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Señores

SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO
DIVISION DE NUEVAS CREACIONES

E.

S.

adición : 03097535 0000001
Fecha (ARB): 2003-11-26 17:39:04
vacita : 011 PCT-PATENT 379 FASE NACI 329 COMPLEN
Dependencia: ER20 DIVISION DE NUEVAS CREACIONES

Re: Expediente No. 03.097.535.

Solicitud de Patente de Invención: "VACUNAS DE
ACIDO NUCLEICO PARA PREVENCION DE LA
INFECCION DE FLAVIVIRUS"

Solicitante: THE GOVERNMENT OF THE UNITED
STATES OF AMERICA AS REPRESENTED BY THE
SECRETARY OF THE DEPARTMENT OF HEALTH
AND HUMAN SERVICES, CENTERS FOR DISEASE
CONTROL AND PREVENTION

MEMORIAL DE ALCANCE

ALVARO CORREA ORDOÑEZ, mayor de edad y vecino de Bogotá,
identificado tal como aparece al pie de mi firma, en mi carácter de apoderado de la
sociedad solicitante, manifiesto lo siguiente:

1. Adjunto copia del reporte de examen preliminar internacional junto con la
su traducción al español.
2. De igual manera, presento una copia del listado de secuencias, puesto que
según me informó el cliente, el listado originalmente presentado tenía unos pequeños

RAISBECK, LARA, RODRÍGUEZ & RUEDA
MIEMBROS DE LA FIRMA
BAKER & M^oKENZIE

- 2 -

errores de digitación. En consecuencia, solicito de manera respetuosa, se tenga en cuenta para el trámite de la solicitud, el listado de secuencias que ahora adjunto.

Atentamente,



ALVARO CORREA ORDÓÑEZ
C.C. No. 79.143.366 de Usaquén
T.P. 20.281

Adjunto: Reporte de Examen Preliminar Internacional y traducción al español
Listado de secuencias.

3
427

TRADUCCIÓN OFICIAL No. 473/03 de un documento escrito en inglés, el cual para su identificación se sella con el sello del Traductor. Esta es una Traducción Oficial efectuada el día 7 de noviembre de 2003 por la Sra. María Teresa Lara R., c.c. 41.568.055 de Bogotá, Traductora Oficial según Resolución No. 01016 del 2 de octubre de 1998, expedida por el Ministerio de Justicia.

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Notificación de Transmisión de Informe de Examen Preliminar Internacional expedido bajo el Tratado de Cooperación en Patentes.

TRATADO DE COOPERACIÓN EN PATENTES

De la
AUTORIDAD EXAMINADORA PRELIMINAR INTERNACIONAL

MARIA TERESA LARA R.
TRADUCTORA OFICIAL
RESOLUCION No. 01016
DE JUSTICIA

Para: MARY L. MILLER MEEDLE & ROSENBERG, P.C. 127 PEACHTREE STREET, N.E. SUITE 1200 ATLANTA, GA 30303-1811	PCT NOTIFICACIÓN DE TRANSMISIÓN DE INFORME DE EXAMEN PRELIMINAR INTERNACIONAL (PCT Regla 71.1)
Fecha de Envío (día/mes/año) 18 MAR 2003	

Referencia del expediente del solicitante o agente		NOTIFICACIÓN IMPORTANTE	
14114.0332P2			
No. de solicitud Internacional	Fecha de presentación Internacional (día/mes/año)	Fecha de prioridad (día/mes/año)	
	04 Abril 2002 (04.04.2002)	04 Abril 2001 (04.04.2001)	
Solicitante			
EL GOBIERNO DE LOS ESTADOS UNIDOS DE AMÉRICA			

1. Por la presente se notifica al solicitante que esta Autoridad Examinadora Preliminar Internacional transmite con la presente el Informe de examen preliminar Internacional y sus anexos, en caso de haberlos, establecidos en la solicitud Internacional.
2. Una copia del Informe y sus anexos, en caso de haberlos, está siendo transmitida a la Oficina Internacional para su comunicación a todas las Oficinas elegidas.

3. Cuando así lo requiera cualquiera de las Oficinas elegidas, la Oficina Internacional elaborará una traducción al Inglés del Informe (pero no de sus anexos) y transmitirá dicha traducción a esas Oficinas.

4. RECORDATORIO

El solicitante deberá ingresar la fase nacional antes de cada Oficina elegida realizando ciertos actos (registro de traducciones y pago de derechos nacionales) dentro de los 30 meses siguientes a la fecha de prioridad (o más tarde en algunas Oficinas)(Artículo 39(1)(ver también el recordatorio enviado por la Oficina Internacional con el Formulario PCT/IB/301).

Cuando sea necesario suministrar una traducción de la solicitud Internacional a una Oficina elegida, dicha traducción deberá incluir una traducción de cualquier anexo al Informe de examen preliminar Internacional. Es responsabilidad del solicitante elaborar y suministrar dicha traducción directamente a cada una de las respectivas Oficinas elegidas.

Para mayores detalles acerca de los plazos y requisitos aplicables de las Oficinas elegidas, véase el Volumen II de la Guía para Solicitantes del PCT.

MARIA TERESA LARA R.
TRADUCCION OFICIAL
RESOLUCION No. 01010
DE MINISTERIO

Nombre y dirección postal del IPEA/US Comisionado de Patentes y Marcas Box PCT Washington, D.C., 20231 Facsimil No. (703)305-3230	Funcionario autorizado James C. House1 (Firmado ilegible) Teléfono (703) 308-1111
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Referencia del expediente del solicitante o agente 14114.0332P2	PARA ACCIÓN ADICIONAL	Véase Notificación de Transmisión de Informe de Examen Preliminar Internacional (Formulario PCT/IPEA/416)
No. de solicitud internacional PCT/US02/10764	Fecha de presentación Internacional (día/mes/año) 04 Abril 2002 (04.04.2002)	Fecha de prioridad (día/mes/año) 04 Abril 2001 (04.04.2001)
Clasificación Internacional de Patentes (IPC) o clasificación nacional e IPC IPC(7): C12Q 1/70; G01N 33/53; C12P 21/06; C07K 16/00; C07H 21/04; A61K 39/12 y Cl. US: 435/5, 7.1, 69.1; 530/387.1; 424/218.1; 536/23.72		
Solicitante EL GOBIERNO DE LOS ESTADOS UNIDOS DE AMÉRICA		

429

1. Este Informe de examen preliminar Internacional ha sido elaborado por esta Autoridad Examinadora Preliminar Internacional y se transmite al solicitante de conformidad con el Artículo 36.

2. Este INFORME consta de un total de 3 hojas, Incluida esta cubierta.

[] Este Informe también va acompañado por ANEXOS, v.g., hojas con las descripción, reivindicaciones y/o dibujos que han sido modificados y constituyen la base de este Informe y/o hojas que contienen rectificaciones efectuadas ante esta Autoridad (véase Regla 70.16 y Sección 607 de las Instrucciones Administrativas bajo el PCT).

Estos anexos constan de un total de 0 hojas.

