<223> X2 se selecciona del grupo que consiste en F y Y

<220>
<221> CARACTERÍSTICA_MISC
<222> (5)..(5)
<223> X3 se selecciona del grupo que consiste en F, I, S y Y

2721

<220>
<221> CARACTERÍSTICA_MISC
<222> (6)..(6)
<223> X4 se selecciona del grupo que consiste en A, S y T

<220>
<221> CARACTERÍSTICA_MISC
<222> (7)..(7)
<223> X5 se selecciona del grupo que consiste en P y S

<400> 1090

Gln Gln Xaa Xaa Xaa Xaa Xaa Ile Thr
1 5

<210> 1091
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<221> CARACTERÍSTICA_MISC
<222> (1)..(1)
<223> X1 se selecciona del grupo que consiste en L y Q

<220>
<221> CARACTERÍSTICA_MISC
<222> (2)..(2)
<223> X2 se selecciona del grupo que consiste en K, N y Q

<220>
<221> CARACTERÍSTICA_MISC
<222> (3)..(3)
<223> X3 se selecciona del grupo que consiste en A, H, S y Y

<220>
<221> CARACTERÍSTICA_MISC
<222> (4)..(4)
<223> X4 se selecciona del grupo que consiste en H, N y Y

<220>
<221> CARACTERÍSTICA_MISC
<222> (5)..(5)
<223> X5 se selecciona del grupo que consiste en N, S y T

<220>
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<222> (6)..(6)
<223> X6 se selecciona del grupo que consiste en A, F, I, T, V y Y

<220>
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<222> (7)..(7)
<223> X7 se selecciona del grupo que consiste en P y ningún aminoácido

<220>
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<222> (8)..(8)
<223> X8 se selecciona del grupo que consiste en F, L y P

<400> 1091

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr
1 5

<210> 1092
<211> 9
<212> PRT
<213> Homo sapiens

<220>
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<223> X1 se selecciona del grupo que consiste en H y Q

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<222> (3)..(3)
<223> X2 se selecciona del grupo que consiste en C y Y

<220>
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<222> (5)..(5)
<223> X3 se selecciona del grupo que consiste en D, I, N, S y Y

<220>
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<222> (8)..(8)
<223> X4 se selecciona del grupo que consiste en F, I y L

<220>
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<222> (9)..(9)
<223> X5 se selecciona del grupo que consiste en A, S y T

<400> 1092

Gln Xaa Xaa Asp Xaa Leu Pro Xaa Xaa
1 5

<210> 1093
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<213> Homo sapiens

2123

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<223> X1 se selecciona del grupo que consiste en H y Y

<220>
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<223> X2 se selecciona del grupo que consiste en G y N

<220>
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<223> X3 se selecciona del grupo que consiste en N y S

<220>
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<223> X4 se selecciona del grupo que consiste en S y W

<220>
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<222> (8)..(8)
<223> X5 se selecciona del grupo que consiste en P y ningún aminoácido

<220>
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<222> (9)..(9)
<223> X6 se selecciona del grupo que consiste en R y W

<220>
<221> CARACTERÍSTICA_MISC
<222> (10)..(10)
<223> X7 se selecciona del grupo que consiste en S y T

<400> 1093

Gln Gln Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa
1 5 10

<210> 1094
<211> 10
<212> PRT
<213> Homo sapiens

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<220>
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<222> (4)..(4)

<223> X2 se selecciona del grupo que consiste en F y Y

<220>
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<222> (5)..(5)
<223> X3 se selecciona del grupo que consiste en G, I y S

<220>
<221> CARACTERÍSTICA_MISC
<222> (6)..(6)
<223> X4 se selecciona del grupo que consiste en F, I y T

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<223> X6 se selecciona del grupo que consiste en F, L, R y W

<220>
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<222> (9)..(9)
<223> X7 se selecciona del grupo que consiste en S y T

<400> 1094

Xaa Gln Tyr Xaa Xaa Xaa Xaa Xaa Xaa Phe
1 5 10

<210> 1095
<211> 10
<212> PRT
<213> Homo sapiens

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<223> X2 se selecciona del grupo que consiste en E, G y S

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<222> (7)..(7)
<223> X3 se selecciona del grupo que consiste en H, L y Y

<220>

<221> CARACTERÍSTICA_MISC
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<223> X4 se selecciona del grupo que consiste en G, S y Y

<220>
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<223> X5 se selecciona del grupo que consiste en I y M

<220>
<221> CARACTERÍSTICA_MISC
<222> (10)..(10)
<223> X6 se selecciona del grupo que consiste en H y S

<400> 1095

Gly Tyr Thr Xaa Thr Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> 1096
<211> 10
<212> PRT
<213> Homo sapiens

<220>
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<222> (3)..(3)
<223> X1 se selecciona del grupo que consiste en R y S

<400> 1096

Gly Tyr Xaa Phe Thr Ser Tyr Trp Ile Gly
1 5 10

<210> 1097
<211> 10
<212> PRT
<213> Homo sapiens

<220>
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<223> X1 se selecciona del grupo que consiste en R y S

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<222> (7)..(7)
<223> X2 se selecciona del grupo que consiste en H y Y

<220>
<221> CARACTERÍSTICA_MISC
<222> (8)..(8)
<223> X3 se selecciona del grupo que consiste en D y G

1726

<400> 1097

Gly Phe Thr Phe Xaa Ser Xaa Xaa Met His
1 5 10

<210> 1098
<211> 10
<212> PRT
<213> Homo sapiens

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<222> (6)..(6)
<223> X2 se selecciona del grupo que consiste en A, R y S

<220>
<221> CARACTERÍSTICA_MISC
<222> (8)..(8)
<223> X3 se selecciona del grupo que consiste en A y S