3. Este Informe contiene indicaciones relacionadas con los siguientes ítems:

- I [X] Base del Informe
- II [] Prioridad
- III [] No establecimiento de Informe con respecto a novedad, altura inventiva y aplicabilidad Industrial
- IV [] Falta de unidad del invento
- V [X] Declaración razonada conforme al Artículo 35(2) con respecto a novedad, altura inventiva y aplicabilidad Industrial; citas y explicaciones en respaldo de dicha declaración
- VI [] Ciertos documentos citados
- VII [] Ciertos defectos en la solicitud Internacional
- VIII [] Ciertas observaciones acerca de la solicitud Internacional

Fecha de presentación de la demanda 01 Octubre 2002 (01.10.2002)	Fecha de terminación de este Informe 06 Marzo 2003 (06.03.2003)
Nombre y dirección postal del IPEA/US Comisionado de Patentes y Marcas Box PCT Washington, D.C., 20231 Facsimil No. (703)305-3230	Funcionario autorizado James C. Housel (Firmado ilegible) Teléfono (703) 308-1111

MARIA TERESA LARA R.
TRADUCTORA OFICIAL
RESOLUCION No. 01616
DE MINISTERIO

430

**INFORME DE EXAMEN
PRELIMINAR INTERNACIONAL**

Solicitud internacional No.

PCT/US02/10764

I. Base del Informe

1. Con respecto a los elementos de la solicitud Internacional:*

☒ la solicitud internacional según se presentó originalmente.

☒ la descripción:

páginas 1-95 , según se presentaron originalmente
páginas NINGUNA , presentadas con la demanda
páginas NINGUNA , presentadas con la carta de _____.

☒ las reivindicaciones:

páginas 96-100 , según se presentaron originalmente
páginas NINGUNA , según fueron modificadas (junto con cualquier
declaración) conforme al Artículo 19
páginas NINGUNA , presentadas con la demanda
páginas NINGUNA , presentadas con la carta de _____.

☒ los dibujos:

páginas 1-8 , según se presentaron originalmente
páginas NINGUNA , presentadas con la demanda
páginas NINGUNA , presentadas con la carta de _____.

☒ la parte del listado de secuencias de la descripción:

páginas 1-63 , según se presentaron originalmente
páginas NINGUNA , presentadas con la demanda
páginas NINGUNA , presentadas con la carta de _____.

2. Con respecto al idioma, todos los elementos antes marcados estuvieron disponibles o fueron suministrados a esta Autoridad en el idioma en el cual se presentó la solicitud internacional, a no ser que se indique algo distinto bajo este ítem. Estos elementos estuvieron disponibles o fueron suministrados a esta Autoridad en el siguiente idioma _____, que es:

☐ el idioma de una traducción suministrada para efectos de una Investigación Internacional (bajo la Regla 23.1(b)).

☐ el idioma de publicación de la solicitud internacional (bajo la Regla 48.3(b)).

☐ el idioma de la traducción suministrada para efectos de un examen preliminar internacional (bajo las Reglas 55.2 y/o 55.3).

3. Con respecto a cualquier secuencia de nucleótidos y/o aminoácidos divulgada en la solicitud internacional, el examen preliminar internacional se realizó con base en el listado de secuencias:

☒ contenida en la solicitud internacional en forma impresa.

☐ presentada junto con la solicitud internacional en forma legible por computador.

☐ suministrada posteriormente a esta Autoridad en forma escrita.

☐ suministrada posteriormente a esta Autoridad en forma legible por computador.

TERESA LARA R.
TRADUCTORA OFICIAL
REGISTRADA EN EL
DEPARTAMENTO DE
COMERCIO EXTERIOR

7
431

- [] Se ha suministrado la declaración de que el listado de secuencias escrito suministrado posteriormente no excede de la divulgación en la solicitud internacional según fue presentada.
- [] Se ha suministrado la declaración de que la información registrada en forma legible por computador es idéntica al listado de secuencias escrito.

4. [] Las modificaciones han resultado en la cancelación de:

- [] la descripción, páginas NINGUNA
- [] las reivindicaciones, Nos. NINGUNA
- [] los dibujos, hojas NINGUNA

5. [] Este Informe se ha establecido como si (algunas de) las modificaciones no se hubiesen efectuado, dado que se ha considerado que exceden de la divulgación presentada, como se indica en la Casilla Suplementaria (Regla 70.2(c)).**

* Las hojas de reemplazo que hayan sido suministradas a la Oficina receptora en respuesta a una invitación bajo el Artículo 14 se denominan en este informe "originalmente presentadas" y no se adjuntan a este Informe, dado que no contienen modificaciones (Reglas 70.16 y 70.17).

** Cualquier hoja de reemplazo que contenga dichas modificaciones deberá mencionarse en el ítem 1 y anexarse a este Informe.

V. Declaración razonada conforme a la Regla 66.2(a)(II) con respecto a novedad, altura inventiva o aplicabilidad industrial; citas y explicaciones que respaldan dicha declaración

1. DECLARACIÓN

Novedad (N)	Reivindicaciones <u>1-43</u>	SI
	Reivindicaciones <u>NINGUNA</u>	NO
Altura Inventiva (IS)	Reivindicaciones <u>1-43</u>	SI
	Reivindicaciones <u>NINGUNA</u>	NO
Aplicabilidad Industrial (IA)	Reivindicaciones <u>1-43</u>	SI
	Reivindicaciones <u>NINGUNA</u>	NO

2. CITAS Y EXPLICACIONES

Las reivindicaciones 1-43 cumplen con los criterios señalados en el PCT Artículo 33(2)-(3), dado que el arte anterior no enseña ni sugiere objetivamente la codificación reivindicada de ácidos nucleicos que codifican una unidad transcripcional que codifica una secuencia de señales de una primera proteína estructural de flavivirus y una porción inmunogénica de una segunda proteína estructural de flavivirus diferente. El arte anterior tampoco enseña ni sugiere los diversos métodos de uso que emplean dicha unidad transcripcional y los inmunógenos codificados por ella. Aunque el arte anterior proporciona quimeras recombinantes del flavivirus, no describe ni sugiere las

8
432

quimeras estructurales reivindicadas del flavivirus. Adicionalmente, las enseñanzas del arte anterior no proporcionan proteínas recombinantes altamente inmunogénicas apropiadas para el uso en ensayos diagnósticos e inmunológicos.

----- NUEVAS CITAS -----

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La anterior es traducción fiel y completa del documento en referencia, de la cual se deja copia en este archivo para su confrontación.

MARIA TERESA LARA R.
TRADUCTORA OFICIAL
RESOLUCION No. 01016
DE MINISTERIO DE JUSTICIA



María Teresa Lara R.
c.c. 41.568.055 de Bogotá
Traductora Oficial según
Resolución No. 01016 del
2 de octubre de 1998, del
Ministerio de Justicia

433

PATENT COOPERATION TREATY

PREVIOUSLY DOCKETED
10/4/03

From the
INTERNATIONAL PRELIMINARY EXAMINING AUTHORITY

To:
MARY L. MILLER
NEEDLE & ROSENBERG, P.C.
127 PEACHTREE STREET, N.E.
SUITE 1200
ATLANTA, GA 30303-1811

RECEIVED
MAR 24 2003
NEEDLE & ROSENBERG

PCT
NOTIFICATION OF TRANSMITTAL OF
INTERNATIONAL PRELIMINARY
EXAMINATION REPORT
(PCT Rule 71.1)

Date of Mailing
(day/month/year) 18 MAR 2003

Applicant's or agent's file reference

14114:0332P2

IMPORTANT NOTIFICATION

International application No.

International filing date (day/month/year)

Priority date (day/month/year)

PCT/US02/10764

04 April 2002 (04.04.2002)

04 April 2001 (04.04.2001)

Applicant

THE GOVERNMENT OF THE UNITED STATES OF AMERICA

1. The applicant is hereby notified that this International Preliminary Examining Authority transmits herewith the international preliminary examination report and its annexes, if any, established on the international application.
2. A copy of the report and its annexes, if any, is being transmitted to the International Bureau for communication to all the elected Offices.
3. Where required by any of the elected Offices, the International Bureau will prepare an English translation of the report (but not of any annexes) and will transmit such translation to those Offices.
4. REMINDER

The applicant must enter the national phase before each elected Office by performing certain acts (filing translations and paying national fees) within 30 months from the priority date (or later in some Offices)(Article 39(1))(see also the reminder sent by the International Bureau with Form PCT/IB/301).