<220>
<221> CARACTERÍSTICA_MISC
<222> (10)..(10)
<223> X4 se selecciona del grupo que consiste en N y S

<400> 1098

Gly Phe Xaa Phe Ser Xaa Tyr Xaa Met Xaa
1 5 10

<210> 1099
<211> 12
<212> PRT
<213> Homo sapiens

<220>
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<223> X1 se selecciona del grupo que consiste en D y G

<220>
<221> CARACTERÍSTICA_MISC
<222> (4)..(4)
<223> X2 se selecciona del grupo que consiste en F, I y V

<220>
<221> CARACTERÍSTICA_MISC
<222> (6)..(6)

<223> X3 se selecciona del grupo que consiste en R, S y ningún aminoácido

<220>
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<222> (7)..(7)
<223> X4 se selecciona del grupo que consiste en G, Y y ningún aminoácido

<220>
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<222> (8)..(8)
<223> X5 se selecciona del grupo que consiste en D, G, S y ningún aminoácido

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<222> (9)..(9)
<223> X6 se selecciona del grupo que consiste en A, S y Y

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<222> (10)..(10)
<223> X7 se selecciona del grupo que consiste en A y Y

<220>
<221> CARACTERÍSTICA_MISC
<222> (12)..(12)
<223> X8 se selecciona del grupo que consiste en N y S

<400> 1099

Gly Xaa Ser Xaa Ser Xaa Xaa Xaa Xaa Xaa Trp Xaa
1 5 10

<210> 1100
<211> 12
<212> PRT
<213> Homo sapiens

<220>
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<222> (5)..(5)
<223> X1 se selecciona del grupo que consiste en S y N

<400> 1100

Gly Phe Ser Leu Xaa Thr Gly Gly Val Gly Val Gly
1 5 10

<210> 1101
<211> 16
<212> PRT

2728

<213> Homo sapiens

<220>
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<223> X1 se selecciona del grupo que consiste en S y W

<220>
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<223> X2 se selecciona del grupo que consiste en F y I

<220>
<221> CARACTERÍSTICA_MISC
<222> (3)..(3)
<223> X3 se selecciona del grupo que consiste en D, N y S

<220>
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<223> X7 se selecciona del grupo que consiste en E, G y N

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<223> X8 se selecciona del grupo que consiste en I y N

<220>
<221> CARACTERÍSTICA_MISC
<222> (11)..(11)
<223> X9 se selecciona del grupo que consiste en C, H y Y

<220>
<221> CARACTERÍSTICA_MISC
<222> (12)..(12)
<223> X10 se selecciona del grupo que consiste en A y T

<220>

2729

<221> CARACTERÍSTICA_MISC
<222> (15)..(15)
<223> X11 se selecciona del grupo que consiste en F y L

<220>
<221> CARACTERÍSTICA_MISC
<222> (16)..(16)
<223> X12 se selecciona del grupo que consiste en D y G

<400> 1101

Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Thr Xaa Xaa Xaa Gln Lys Xaa Xaa
1 5 10 15

<210> 1102
<211> 17
<212> PRT
<213> Homo sapiens

<220>
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<223> X1 se selecciona del grupo que consiste en D y G

<220>
<221> CARACTERÍSTICA_MISC
<222> (9)..(9)
<223> X2 se selecciona del grupo que consiste en A, I y T

<400> 1102

Ile Ile Tyr Pro Xaa Asp Ser Asp Xaa Arg Tyr Ser Pro Ser Phe Gln
1 5 10 15

Gly

<210> 1103
<211> 17
<212> PRT
<213> Homo sapiens

<220>
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<223> X1 se selecciona del grupo que consiste en F y V

<220>
<221> CARACTERÍSTICA_MISC
<222> (3)..(3)
<223> X2 se selecciona del grupo que consiste en S y W

<220>

2730

<221> CARACTERÍSTICA_MISC
<222> (4)..(4)
<223> X3 se selecciona del grupo que consiste en D, S y Y

<220>
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<222> (8)..(8)
<223> X4 se selecciona del grupo que consiste en I, N y T

<220>
<221> CARACTERÍSTICA_MISC
<222> (9)..(9)
<223> X5 se selecciona del grupo que consiste en K y Q

<220>
<221> CARACTERÍSTICA_MISC
<222> (10)..(10)
<223> X6 se selecciona del grupo que consiste en N, R y Y

<220>
<221> CARACTERÍSTICA_MISC
<222> (12)..(12)
<223> X7 se selecciona del grupo que consiste en A, T y V

<220>
<221> CARACTERÍSTICA_MISC
<222> (16)..(16)
<223> X8 se selecciona del grupo que consiste en K y R

<400> 1103

Xaa Ile Xaa Xaa Asp Gly Ser Xaa Xaa Xaa Tyr Xaa Asp Ser Val Xaa
1 5 10 15

Gly

<210> 1104
<211> 17
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<222> (4)..(4)
<223> X2 se selecciona del grupo que consiste en G, R y S

<220>

<221> CARACTERÍSTICA_MISC
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<223> X3 se selecciona del grupo que consiste en G y S

<220>
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<223> X4 se selecciona del grupo que consiste en G, R y S

<220>
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<223> X5 se selecciona del grupo que consiste en S, T y Y

<220>
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<222> (9)..(9)
<223> X6 se selecciona del grupo que consiste en I y T

<400> 1104

Xaa Ile Ser Xaa Ser Xaa Xaa Xaa Xaa Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 1105
<211> 18
<212> PRT
<213> Homo sapiens

<220>
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<223> X1 se selecciona del grupo que consiste en E, R y Y

<220>
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<222> (2)..(2)
<223> X2 se selecciona del grupo que consiste en I y T

<220>
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<220>
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<222> (4)..(4)
<223> X4 se selecciona del grupo que consiste en C, H, S, T y Y

<220>

2732

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<223> X5 se selecciona del grupo que consiste en S y R

<220>
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<220>
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<220>
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<223> X8 se selecciona del grupo que consiste en T y W

<220>
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<222> (9)..(9)
<223> X9 se selecciona del grupo que consiste en N y Y

<220>
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<220>
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<222> (11)..(11)
<223> X11 se selecciona del grupo que consiste en D y ningún aminoácido

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<222> (13)..(13)
<223> X12 se selecciona del grupo que consiste en A y N

<220>
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<222> (14)..(14)
<223> X13 se selecciona del grupo que consiste en P y V

<220>
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<222> (16)..(16)
<223> X14 se selecciona del grupo que consiste en L y V

<400> 1105

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Xaa Ser Xaa
1 5 10 15

Lys Ser

<210> 1106
<211> 16
<212> PRT
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<223> X1 se selecciona del grupo que consiste en K y R

<220>
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<222> (7)..(7)
<223> X2 se selecciona del grupo que consiste en L y V

<220>
<221> CARACTERÍSTICA_MISC
<222> (8)..(8)
<223> X3 se selecciona del grupo que consiste en H y Y

<220>
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<222> (12)..(12)
<223> X4 se selecciona del grupo que consiste en K y N

<220>
<221> CARACTERÍSTICA_MISC
<222> (16)..(16)
<223> X5 se selecciona del grupo que consiste en N, S y Y

<400> 1106

Xaa Ser Ser Gln Ser Leu Xaa Xaa Ser Asp Gly Xaa Thr Tyr Leu Xaa
1 5 10 15

<210> 1107
<211> 11
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<213> Homo sapiens

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<223> X1 se selecciona del grupo que consiste en R, S y T

<220>
<221> CARACTERÍSTICA_MISC
<222> (8)..(8)
<223> X2 se selecciona del grupo que consiste en R y S

<400> 1107

Arg Ala Ser Gln Xaa Ile Ser Xaa Tyr Leu Asn
1 5 10

<210> 1108
<211> 11
<212> PRT
<213> Homo sapiens

<220>
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<223> X1 se selecciona del grupo que consiste en D, G, S y T

<220>
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<222> (7)..(7)
<223> X2 se selecciona del grupo que consiste en A, R y S

<220>
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<222> (8)..(8)
<223> X3 se selecciona del grupo que consiste en H, I, N, R, S y T

<220>
<221> CARACTERÍSTICA_MISC
<222> (9)..(9)
<223> X4 se selecciona del grupo que consiste en D, W y Y

<220>
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<222> (11)..(11)
<223> X5 se selecciona del grupo que consiste en A, G y N

<400> 1108

Arg Ala Ser Gln Xaa Ile Xaa Xaa Xaa Leu Xaa
1 5 10

<210> 1109
<211> 11
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<220>
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<223> X1 se selecciona del grupo que consiste en S y T

<220>
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<222> (8)..(8)

<223> X2 se selecciona del grupo que consiste en D y N

<220>
<221> CARACTERÍSTICA_MISC
<222> (9)..(9)
<223> X3 se selecciona del grupo que consiste en S y Y

<400> 1109

Gln Ala Ser Gln Asp Ile Xaa Xaa Xaa Leu Asn
1 5 10

<210> 1110
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<213> Homo sapiens

<220>
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<223> X1 se selecciona del grupo que consiste en S y T

<220>
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<222> (7)..(7)
<223> X2 se selecciona del grupo que consiste en I y S

<220>
<221> CARACTERÍSTICA_MISC
<222> (8)..(8)
<223> X3 se selecciona del grupo que consiste en R y S

<220>
<221> CARACTERÍSTICA_MISC
<222> (9)..(9)
<223> X4 se selecciona del grupo que consiste en S, N y ningún aminoácido

<220>
<221> CARACTERÍSTICA_MISC
<222> (10)..(10)
<223> X5 se selecciona del grupo que consiste en Y y ningún aminoácido

<400> 1110

Arg Ala Ser Gln Xaa Val Xaa Xaa Xaa Xaa Leu Ala
1 5 10

<210> 1111
<211> 17
<212> PRT
<213> Homo sapiens

<220>
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<223> X1 se selecciona del grupo que consiste en N y S

<220>
<221> CARACTERÍSTICA_MISC
<222> (6)..(6)
<223> X2 se selecciona del grupo que consiste en I y V

<220>
<221> CARACTERÍSTICA_MISC
<222> (8)..(8)
<223> X3 se selecciona del grupo que consiste en D y Y

<220>
<221> CARACTERÍSTICA_MISC
<222> (9)..(9)
<223> X4 se selecciona del grupo que consiste en N, R y S

<220>
<221> CARACTERÍSTICA_MISC
<222> (17)..(17)
<223> X5 se selecciona del grupo que consiste en A y V

<400> 1111

Lys Ser Ser Gln Xaa Xaa Leu Xaa Xaa Ser Asn Asn Lys Asn Tyr Leu
1 5 10 15

Xaa

<210> 1112
<211> 7
<212> PRT
<213> Homo sapiens

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<223> X1 se selecciona del grupo que consiste en E y K

<220>
<221> CARACTERÍSTICA_MISC
<222> (2)..(2)
<223> X2 se selecciona del grupo que consiste en I y V

<220>
<221> CARACTERÍSTICA_MISC
<222> (5)..(5)
<223> X3 se selecciona del grupo que consiste en R y W

<220>
<221> CARACTERÍSTICA_MISC
<222> (6)..(6)
<223> X4 se selecciona del grupo que consiste en D y F