Where a translation of the international application must be furnished to an elected Office, that translation must contain a translation of any annexes to the international preliminary examination report. It is the applicant's responsibility to prepare and furnish such translation directly to each elected Office concerned.

For further details on the applicable time limits and requirements of the elected Offices, see Volume II of the PCT Applicant's Guide.

Name and mailing address of the IPEA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. (703)305-3230

Form PCT/IPEA/416 (July 1992)

Authorized officer

James C. Howell

Telephone No. (703) 308-1111

EDS / WBD / ACS

By	DOCKETED	03/25/03
Date		
Reviewed		
Name/Date		

MANAGING ATTORNEY

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434

PATENT COOPERATION TREATY

PCT

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

(PCT Article 36 and Rule 70)

Applicant's or agent's file reference 14114.0332P2		FOR FURTHER ACTION See Notification of Transmittal of International Preliminary Examination Report (Form PCT/IEPA/416)
International application No. PCT/US02/10764	International filing date (day/month/year) 04 April 2002 (04.04.2002)	Priority date (day/month/year) 04 April 2001 (04.04.2001)
International Patent Classification (IPC) or national classification and IPC IPC(7): C12Q 1/70; G01N 33/53; C12P 21/06; C07K 16/00; C07H 21/04; A61K 39/12 and US Cl.: 435/5, 7.1, 69.1; 530/387.1; 424/218.1; 536/23.72		
Applicant THE GOVERNMENT OF THE UNITED STATES OF AMERICA		
1. This international preliminary examination report has been prepared by this International Preliminary Examining Authority and is transmitted to the applicant according to Article 36. 2. This REPORT consists of a total of <u>2</u> sheets, including this cover sheet. ☐ This report is also accompanied by ANNEXES, i.e., sheets of the description, claims and/or drawings which have been amended and are the basis for this report and/or sheets containing rectifications made before this Authority (see Rule 70.16 and Section 607 of the Administrative Instructions under the PCT). These annexes consist of a total of <u>0</u> sheets.		
3. This report contains indications relating to the following items: I ☒ Basis of the report II ☐ Priority III ☐ Non-establishment of report with regard to novelty, inventive step and industrial applicability IV ☐ Lack of unity of invention V ☒ Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement VI ☐ Certain documents cited VII ☐ Certain defects in the international application VIII ☐ Certain observations on the international application		
Date of submission of the demand 01 October 2002 (01.10.2002)		Date of completion of this report 06 March 2003 (06.03.2003)
Name and mailing address of the IEPA/US Comptroller of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703)305-3230		Authorized officer James C. Howell Telephone No. (703) 308-1111

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

International application No.

PCT/US02/10764

I. Basis of the report

1. With regard to the elements of the international application:*

- ☒ the international application as originally filed.
- ☒ the description:
 pages 1-93 as originally filed
 pages NONE, filed with the demand
 pages NONE, filed with the letter of _____
- ☒ the claims:
 pages 96-100 as originally filed
 pages NONE, as amended (together with any statement) under Article 19
 pages NONE, filed with the demand
 pages NONE, filed with the letter of _____
- ☒ the drawings:
 pages 1-8 as originally filed
 pages NONE, filed with the demand
 pages NONE, filed with the letter of _____
- ☒ the sequence listing part of the description:
 pages 1-63 as originally filed
 pages NONE, filed with the demand
 pages NONE, filed with the letter of _____

2. With regard to the language, all the elements marked above were available or furnished to this Authority in the language in which the international application was filed, unless otherwise indicated under this item.

These elements were available or furnished to this Authority in the following language _____ which is:

- ☐ the language of a translation furnished for the purposes of international search (under Rule 23.1(b)).
- ☐ the language of publication of the international application (under Rule 48.3(b)).
- ☐ the language of the translation furnished for the purposes of international preliminary examination (under Rules 55.2 and/or 55.3).

3. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international preliminary examination was carried out on the basis of the sequence listing:

- ☒ contained in the international application in printed form.
- ☐ filed together with the international application in computer readable form.
- ☐ furnished subsequently to this Authority in written form.
- ☐ furnished subsequently to this Authority in computer readable form.
- ☐ The statement that the subsequently furnished written sequence listing does not go beyond the disclosure in the international application as filed has been furnished.
- ☐ The statement that the information recorded in computer readable form is identical to the written sequence listing has been furnished.

4. ☐ The amendments have resulted in the cancellation of:

- ☐ the description, pages NONE
- ☐ the claims, Nos. NONE
- ☐ the drawings, sheets/fig NONE

5. ☐ This report has been established as if (some of) the amendments had not been made, since they have been considered to go beyond the disclosure as filed, as indicated in the Supplemental Box (Rule 70.2(c)).**

* Replacement sheets which have been furnished to the receiving Office in response to an invitation under Article 14 are referred to in this report as "originally filed" and are not annexed to this report since they do not contain amendments (Rules 70.16 and 70.17).

** Any replacement sheet containing such amendments must be referred to under item 1 and annexed to this report.

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

International application No.
PCT/US02/10764**V. Reasoned statement under Rule 66.2(a)(II) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement****1. STATEMENT**

Novelty (N)	Claims <u>1-43</u>	YES
	Claims <u>NONE</u>	NO
Inventive Step (IS)	Claims <u>1-43</u>	YES
	Claims <u>NONE</u>	NO
Industrial Applicability (IA)	Claims <u>1-43</u>	YES
	Claims <u>NONE</u>	NO

2. CITATIONS AND EXPLANATIONS

Claims 1-43 meet the criteria set out in PCT Article 33(2)-(3), because the prior art does not teach or fairly suggest the claimed nucleic acids encoding a transcriptional unit encoding a signal sequence from a first flavivirus structural protein and an immunogenic portion from a second, different flavivirus structural protein. The prior art also fails to teach or suggest the various methods of use employing said transcriptional unit and the immunogens encoded thereby. While the prior art provides recombinant flavivirus chimeras, it does not describe or suggest the claimed flavivirus structural chimeras. Moreover, the teachings of the prior art fail to provide highly immunogenic recombinant proteins suitable for use in diagnostic and immunological assays.

NEW CITATIONS

PATENT COOPERATION TREATY

CDC/TMHT
6395-64909
PREVIOUSLY DOCKETED 437
10/4/03From the
INTERNATIONAL PRELIMINARY EXAMINING AUTHORITYTo:
MARY L. MILLER
NEEDLE & ROSENBERG, P.C.
127 PEACHTREE STREET, N.E.
SUITE 1200
ATLANTA, GA 30303-1811

RECEIVED

MAR 24 2003

NEEDLE & ROSENBERG

PCT

NOTIFICATION OF TRANSMITTAL OF
INTERNATIONAL PRELIMINARY
EXAMINATION REPORT

(PCT Rule 71.1)

Date of Mailing
(day/month/year)

18 MAR 2003

Applicant's or agent's file reference

14114:0332P2

IMPORTANT NOTIFICATION

International application No.

PCT/US02/10764

International filing date (day/month/year)

04 April 2002 (04.04.2002)

Priority date (day/month/year)

04 April 2001 (04.04.2001)

Applicant

THE GOVERNMENT OF THE UNITED STATES OF AMERICA

1. The applicant is hereby notified that this International Preliminary Examining Authority transmits herewith the international preliminary examination report and its annexes, if any, established on the international application.
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4. REMINDER

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For further details on the applicable time limits and requirements of the elected Offices, see Volume II of the PCT Applicant's Guide.