<400> 1112

Xaa Xaa Ser Asn Xaa Xaa Ser
1 5

<210> 1113
<211> 7
<212> PRT
<213> Homo sapiens

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<223> X1 se selecciona del grupo que consiste en A y T

<220>
<221> CARACTERÍSTICA_MISC
<222> (2)..(2)
<223> X2 se selecciona del grupo que consiste en A, E y V

<220>
<221> CARACTERÍSTICA_MISC
<222> (4)..(4)
<223> X3 se selecciona del grupo que consiste en S y T

<400> 1113

Xaa Xaa Ser Xaa Leu Gln Ser
1 5

<210> 1114
<211> 7
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<222> (4)..(4)
<223> X2 se selecciona del grupo que consiste en S y T

<400> 1114

Xaa Ala Ser Xaa Leu Gln Ser
1 5

<210> 1115
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<221> CARACTERÍSTICA_MISC
<222> (4)..(4)
<223> X1 se selecciona del grupo que consiste en I y N

<400> 1115

Asp Ala Ser Xaa Leu Glu Thr
1 5

<210> 1116
<211> 7
<212> PRT
<213> Homo sapiens

<220>
<221> CARACTERÍSTICA_MISC
<222> (4)..(4)
<223> X1 se selecciona del grupo que consiste en A y T

<400> 1116

Trp Ala Ser Xaa Arg Glu Ser
1 5

2739

INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2008/008233

A. CLASSIFICATION OF SUBJECT MATTER
INV. C07K16/22 A61K39/395 A61K33/24 A61P35/00
ADD. C07K16/28

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C07K A61K A61P

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)
EPO-Internal, BIOSIS, Sequence Search, EMBASE, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2005/100403 A (ABBOTT LAB [US]; REILLY EDWARD B [US]; LACY SUSAN E [US]; FUNG EMMA [U) 27 October 2005 (2005-10-27) sequence 16	1,5-10, 12-16
X	WO 2005/010151 A (ABGENIX INC [US]; WEBER RICHARD [US]; FENG XIAO [US]; FOORD ORIT [US];) 3 February 2005 (2005-02-03) sequence 131	1,5-10, 12-16, 20-30, 44-54, 56-64, 67-72,74

-/--

[X] Further documents are listed in the continuation of Box C.

[X] See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier document but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
15 January 2009	28/01/2009

Name and mailing address of the ISA/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Bumb, Peter

Form PCT/ISA/210 (second sheet) (April 2005)

INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2008/008233

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	ITOH Y ET AL: "IL-8 promotes cell proliferation and migration through metalloproteinase-cleavage proHB-EGF in human colon carcinoma cells" CYTOKINE, ACADEMIC PRESS LTD, PHILADELPHIA, PA, US, vol. 29, no. 6, 21 March 2005 (2005-03-21), pages 275-282, XP004769509 ISSN: 1043-4666 paragraph [02.1] paragraph [03.6] figure 6	1-50, 70-72,74
Y		51-64, 67-69,73
X	MISHIMA KAZUHIKO ET AL: "Heparin-binding epidermal growth factor-like growth factor stimulates mitogenic signaling and is highly expressed in human malignant gliomas" ACTA NEUROPATHOLOGICA, vol. 96, no. 4, October 1998 (1998-10), pages 322-328, XP002510490 ISSN: 0001-6322 page 323, left-hand column, lines 26-33 page 325, left-hand column, lines 17-24 figure 3B	1-50, 70-72,74
Y		51-64, 67-69,73
Y	MIYAMOTO S ET AL: "Heparin-Binding EGF-Like Growth Factor is a Promising Target for Ovarian Cancer Therapy" CANCER RESEARCH, AMERICAN ASSOCIATION FOR CANCER RESEARCH, BALTIMORE, MD.; US, vol. 64, no. 16, 15 August 2004 (2004-08-15), pages 5720-5727, XP003000585 page 344 - page 346 page 346, right-hand column, lines 22-25	51-64, 67-69,73
A	MIYAMOTO S ET AL: "Heparin-binding epidermal growth factor-like growth factor as a novel targeting molecule for cancer therapy" CANCER SCIENCE, JAPANESE CANCER ASSOCIATION, TOKYO, JP, vol. 97, 1 May 2006 (2006-05-01), pages 341-347, XP003020176 ISSN: 1347-9032 the whole document	1-74

-/--

INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2008/008233

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	WO 2008/047925 A (FORERUNNER PHARMA RES CO LTD [JP]; KIMURA NAOKI [JP]) 24 April 2008 (2008-04-24) paragraphs [0070], [0076] - [0083] paragraphs [0103], [0106] paragraphs [0155] - [0169] examples 1-10	11,12, 31-41, 43-53, 57-74
P,X	WO 2008/047914 A (FORERUNNER PHARMA RES CO LTD [JP]; KIMURA NAOKI [JP]) 24 April 2008 (2008-04-24) examples 1-3 paragraphs [0051], [0057] - [0067] paragraphs [0081], [0082], [0085] paragraphs [0113], [0140] - [0145] examples 1-3	11,12, 31-41, 43-53, 57-74
P,X	WO 2007/142277 A (KYOWA HAKKO KOGYO KK [JP]; UNIV OSAKA; FUKUOKA UNIVERSITY; MEKADA EISU) 13 December 2007 (2007-12-13) paragraphs [0019] - [0022] paragraphs [0049] - [0058] examples 1-10	11,12, 31-41, 43-53, 57-74

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/EP2008/008233

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2005100403 A	27-10-2005	CA 2563295 A1	27-10-2005
		EP 1732950 A2	20-12-2006
		JP 2008505612 T	28-02-2008
WO 2005010151 A	03-02-2005	AU 2004259398 A1	03-02-2005
		AU 2004260936 A1	10-02-2005
		BR PI0411803 A	23-05-2006
		BR PI0411852 A	23-05-2006
		CA 2530172 A1	10-02-2005
		CA 2530285 A1	03-02-2005
		EP 1638606 A2	29-03-2006
		EP 1639092 A2	29-03-2006
		JP 2007526880 T	20-09-2007
		JP 2007526233 T	13-09-2007
		KR 20060073540 A	28-06-2006
		KR 20060054203 A	22-05-2006
		MX PA05014152 A	25-05-2006
		MX PA05014155 A	25-05-2006
		WO 2005012479 A2	10-02-2005
WO 2008047925 A	24-04-2008	NONE	
WO 2008047914 A	24-04-2008	NONE	
WO 2007142277 A	13-12-2007	NONE	

2743

PATENT COOPERATION TREATY PCT/EP2008/008233

From the INTERNATIONAL BUREAU

PCT

NOTIFICATION OF THE RECORDING OF A CHANGE

(PCT Rule 92*bis*.1 and Administrative Instructions, Section 422)

To:

WEICKMANN & WEICKMANN
Postfach 860 820
81635 Munich
ALLEMAGNE

Date of mailing *(day/month/year)*
26 March 2010 (26.03.2010)

Applicant's or agent's file reference
39562P WO

IMPORTANT NOTIFICATION

International application No.
PCT/EP2008/008233

International filing date *(day/month/year)*
26 September 2008 (26.09.2008)

1. The following indications appeared on record concerning:

☒ the applicant ☐ the inventor ☐ the agent ☐ the common representative

Name and Address
U3 PHARMA GMBH
Bunsenstrasse 1
82152 Martinsried
Germany

State of Nationality: DE
State of Residence: DE
Telephone No.:
Facsimile No.:
E-mail address:

2. The International Bureau hereby notifies the applicant that the following change has been recorded concerning:

☐ the person ☐ the name ☒ the address ☐ the nationality ☐ the residence

Name and Address
U3 PHARMA GMBH
Fraunhoferstr. 22
82152 Martinsried
Germany

State of Nationality: DE
State of Residence: DE
Telephone No.:
Facsimile No.:
E-mail address:
☐ Notifications by e-mail authorized

3. Further observations, if necessary:

4. A copy of this notification has been sent to:

☒ the receiving Office
☐ the International Searching Authority
☐ the Authority(ies) specified for supplementary search
☐ the International Preliminary Examining Authority
☒ the designated Offices concerned
☐ the elected Offices concerned
☐ other:

The International Bureau of WIPO
34, chemin des Colombettes
1211 Geneva 20, Switzerland

Facsimile No. +41 22 338 89 75

Authorized officer
Cabot Daniele
e-mail pt05.pct@wipo.int
Telephone No. +41 22 338 74 05

2744

PATENT COOPERATION TREATY PCT/EP2008/008233

From the INTERNATIONAL BUREAU

PCT

NOTIFICATION OF THE RECORDING OF A CHANGE

(PCT Rule 92*bis*.1 and Administrative Instructions, Section 422)

To:

WEICKMANN & WEICKMANN
Postfach 860 820
81635 Munich
ALLEMAGNE

Date of mailing *(day/month/year)*
26 March 2010 (26.03.2010)

Applicant's or agent's file reference
39562P WO

IMPORTANT NOTIFICATION

International application No.
PCT/EP2008/008233

International filing date *(day/month/year)*
26 September 2008 (26.09.2008)

1. The following indications appeared on record concerning:

☒ the applicant ☒ the inventor ☐ the agent ☐ the common representative

Name and Address

State of Nationality | State of Residence

Telephone No.

Facsimile No.

E-mail address

2. The International Bureau hereby notifies the applicant that the following change has been recorded concerning:

☒ the person ☐ the name ☐ the address ☐ the nationality ☐ the residence

Name and Address

FOORD, Orit
712 Cayman Lane
Foster City, CA 94404
United States of America

State of Nationality: US | State of Residence: US

Telephone No.

Facsimile No.

E-mail address
☐ Notifications by e-mail authorized

3. Further observations, if necessary:
The person identified in Box 2 should be added to the record as applicant for the United States of America only and inventor for all designated States.