Name and mailing address of the IPEA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. (703)305-3230

Form PCT/IPEA/416 (July 1992)

Authorized officer

James C. Howell

Telephone No. (703) 308-1111

EDS / WBD / ACS

By	WBD	DOCKETED	03/25/03
		Date	
Reviewed		Name/Date	

instruct - other myself

PCT

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

(PCT Article 36 and Rule 70)

Applicant's or agent's file reference 14114.0332P2	FOR FURTHER ACTION See Notification of Transmittal of International Preliminary Examination Report (Form PCT/IPEA/416)	
International application No. PCT/US02/10764	International filing date (day/month/year) 04 April 2002 (04.04.2002)	Priority date (day/month/year) 04 April 2001 (04.04.2001)
International Patent Classification (IPC) or national classification and IPC IPC(7): C12Q 1/70; G01N 33/53; C12P 21/06; C07K 16/00; C07H 21/04; A61K 39/12 and US Cl.: 435/5, 7.1, 69.1; 530/387.1; 424/218.1; 536/23.72		
Applicant THE GOVERNMENT OF THE UNITED STATES OF AMERICA		
1. This international preliminary examination report has been prepared by this International Preliminary Examining Authority and is transmitted to the applicant according to Article 36. 2. This REPORT consists of a total of 2 sheets, including this cover sheet. ☐ This report is also accompanied by ANNEXES, i.e., sheets of the description, claims and/or drawings which have been amended and are the basis for this report and/or sheets containing rectifications made before this Authority (see Rule 70.16 and Section 607 of the Administrative Instructions under the PCT). These annexes consist of a total of 4 sheets.		
3. This report contains indications relating to the following items: I ☒ Basis of the report II ☐ Priority III ☐ Non-establishment of report with regard to novelty, inventive step and industrial applicability IV ☐ Lack of unity of invention V ☒ Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement VI ☐ Certain documents cited VII ☐ Certain defects in the international application VIII ☐ Certain observations on the international application		
Date of submission of the demand 01 October 2002 (01.10.2002)	Date of completion of this report 06 March 2003 (06.03.2003)	
Name and mailing address of the IPEA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703)305-3230	Authorized officer James C. Flouzel Telephone No. (703) 308-1111	

Form PCT/IPEA/409 (cover sheet) (July 1998)

PRELIMINARY EXAMINATION REPORT

International application No.

PCT/US02/10764

1. Basis of the report

1. With regard to the elements of the international application:*

- ☒ the international application as originally filed.
- ☒ the description:
 pages 1-93 as originally filed
 pages NONE filed with the demand
 pages NONE filed with the letter of _____.
- ☒ the claims:
 pages 96-100 as originally filed
 pages NONE as amended (together with any statement) under Article 19
 pages NONE filed with the demand
 pages NONE filed with the letter of _____.
- ☒ the drawings:
 pages 1-8 as originally filed
 pages NONE filed with the demand
 pages NONE filed with the letter of _____.
- ☒ the sequence listing part of the description:
 pages 1-63 as originally filed
 pages NONE filed with the demand
 pages NONE filed with the letter of _____.

2. With regard to the language, all the elements marked above were available or furnished to this Authority in the language in which the international application was filed, unless otherwise indicated under this item.

These elements were available or furnished to this Authority in the following language _____ which is:

- ☐ the language of a translation furnished for the purposes of international search (under Rule 23.1(b)).
- ☐ the language of publication of the international application (under Rule 48.3(b)).
- ☐ the language of the translation furnished for the purposes of international preliminary examination (under Rules 55.2 and/or 55.3).

3. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international preliminary examination was carried out on the basis of the sequence listing:

- ☒ contained in the international application in printed form.
- ☐ filed together with the international application in computer readable form.
- ☐ furnished subsequently to this Authority in written form.
- ☐ furnished subsequently to this Authority in computer readable form.
- ☐ The statement that the subsequently furnished written sequence listing does not go beyond the disclosure in the international application as filed has been furnished.
- ☐ The statement that the information recorded in computer readable form is identical to the written sequence listing has been furnished.

4. ☐ The amendments have resulted in the cancellation of:

- ☐ the description, pages NONE.
- ☐ the claims, Nos. NONE.
- ☐ the drawings, sheets/fig NONE.

5. ☐ This report has been established as if (some of) the amendments had not been made, since they have been considered to go beyond the disclosure as filed, as indicated in the Supplemental Box (Rule 70.2(c)).**

* Replacement sheets which have been furnished to the receiving Office in response to an invitation under Article 14 are referred to in this report as "originally filed" and are not annexed to this report since they do not contain amendments (Rules 70.16 and 70.17).

** Any replacement sheet containing such amendments must be referred to under item 1 and annexed to this report.

V. Reasoned statement under Rule 66.2(a)(II) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement

1. STATEMENT

Novelty (N)	Claims <u>1-43</u>	YES
	Claims <u>NONE</u>	NO
Inventive Step (IS)	Claims <u>1-43</u>	YES
	Claims <u>NONE</u>	NO
Industrial Applicability (IA)	Claims <u>1-43</u>	YES
	Claims <u>NONE</u>	NO

2. CITATIONS AND EXPLANATIONS

Claims 1-43 meet the criteria set out in PCT Article 33(2)-(3), because the prior art does not teach or fairly suggest the claimed nucleic acids encoding a transcriptional unit encoding a signal sequence from a first flavivirus structural protein and an immunogenic portion from a second, different flavivirus structural protein. The prior art also fails to teach or suggest the various methods of use employing said transcriptional unit and the immunogens encoded thereby. While the prior art provides recombinant flavivirus chimeras, it does not describe or suggest the claimed flavivirus structural chimeras. Moreover, the teachings of the prior art fail to provide highly immunogenic recombinant proteins suitable for use in diagnostic and immunological assays.

NEW CITATIONS

SEQUENCE LISTING

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<110> The Government of the United States of America, as
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      Services, c/o Centers for Disease Control and Prevention
      Chang, Gwong-Jen J.

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 cacctagatc cttttaaatt aaaaatgaag ttttaaatca atctaaagta tatatgagta 6489
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atttcgttca tccatagttg cctgactccc cgtcgtgtag ataactacga tacgggaggg 6609
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aagcatttat cagggttatt gtctcatgag cggatacata tttgaatgta tttagaaaaa 7449
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<210> 11
<211> 697
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of artificial sequence; note = synthetic construct

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<400> 11

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Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu Gly Ser Ile Met
1           5           10          15

```

```

Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met Lys
          20          25          30

```

```

Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile Asn Asn Thr Asp
          35          40          45

```