4. A copy of this notification has been sent to:

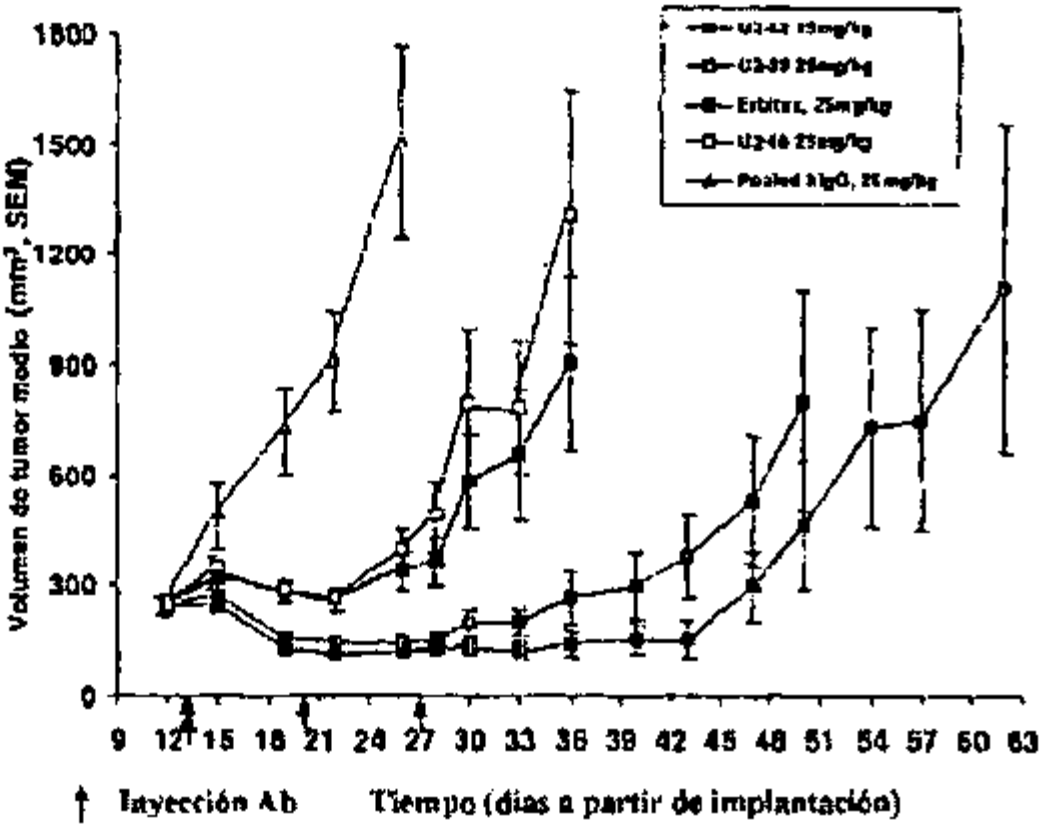
☒ the receiving Office
☐ the International Searching Authority
☐ the Authority(ies) specified for supplementary search
☐ the International Preliminary Examining Authority
☒ the designated Offices concerned
☐ the elected Offices concerned
☐ other:

The International Bureau of WIPO
34, chemin des Colombettes
1211 Geneva 20, Switzerland

Facsimile No. +41 22 338 89 75

Authorized officer
Cabot Daniele
e-mail pt05.pct@wipo.int
Telephone No. +41 22 338 74 05

FIGURA 38A



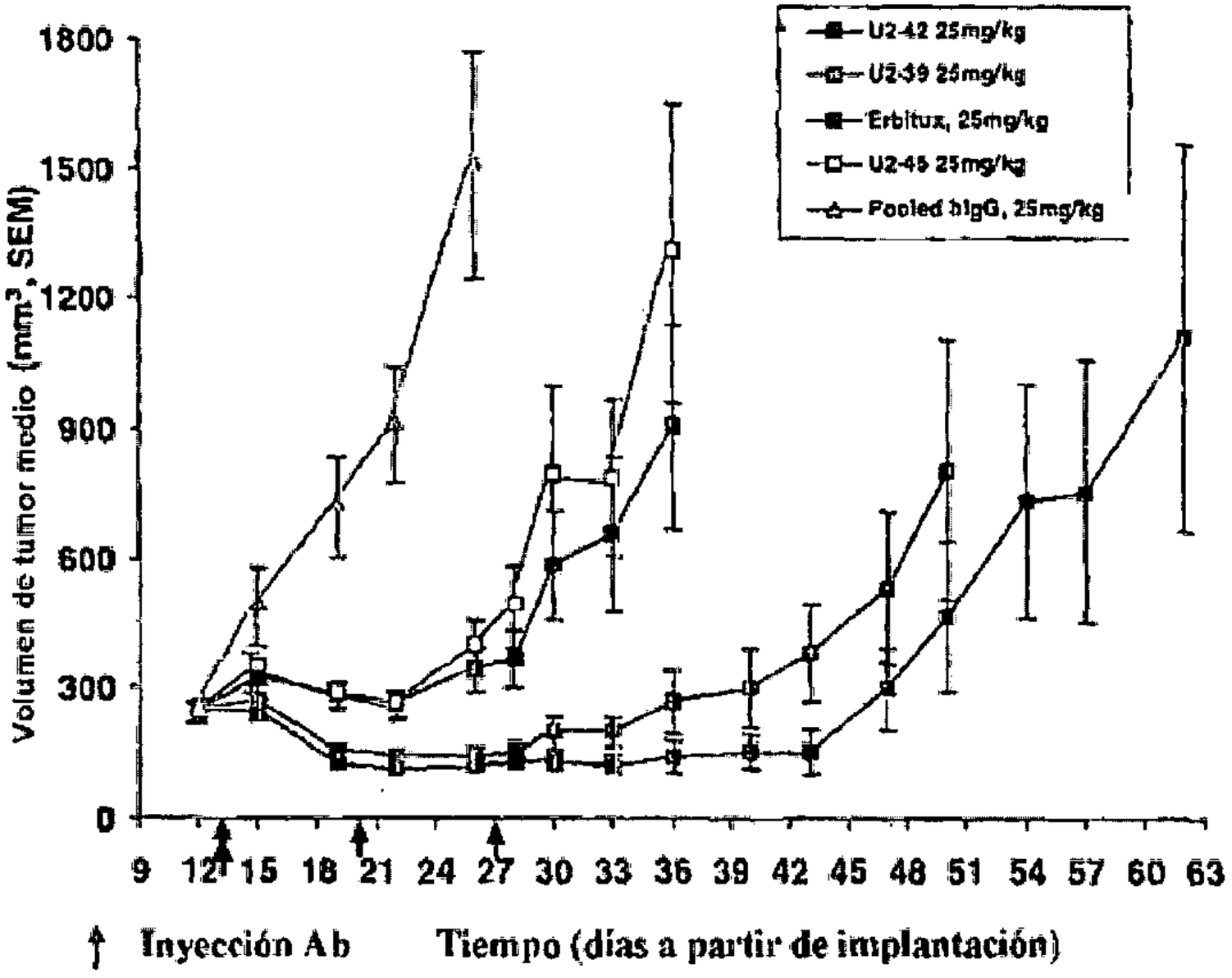
3x10⁶ sc, matrigel, ratones SCID, n=9, Inicio de tratamiento (d13) @ ~ 250 mm³

Dosis inicial (ip): 50 mg/kg Dosis semanal (ip): 25 mg/kg

Combinación de cHOEGF con Erbitux en dia +12,5 mg/kg cada uno

Cisplatino subóptimo dado una vez por semana a 5 mg/kg

FIGURA 38A



$3x10^6$ sc, matrigel, ratones SCID, n=9; Inicio de tratamiento (d13) @ ~ 250 mm^3

Dosis Inicial (ip): 50 mg/kg; Dosis semanal (ip): 25 mg/kg,

Combinación de αHBEGF con Erbitux se dio a 12,5 mg/kg cada uno

Cisplatino administrado una vez por semana a 5 mg/kg

7748

SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO

NIT : 800176089-2

RECIBO OFICIAL DE CAJA : 10 - 24,711
FECHA : ABRIL 5 DE 2010

SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO
No. 10-048790- -00000-0000
Fecha: 2010-04-26 16:26:55 Dep. 2020 DIR.NUEVASCR
Tra. 11 PATENTEIYII Eve: 378 FASENACIONALI
Act. 411 PRESENTACION Folios: 2752

***** C O N S I G N A C I O N *****

DEPOSITANTE	TIPO PAGO	BANCO	CUENTA	No. PAGO	FECHA PGO	Vr. PAGO
CAVELIER ABOGADOS	CONSIGNACION	BANCO DE BOGOTA	062754387	175534531	31/03/2010	95,531,000.00

***** C O N C E P T O *****

CANT.	RENTISTICO	CONCEPTO		TOTAL CONCEPTO
1	50005-01-01 SOLICITUDES	1 TRAMITES DE SOL. DE PATENTE DE IN		554,000.00
		TOTAL :	$	554,000.00

SON: QUINIENTOS CINCUENTA Y CUATRO MIL PESOS

RESPONSABLE : _____

RECIBO DE CAJA APLICADO AL EXPEDIENTE No._____

COLO_16571-841-002-1

7749

SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO

NIT : 800176089-2

RECIBO OFICIAL DE CAJA : 10 - 20,579
FECHA : MARZO 15 DE 2010

SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO

No. 10-048790- -00000-0000

Fecha: 2010-04-26 16:26:55 Dep. 2020 DIR.NUEVASCR
Tra. 11 PATENTEIYII Eve: 378 FASENACIONALI
Act. 411 PRESENTACION Folios: 2752

***** C O N S I G N A C I O N *****

DEPOSITANTE	TIPO PAGO	BANCO	CUENTA	No. PAGO	FECHA PGO	Vr. PAGO
CAVELIER ABOGADOS	CONSIGNACION	BANCO DE BOGOTA	062754387	175526956	15/03/2010	56,869,000.00

***** C O N C E P T O *****

CANT.	RENTISTICO	CONCEPTO	TOTAL CONCEPTO
1	50005-01-09 OTROS SERVICIOS DE PROPIEDAD I	*** TASA ANUAL A#OS 9 a 12 CUATRENIO	437,000.00

****

TOTAL : $ 437,000.00

SON: CUATROCIENTOS TREINTA Y SIETE MIL PESOS

RESPONSABLE : _____

RECIBO DE CAJA APLICADO AL EXPEDIENTE No._____

COLO: 16571-841-002-1

2750

SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO

NIT : 800176089-2

RECIBO OFICIAL DE CAJA : 10 - 20,607
FECHA : MARZO 15 DE 2010

SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO

No. 10-048790- -00000-0000

Fecha: 2010-04-26 16:26:55 Dep. 2020 DIR.NUEVASCR
Tra. 11 PATENTEIYII Eve: 378 FASENACIONALI
Act. 411 PRESENTACION Folios: 2752

***** C O N S I G N A C I O N *****

DEPOSITANTE	TIPO PAGO	BANCO	CUENTA	No. PAGO	FECHA PGO	Vr. PAGO
CAVELIER ABOGADOS	CONSIGNACION	BANCO DE BOGOTA	062754387	175526956	15/03/2010	56,869,000.00

***** C O N C E P T O *****

CANT.	RENTISTICO	CONCEPTO	TOTAL CONCEPTO
1	50005-01-09 OTROS SERVICIOS DE PROPIEDAD I	*** TASA ANUAL C.RECARGO A#OS 17 a 30	1,207,000.00

****

TOTAL : $ 1,207,000.00

SON: UN MILLON DOSCIENTOS SIETE MIL PESOS

RESPONSABLE : _____

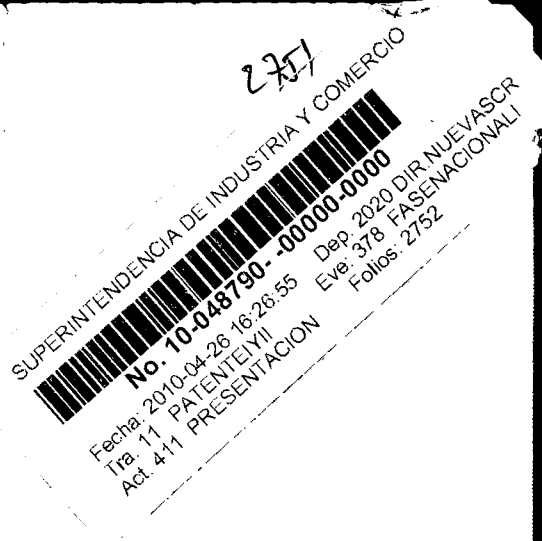
RECIBO DE CAJA APLICADO AL EXPEDIENTE No._____