```

Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly Glu Asn Arg Cys
          50          55          60

```

Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu Asp Thr Ile Thr
 65 70 75 80

Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro Glu Asp Val Asp
 85 90 95

Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr Gly Arg Cys Thr
 100 105 110

Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val Ser Val Gln Thr
 115 120 125

His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala Trp Leu Asp Ser
 130 135 140

Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn Trp Ile Ile Arg
 145 150 155 160

Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly Trp Met Leu Gly
 165 170 175

Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu Leu Leu Leu Val
 180 185 190

Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly Asn Arg Asp Phe
 195 200 205

Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly
 210 215 220

Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val
 225 230 235 240

Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu Val Arg Ser Tyr
 245 250 255

Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro
 260 265 270

Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val
 275 280 285

Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu
 290 295 300

Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Ser
 305 310 315 320

Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val
 325 330 335

Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn His Gly Asn Tyr
 340 345 350

Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro
 355 360 365

Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr Gly Glu Val Thr
 370 375 380

Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu Ala Phe Tyr Val
 385 390 395 400

Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg Glu Trp Phe His
 405 410 415

Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr Ala Trp Arg Asn
 420 425 430

Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser
 435 440 445

Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His Gln Ala Leu Ala
 450 455 460

Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys Leu Thr Ser Gly
 465 470 475 480

His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr
 485 490 495

Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala
 500 505 510

Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser Tyr Ser Gly Ser
 515 520 525

Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala Ser Leu Asn Asp
 530 535 540

Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr
545 550 555 560

Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly
565 570 575

Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln Ile Asn His His
580 585 590

Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu
595 600 605

Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe
610 615 620

Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln
625 630 635 640

Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile
645 650 655

Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala
660 665 670

Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr Gly Gly Val Leu
675 680 685

Val Phe Leu Ala Thr Asn Val His Ala
690 695

<210> 12
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> misc_feature
<222> (1)..(46)
<223> WN 466

<400> 12
cttggtaccc gtctcggcgc cgtgaccctc tcgaacttcc agggca 46

<210> 13
<211> 43

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <220>
 <221> misc_feature
 <222> (1)..(43)
 <223> CWN2444

 <400> 13
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 <210> 14
 <211> 24
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <220>
 <221> MISC_FEATURE
 <223> JE Signal

 <400> 14

 Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
 1 5 10 15

 Val Val Ile Ala Cys Ala Gly Ala
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 <210> 15
 <211> 5308
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <220>
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 <222> (1)..(5308)
 <223> pCBWN

 <220>
 <221> CDS
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ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgt gagtagtgcg	120
cgagcaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc	180
ttagggtag gcgttttgcg ctgcttcgcy atgtacgggc cagatatacg cgttgacatt	240
gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata	300
tggagttccg cgttacataa cttacggtaa atggcccgc tggctgaccg cccaacgacc	360
cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc	420
attgacgtca atgggtggag tatttacggg aaactgcccc cttggcagta catcaagtgt	480
atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt	540
atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca	600
tcgctattac catggtgatg cggtttttgg cagtacatca atgggcgtgg atagcggttt	660
gactcacggg gatttccaag tctccacccc attgacgtca atgggagttt gttttggcac	720
caaatcaac gggactttcc aaaatgtcgt aacaactccg ccccatgac gcaaatgggc	780
gtaggcgtg tacgggtggga ggtctatata agcagagctc tctggctaac tagagaaccc	840
actgcttact ggcttatcga aattaatacg actcactata gggagaccca agcttggtac	900
cgccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg	949
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala	
1 5 10	
agc ttg gca gtt gtc ata gct tgt gca ggc gcc gtg acc ctc tcg aac	997
Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Val Thr Leu Ser Asn	
15 20 25	
ttc cag ggc aag gtg atg atg acg gta aat gct act gac gtc aca gat	1045
Phe Gln Gly Lys Val Met Met Thr Val Asn Ala Thr Asp Val Thr Asp	
30 35 40 45	
gtc atc acg att cca aca gct gct gga aag aac cta tgc att gtc aga	1093
Val Ile Thr Ile Pro Thr Ala Ala Gly Lys Asn Leu Cys Ile Val Arg	
50 55 60	
gca atg gat gtg gga tac atg tgc gat gat act atc act tat gaa tgc	1141
Ala Met Asp Val Gly Tyr Met Cys Asp Asp Thr Ile Thr Tyr Glu Cys	
65 70 75	
cca gtg ctg tcg gct ggt aat gat cca gaa gac atc gac tgt tgg tgc	1189
Pro Val Leu Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys	
80 85 90	
aca aag tca gca gtc tac gtc agg tat gga aga tgc acc aag aca cgc	1237
Thr Lys Ser Ala Val Tyr Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg	
95 100 105	
cac tca aga cgc agt cgg agg tca ctg aca gtg cag aca cac gga gaa	1285
His Ser Arg Arg Ser Arg Arg Ser Leu Thr Val Gln Thr His Gly Glu	
110 115 120 125	

agc act cta gcg aac aag aag ggg gct tgg atg gac agc acc aag gcc Ser Thr Leu Ala Asn Lys Lys Gly Ala Trp Met Asp Ser Thr Lys Ala 130 135 140	1333
aca agg tat ttg gta aaa aca gaa tca tgg atc ttg agg aac cct gga Thr Arg Tyr Leu Val Lys Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly 145 150 155	1381
tat gcc ctg gtg gca gcc gtc att ggt tgg atg ctt ggg agc aac acc Tyr Ala Leu Val Ala Ala Val Ile Gly Trp Met Leu Gly Ser Asn Thr 160 165 170	1429
atg cag aga gtt gtg ttt gtc gtg cta ttg ctt ttg gtg gcc cca gct Met Gln Arg Val Val Phe Val Val Leu Leu Leu Leu Val Ala Pro Ala 175 180 185	1477
tac agc ttc aac tgc ctt gga atg agc aac aga gac ttc ttg gaa gga Tyr Ser Phe Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly 190 195 200 205	1525
gtg tct gga gca aca tgg gtg gat ttg gtt ctc gaa ggc gac agc tgc Val Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys 210 215 220	1573
gtg act atc atg tct aag gac aag cct acc atc gat gtg aag atg atg Val Thr Ile Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met 225 230 235	1621
aat atg gag gcg gcc aac ctg gca gag gtc cgc agt tat tgc tat ttg Asn Met Glu Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu 240 245 250	1669
gct acc gtc agc gat ctc tcc acc aaa gct gcg tgc ccg acc atg gga Ala Thr Val Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly 255 260 265	1717
gaa gct cac aat gac aaa cgt gct gac cca gct ttt gtg tgc aga caa Glu Ala His Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln 270 275 280 285	1765
gga gtg gtg gac agg ggc tgg ggc aac ggc tgc gga cta ttt ggc aaa Gly Val Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys 290 295 300	1813
gga agc att gac aca tgc gcc aaa ttt gcc tgc tct acc aag gca ata Gly Ser Ile Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile 305 310 315	1861
gga aga acc atc ttg aaa gag aat atc aag tac gaa gtg gcc att ttt Gly Arg Thr Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe 320 325 330	1909
gtc cat gga cca act act gtg gag tgc cac gga aac tac tcc aca cag Val His Gly Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln 335 340 345	1957
gtt gga gcc act cag gca ggg aga ttc agc atc act cct gcg gcg cct Val Gly Ala Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro 350 355 360 365	2005

tca tac aca cta aag ctt gga gaa tat gga gag gtg aca gtg gac tgt Ser Tyr Thr Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys 370 375 380	2053
gaa cca cgg tca ggg att gac acc aat gca tac tac gtg atg act gtt Glu Pro Arg Ser Gly Ile Asp Thr Asn Ala Tyr Tyr Val Met Thr Val 385 390 395	2101
gga aca aag acg ttc ttg gtc cat cgt gag tgg ttc atg gac ctc aac Gly Thr Lys Thr Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn 400 405 410	2149
ctc cct tgg agc agt gct gga agt act gtg tgg agg aac aga gag acg Leu Pro Trp Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr 415 420 425	2197
tta atg gag ttt gag gaa cca cac gcc acg aag cag tct gtg ata gca Leu Met Glu Phe Glu Glu Pro His Ala Thr Lys Gln Ser Val Ile Ala 430 435 440 445	2245
ttg ggc tca caa gag gga gct ctg cat caa gct ttg gct gga gcc att Leu Gly Ser Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile 450 455 460	2293
cct gtg gaa ttt tca agc aac act gtc aag ttg acg tcg ggt cat ttg Pro Val Glu Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu 465 470 475	2341
aag tgt aga gtg aag atg gaa aaa ttg cag ttg aag gga aca acc tat Lys Cys Arg Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr 480 485 490	2389
ggc gtc tgt tca aag gct ttc aag ttt ctt ggg act ccc gcg gac aca Gly Val Cys Ser Lys Ala Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr 495 500 505	2437
ggt cac ggc act gtg gtg ttg gaa ttg cag tac act ggc acg gat gga Gly His Gly Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly 510 515 520 525	2485
cct tgc aaa gtt cct atc tcg tca gtg gct tca ttg aac gac cta acg Pro Cys Lys Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr 530 535 540	2533
cca gtg ggc aga ttg gtc act gtc aac cct ttt gtt tca gtg gcc acg Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr 545 550 555	2581
gcc aac gct aag gtc ctg att gaa ttg gaa cca ccc ttt gga gac tca Ala Asn Ala Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser 560 565 570	2629
tac ata gtg gtg ggc aga gga gaa caa cag atc aat cac cat tgg cac Tyr Ile Val Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His 575 580 585	2677
aag tct gga agc agc att ggc aaa gcc ttt aca acc acc ctc aaa gga Lys Ser Gly Ser Ser Ile Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly 590 595 600 605	2725

gcg cag aga cta gcc gct cta gga gac aca gct tgg gac ttt gga tca Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser 610 615 620	2773
gtt gga ggg gtg ttc acc tca gtt ggg aag gct gtc cat caa gtg ttc Val Gly Gly Val Phe Thr Ser Val Gly Lys Ala Val His Gln Val Phe 625 630 635	2821
gga gga gca ttc cgc tca ctg ttc gga ggc atg tcc tgg ata acg caa Gly Gly Ala Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln 640 645 650	2869
gga ttg ctg ggg gct ctc ctg ttg tgg atg ggc atc aat gct cgt gat Gly Leu Leu Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp 655 660 665	2917
agg tcc ata gct ctc acg ttt ctc gca gtt gga gga gtt ctg ctc ttc Arg Ser Ile Ala Leu Thr Phe Leu Ala Val Gly Gly Val Leu Leu Phe 670 675 680 685	2965
ctc tcc gtg aac gtg cac gcc tgaaggcggc cgctcgagca tgcattctaga Leu Ser Val Asn Val His Ala 690	3016
gggccctatt ctatagtgtc acctaaatgc tagagctcgc tgatcagcct cgactgtgcc	3076
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aggattagca gagcgaggta tgtaggcggg gctacagagt tcttgaagtg gtggcctaac	3976
tacggctaca ctagaagaac agtatttggg atctgcgctc tgctgaagcc agttaccttc	4036
ggaaaaagag ttggtagctc ttgatccggc aaacaaacca ccgctggtag cggtaggtttt	4096

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tttgtttgca agcagcagat tacgcgcaga aaaaaaggat ctcaagaaga tcctttgatc 4156
ttttctacgg ggtctgacgc tcagtggaaac gaaaactcac gttaagggat tttgggcatg 4216
agattatcaa aaaggatcctt cacctagatc cttttaaat aaaaatgaag ttttaaatca 4276
atctaaagta tatatgagta aacttgggtct gacagttacc aatgcttaat cagtgaggca 4336
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tcattctgag aatagtgtat gcggcgaccg agttgctctt gcccggcgtc aatacgggat 4936
aataccgcgc cacatagcag aactttaaaa gtgctcatca ttggaaaacg ttcttcgggg 4996
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ccacctgacg tc 5308

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<210> 16

<211> 692

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 16

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Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1           5           10           15