COLO: 16571-841-002-1

SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO

NIT : 800176089-2

RECIBO OFICIAL DE CAJA : 10 - 27,472
FECHA : ABRIL 12 DE 2010



***** C O N S I G N A C I O N *****

DEPOSITANTE	TIPO PAGO	BANCO	CUENTA	No. PAGO	FECHA PGO	Vr. PAGO
CAVELIER ABOGADOS	CONSIGNACION	BANCO DE BOGOTA	062754387	175534542	12/04/2010	49,791,000.00

***** C O N C E P T O *****

CANT.	RENTISTICO	CONCEPTO	TOTAL CONCEPTO
1	50005-01-01 SOLICITUDES	*** REIVINDICACION UNITARIA ADICIONAL	26,000.00
		TOTAL : $	26,000.00

SON: VEINTISEIS MIL PESOS

RESPONSABLE : _____

RECIBO DE CAJA APLICADO AL EXPEDIENTE No._____

Colo: 165571 - 841 - 0021

Industria y Comercio
SUPERINTENDENCIA

SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO

No. 10-048790- -00000-0000

Fecha: 2010-04-26 16:26:55 Dep: 2020 DIR.NUEVASCR
Tra: 11 PATENTEIYII Eve: 378 FASENACIONALI
Act: 411 PRESENTACION Folios: 2752

PATENTE DE INVENCIÓN ☐ **MODELO DE UTILIDAD** ☐ **Art 33 Decisión 486/00**

- ☐ Indicación que se solicita una patente.
- ☐ Datos de identificación del solicitante o de la persona que presenta la solicitud
- ☐ Descripción de la invención
- ☐ Dibujos de ser estos pertinentes
- ☐ Comprobante de pago de las tasas establecidas (De ser el caso formato de descuento)

Completa ☐ Incompleta ☐

PATENTE DE INVENCIÓN PCT ☑ **MODELO DE UTILIDAD PCT** ☐ **Art.33 Decisión 486/00, Circular Única**

- ☑ Indicación que se solicita una PCT
- ☑ Copia de la solicitud en español, tal como fue presentada inicialmente (capítulo descriptivo, reivindicatorio, resumen)
- ☑ Dibujos de ser estos pertinentes
- ☑ Comprobante de pago de las tasas establecidas (de ser el caso formato de descuento)

Completa ☑ Incompleta ☐

DISEÑO INDUSTRIAL ☐ **(Art. 119 Decisión 486/00)**

- ☐ Indicación que se solicita Diseño industrial
- ☐ Datos de identificación del solicitante o de la persona que presenta la solicitud
- ☐ Representación gráfica y fotográfica del Diseño industrial o muestra del material que incorpora el diseño
- ☐ Comprobante de pago de las tasas establecidas

Completa ☐ Incompleta ☐

ESQUEMA DE TRAZADO ☐ **(Art. 92 Decisión 486/00)**

- ☐ Indicación que se solicita un esquema de trazado
- ☐ Datos de identificación del solicitante o de la persona que presenta la solicitud
- ☐ Representación gráfica de un esquema de trazado
- ☐ Comprobante de pago de las tasas establecidas

Completa ☐ Incompleta ☐

Industria y Comercio
SUPERINTENDENCIA

Bogotá D.C.,
2020

Doctor(a)
SUAREZ DE PAEZ LUZ CLEMENCIA
Apoderado(a) y/o Representante de
AMGEN INC.

REFERENCIA	Radicación No.	10 048790
	Solicitud internacional	PCT/EP2008/008233
	Fecha inicio fase nacional	26/04/2010
	Trámite	11
	Evento	378
	Actuación	430
	Oficio No.	0 0 5 6 0 6

Como resultado del examen de forma, realizado con fundamento en el artículo 38 de la Decisión 486 de la Comisión de la Comunidad Andina, artículo 27 del Tratado de Cooperación en Materia de Patentes (PCT), regla 51 bis del Reglamento y Circular Única de la Superintendencia de Industria y Comercio, se le comunica que:

1. La solicitud no contiene la copia del documento en que consta la cesión del derecho a la patente del inventor al solicitante o a su causante, conforme a lo establecido por el artículo 26 literal k) de la Decisión 486 de la Comisión de la Comunidad Andina. Cuando se trate de documentos otorgados en el extranjero, estos deberán legalizarse de conformidad con lo dispuesto por los artículos 259 y 260 del Código de Procedimiento Civil. Cuando se trate de las declaraciones a que hace referencia la Regla 4.17 ii) del Tratado de Cooperación en Materia de Patentes PCT., el alcance de las tales declaraciones se determinará según indiquen claramente una cesión de derechos del inventor al solicitante o su causante, de conformidad con lo dispuesto en el numeral 5.2.15 del Capítulo Quinto, Título X de la Circular Única de Superintendencia de Industria y Comercio.

En cumplimiento de lo dispuesto por el artículo 39 de la Decisión 486, se le requiere para que dentro del término de dos meses siguientes a la fecha de notificación del presente oficio, complete los requisitos anteriormente enunciados. En caso de no dar cumplimiento al presente requerimiento, la solicitud se considerará abandonada y perderá su prelación.

Notifíquese el presente oficio conforme a lo dispuesto en el numeral 5.2, literal e), del capítulo quinto del título primero de la Circular Unica No.10 de 2001.

ALIX CARMENZA CESPEDES DE VERGEL
Directora de Nuevas Creaciones (c)

El anterior requerimiento fue notificado por fijación en lista de fecha 30 ABR. 2010.
adpa11