```

```

Val Val Ile Ala Cys Ala Gly Ala Val Thr Leu Ser Asn Phe Gln Gly
          20          25          30

```

Lys Val Met Met Thr Val Asn Ala Thr Asp Val Thr Asp Val Ile Thr
 35 40 45
 Ile Pro Thr Ala Ala Gly Lys Asn Leu Cys Ile Val Arg Ala Met Asp
 50 55 60
 Val Gly Tyr Met Cys Asp Asp Thr Ile Thr Tyr Glu Cys Pro Val Leu
 65 70 75 80
 Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Thr Lys Ser
 85 90 95
 Ala Val Tyr Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg His Ser Arg
 100 105 110
 Arg Ser Arg Arg Ser Leu Thr Val Gln Thr His Gly Glu Ser Thr Leu
 115 120 125
 Ala Asn Lys Lys Gly Ala Trp Met Asp Ser Thr Lys Ala Thr Arg Tyr
 130 135 140
 Leu Val Lys Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly Tyr Ala Leu
 145 150 155 160
 Val Ala Ala Val Ile Gly Trp Met Leu Gly Ser Asn Thr Met Gln Arg
 165 170 175
 Val Val Phe Val Val Leu Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe
 180 185 190
 Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly Val Ser Gly
 195 200 205
 Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys Val Thr Ile
 210 215 220
 Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met Asn Met Glu
 225 230 235 240
 Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu Ala Thr Val
 245 250 255
 Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly Glu Ala His
 260 265 270

Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln Gly Val Val
275 280 285

Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile
290 295 300

Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile Gly Arg Thr
305 310 315 320

Ile Leu Lys Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His Gly
325 330 335

Pro Thr Thr Val Glu Ser His Gly Asn Tyr Ser Thr Gln Val Gly Ala
340 345 350

Thr Gln Ala Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro Ser Tyr Thr
355 360 365

Leu Lys Leu Gly Glu Tyr Gly Glu Val Thr Val Asp Cys Glu Pro Arg
370 375 380

Ser Gly Ile Asp Thr Asn Ala Tyr Tyr Val Met Thr Val Gly Thr Lys
385 390 395 400

Thr Phe Leu Val His Arg Glu Trp Phe Met Asp Leu Asn Leu Pro Trp
405 410 415

Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr Leu Met Glu
420 425 430

Phe Glu Glu Pro His Ala Thr Lys Gln Ser Val Ile Ala Leu Gly Ser
435 440 445

Gln Glu Gly Ala Leu His Gln Ala Leu Ala Gly Ala Ile Pro Val Glu
450 455 460

Phe Ser Ser Asn Thr Val Lys Leu Thr Ser Gly His Leu Lys Cys Arg
465 470 475 480

Val Lys Met Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr Gly Val Cys
485 490 495

Ser Lys Ala Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr Gly His Gly
500 505 510

Thr Val Val Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly Pro Cys Lys
515 520 525

Val Pro Ile Ser Ser Val Ala Ser Leu Asn Asp Leu Thr Pro Val Gly
530 535 540

Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr Ala Asn Ala
545 550 555 560

Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val
565 570 575

Val Gly Arg Gly Glu Gln Gln Ile Asn His His Trp His Lys Ser Gly
580 585 590

Ser Ser Ile Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly Ala Gln Arg
595 600 605

Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly
610 615 620

Val Phe Thr Ser Val Gly Lys Ala Val His Gln Val Phe Gly Gly Ala
625 630 635 640

Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu
645 650 655

Gly Ala Leu Leu Leu Trp Met Gly Ile Asn Ala Arg Asp Arg Ser Ile
660 665 670

Ala Leu Thr Phe Leu Ala Val Gly Gly Val Leu Leu Phe Leu Ser Val
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Asn Val His Ala
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<210> 17
<211> 5334
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

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<221> misc_feature

<222> (1)..(5334)

<223> pCBE 1-14

<220>

<221> CDS

<222> (916)..(3006)

<400> 17

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ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt      240
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atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt      540
atgccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca      600
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ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa gcttgggtacc      900
tctagagccg ccgcc atg ggc aga aag caa aac aaa aga gga gga aat gaa      951
          Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu
          1             5             10

ggc tca atc atg tgg ctc gcg agc ttg gca gtt gtc ata gct tgt gcg      999
Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala
          15             20             25

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Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile
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aac aac acg gac att gca gac gtt atc gtg att ccc acc tca aaa gga      1095
Asn Asn Thr Asp Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly
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gag aac aga tgc tgg gtc cgg gca atc gac gtc ggc tac atg tgt gag      1143
Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu
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gac act atc acg tac gaa tgt cct aag ctt acc atg ggc aat gat cca      1191
Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro

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gga cgg tgc acg cgg acc agg cat tcc aag cga agc agg aga tcc gtg Gly Arg Cys Thr Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val 110 115 120			1287
tcg gtc caa aca cat ggg gag agt tca cta gtg aat aaa aaa gag gct Ser Val Gln Thr His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala 125 130 135 140			1335
tgg ctg gat tca acg aaa gcc aca cga tat ctc atg aaa act gag aac Trp Leu Asp Ser Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn 145 150 155			1383
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gct cgg tgc ccc acg act gga gaa gcc cac aac gag aag cga gct gat Ala Arg Cys Pro Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp 270 275 280			1767
agt agc tat gtg tgc aaa caa ggc ttc act gac cgt ggg tgg ggc aac Ser Ser Tyr Val Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn 285 290 295 300			1815
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tcc tgc acc agt aaa gcg att ggg aga aca atc cag cca gaa aac atc Ser Cys Thr Ser Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile			1911

29
453

320	325	330	
aaa tac gaa gtt ggc att ttt gtg cat gga acc acc act tcg gaa aac Lys Tyr Glu Val Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn 335 340 345			1959
cat ggg aat tat tca gcg caa gtt ggg gcg tcc cag gcg gca aag ttt His Gly Asn Tyr Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe 350 355 360			2007
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gga gaa gtc aca ctg gac tgt gag cca agg agt gga ctg aac act gaa Gly Glu Val Thr Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu 385 390 395			2103
gcg ttt tac gtc atg acc gtg ggg tca aag tca ttt ctg gtc cat agg Ala Phe Tyr Val Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg 400 405 410			2151
gag tgg ttt cat gac ctc gct ctc ccc tgg acg tcc cct tcg agc aca Glu Trp Phe His Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr 415 420 425			2199
gcg tgg aga aac aga gaa ctc ctc atg gaa ttt gaa gag gcg cac gcc Ala Trp Arg Asn Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala 430 435 440			2247
aca aaa cag tcc gtt gtt gct ctt ggg tca cag gaa gga ggc ctc cat Thr Lys Gln Ser Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His 445 450 455 460			2295
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ctg aaa ggc aca acc tat ggc atg tgt aca gaa aaa ttc tcg ttc gcg Leu Lys Gly Thr Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala 495 500 505			2439
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560	565	570	
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30
454

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<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of artificial sequence; note = synthetic construct

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20 25 30

Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile Asn Asn Thr Asp
35 40 45

Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly Glu Asn Arg Cys
50 55 60

Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu Asp Thr Ile Thr
65 70 75 80

Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro Glu Asp Val Asp
85 90 95

Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr Gly Arg Cys Thr
100 105 110

Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val Ser Val Gln Thr
115 120 125

His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala Trp Leu Asp Ser
130 135 140

Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn Trp Ile Ile Arg
145 150 155 160

Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly Trp Met Leu Gly
165 170 175

Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu Leu Leu Leu Val
180 185 190

Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly Asn Arg Asp Phe
195 200 205

Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly
210 215 220

Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro Thr Leu Asp Val

465	470	475	480
His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr	485	490	495
Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala	500	505	510
Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser Tyr Ser Gly Ser	515	520	525
Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala Ser Leu Asn Asp	530	535	540
Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr	545	550	555
Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly	565	570	575
Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln Ile Asn His His	580	585	590
Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu	595	600	605
Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe	610	615	620
Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln	625	630	635
Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile	645	650	655
Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met Gly Val Asn Ala	660	665	670
Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr Gly Gly Val Leu	675	680	685
Val Phe Leu Ala Thr Asn Val His Ala	690	695	

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<211> 5283
<212> DNA
<213> Artificial Sequence

<220>
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<220>
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<222> (910)..(2964)

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gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc 951
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1 5 10
ttg gca gtt gtc ata gct ggt aca agc gct acc acc atc cac cgg gac 999
Leu Ala Val Val Ile Ala Gly Thr Ser Ala Thr Thr Ile His Arg Asp
15 20 25 30
agg gaa gga tac atg gtt atg cgg gcc agt gga agg gac gct gca agc 1047
Arg Glu Gly Tyr Met Val Met Arg Ala Ser Gly Arg Asp Ala Ala Ser
35 40 45
cag gtc agg gta caa aac gga acg tgc gtc atc ctg gca aca gac atg 1095
Gln Val Arg Val Gln Asn Gly Thr Cys Val Ile Leu Ala Thr Asp Met
50 55 60
gga gag tgg tgt gaa gat tca atc acc tac tct tgc gtc acg att gac 1143

Gly	Glu	Trp	Cys	Glu	Asp	Ser	Ile	Thr	Tyr	Ser	Cys	Val	Thr	Ile	Asp		
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cag	gag	gaa	gaa	ccc	gtt	gac	gtg	gac	tgc	ttc	tgc	cga	ggt	gtt	gat	1191	
Gln	Glu	Glu	Glu	Pro	Val	Asp	Val	Asp	Cys	Phe	Cys	Arg	Gly	Val	Asp		
	80					85				90							
agg	gtt	aag	tta	gag	tat	gga	cgc	tgt	gga	agg	caa	gct	gga	tct	agg	1239	
Arg	Val	Lys	Leu	Glu	Tyr	Gly	Arg	Cys	Gly	Arg	Gln	Ala	Gly	Ser	Arg		
	95				100				105					110			
ggg	aaa	agg	tct	gtg	gtc	att	cca	aca	cat	gca	caa	aaa	gac	atg	gtc	1287	
Gly	Lys	Arg	Ser	Val	Val	Ile	Pro	Thr	His	Ala	Gln	Lys	Asp	Met	Val		
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ggg	cga	ggt	cat	gca	tgg	ctt	aaa	ggt	gac	aat	att	cga	gat	cat	gtc	1335	
Gly	Arg	Gly	His	Ala	Trp	Leu	Lys	Gly	Asp	Asn	Ile	Arg	Asp	His	Val		
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acc	cga	gtc	gag	ggc	tgg	atg	tgg	aag	aac	aag	ctt	cta	act	gcc	gcc	1383	
Thr	Arg	Val	Glu	Gly	Trp	Met	Trp	Lys	Asn	Lys	Leu	Leu	Thr	Ala	Ala		
	145					150					155						
att	gtg	gcc	ttg	gct	tgg	ctc	atg	gtt	gat	agt	tgg	atg	gcc	aga	gtg	1431	
Ile	Val	Ala	Leu	Ala	Trp	Leu	Met	Val	Asp	Ser	Trp	Met	Ala	Arg	Val		
	160				165						170						
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Thr	Val	Ile	Leu	Leu	Ala	Leu	Ser	Leu	Gly	Pro	Val	Tyr	Ala	Thr	Arg		
	175			180				185					190				
tgc	acg	cat	ctt	gag	aac	aga	gat	ttt	gtg	aca	gga	act	caa	ggg	acc	1527	
Cys	Thr	His	Leu	Glu	Asn	Arg	Asp	Phe	Val	Thr	Gly	Thr	Gln	Gly	Thr		
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acc	aga	gtg	tcc	cta	gtt	ttg	gaa	ctt	gga	ggc	tgc	gtg	acc	atc	aca	1575	
Thr	Arg	Val	Ser	Leu	Val	Leu	Glu	Leu	Gly	Gly	Cys	Val	Thr	Ile	Thr		
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gct	gag	ggc	aag	cca	tcc	att	gat	gta	tgg	ctc	gaa	gac	att	ttt	cag	1623	
Ala	Glu	Gly	Lys	Pro	Ser	Ile	Asp	Val	Trp	Leu	Glu	Asp	Ile	Phe	Gln		
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gaa	agc	ccg	gct	gaa	acc	aga	gaa	tac	tgc	ctg	cac	gcc	aaa	ttg	acc	1671	
Glu	Ser	Pro	Ala	Glu	Thr	Arg	Glu	Tyr	Cys	Leu	His	Ala	Lys	Leu	Thr		
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aac	aca	aaa	gtg	gag	gct	cgc	tgt	cca	acc	act	gga	ccg	gcg	aca	ctt	1719	
Asn	Thr	Lys	Val	Glu	Ala	Arg	Cys	Pro	Thr	Thr	Gly	Pro	Ala	Thr	Leu		
	255				260				265					270			
ccg	gag	gag	cat	cag	gct	aat	atg	gtg	tgc	aag	aga	gac	caa	agc	gac	1767	
Pro	Glu	Glu	His	Gln	Ala	Asn	Met	Val	Cys	Lys	Arg	Asp	Gln	Ser	Asp		
			275					280					285				
cgt	gga	tgg	gga	aac	cac	tgc	ggg	ttt	ttt	ggg	aag	ggc	agt	ata	gtg	1815	
Arg	Gly	Trp	Gly	Asn	His	Cys	Gly	Phe	Phe	Gly	Lys	Gly	Ser	Ile	Val		
		290				295						300					
gct	tgt	gca	aag	ttt	gaa	tgc	gag	gaa	gca	aaa	aaa	gct	gtg	ggc	cac	1863	

Ala Cys Ala Lys Phe Glu Cys Glu Glu Ala Lys Lys Ala Val Gly His	
305 310 315	
gtc tat gac tcc aca aag atc acg tat gtt gtc aag gtt gag ccc cac	1911
Val Tyr Asp Ser Thr Lys Ile Thr Tyr Val Val Lys Val Glu Pro His	
320 325 330	
aca ggg gat tac ttg gct gca aat gag acc aat tca aac agg aaa tca	1959
Thr Gly Asp Tyr Leu Ala Ala Asn Glu Thr Asn Ser Asn Arg Lys Ser	
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gca cag ttt acg gtg gca tcc gag aaa gtg atc ctg cgg ctc ggc gac	2007
Ala Gln Phe Thr Val Ala Ser Glu Lys Val Ile Leu Arg Leu Gly Asp	
355 360 365	
tat gga gat gtg tgg ctg acg tgt aaa gtg gca agt ggg att gat gtc	2055
Tyr Gly Asp Val Ser Leu Thr Cys Lys Val Ala Ser Gly Ile Asp Val	
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gcc caa act gtg gtg atg tca ctc gac agc agc aag gac cac ctg cct	2103
Ala Gln Thr Val Val Met Ser Leu Asp Ser Ser Lys Asp His Leu Pro	
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tct gca tgg caa gtg cac cgt gac tgg ttt gag gac ttg gcg ctg ccc	2151
Ser Ala Trp Gln Val His Arg Asp Trp Phe Glu Asp Leu Ala Leu Pro	
400 405 410	
tgg aaa cac aag gac aac caa gat tgg aac agt gtg gag aaa ctt gtg	2199
Trp Lys His Lys Asp Asn Gln Asp Trp Asn Ser Val Glu Lys Leu Val	
415 420 425 430	
gaa ttt gga cca cca cat gct gtg aaa atg gat gtt ttc aat ctg ggg	2247
Glu Phe Gly Pro Pro His Ala Val Lys Met Asp Val Phe Asn Leu Gly	
435 440 445	
gac cag acg gct gtg ctg ctc aaa tca ctg gca gga gtt ccg ctg gcc	2295
Asp Gln Thr Ala Val Leu Leu Lys Ser Leu Ala Gly Val Pro Leu Ala	
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Ser Val Glu Gly Gln Lys Tyr His Leu Lys Ser Gly His Val Thr Cys	
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Asp Val Gly Leu Glu Lys Leu Lys Leu Lys Gly Thr Thr Tyr Ser Met	
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Cys Asp Lys Ala Lys Phe Lys Trp Lys Arg Val Pro Val Asp Ser Gly	
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His Asp Thr Val Val Met Glu Val Ser Tyr Thr Gly Ser Asp Lys Pro	
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Cys Arg Ile Pro Val Arg Ala Val Ala His Gly Val Pro Ala Val Asn	
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gta gcc atg ctc ata acc ccc aat cca acc att gaa aca aat ggt ggc	2583

Val Ala Met Leu Ile Thr Pro Asn Pro Thr Ile Glu Thr Asn Gly Gly	
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gga ttc ata gaa atg cag ctg cca cca ggg gat aac atc atc tat gtg	2631
Gly Phe Ile Glu Met Gln Leu Pro Pro Gly Asp Asn Ile Ile Tyr Val	
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Met Phe Glu Lys Thr Arg Arg Gly Leu Glu Arg Leu Ser Val Val Gly	
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<212> PRT
<213> Artificial Sequence

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<223> Description of artificial sequence; note = synthetic construct

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35 40 45

Arg Val Gln Asn Gly Thr Cys Val Ile Leu Ala Thr Asp Met Gly Glu
50 55 60

Trp Cys Glu Asp Ser Ile Thr Tyr Ser Cys Val Thr Ile Asp Gln Glu
65 70 75 80

Glu Glu Pro Val Asp Val Asp Cys Phe Cys Arg Gly Val Asp Arg Val
85 90 95

Lys Leu Glu Tyr Gly Arg Cys Gly Arg Gln Ala Gly Ser Arg Gly Lys
100 105 110

Arg Ser Val Val Ile Pro Thr His Ala Gln Lys Asp Met Val Gly Arg
115 120 125

Gly His Ala Trp Leu Lys Gly Asp Asn Ile Arg Asp His Val Thr Arg
130 135 140

Val Glu Gly Trp Met Trp Lys Asn Lys Leu Leu Thr Ala Ala Ile Val
145 150 155 160

Ala Leu Ala Trp Leu Met Val Asp Ser Trp Met Ala Arg Val Thr Val
165 170 175

Ile Leu Leu Ala Leu Ser Leu Gly Pro Val Tyr Ala Thr Arg Cys Thr
180 185 190

His Leu Glu Asn Arg Asp Phe Val Thr Gly Thr Gln Gly Thr Thr Arg
195 200 205

Val Ser Leu Val Leu Glu Leu Gly Gly Cys Val Thr Ile Thr Ala Glu
210 215 220

Gly Lys Pro Ser Ile Asp Val Trp Leu Glu Asp Ile Phe Gln Glu Ser
225 230 235 240

Pro Ala Glu Thr Arg Glu Tyr Cys Leu His Ala Lys Leu Thr Asn Thr
245 250 255

Lys Val Glu Ala Arg Cys Pro Thr Thr Gly Pro Ala Thr Leu Pro Glu
260 265 270

Glu His Gln Ala Asn Met Val Cys Lys Arg Asp Gln Ser Asp Arg Gly
275 280 285

Trp Gly Asn His Cys Gly Phe Phe Gly Lys Gly Ser Ile Val Ala Cys
290 295 300

Ala Lys Phe Glu Cys Glu Glu Ala Lys Lys Ala Val Gly His Val Tyr
305 310 315 320

Asp Ser Thr Lys Ile Thr Tyr Val Val Lys Val Glu Pro His Thr Gly
325 330 335

Asp Tyr Leu Ala Ala Asn Glu Thr Asn Ser Asn Arg Lys Ser Ala Gln
340 345 350

Phe Thr Val Ala Ser Glu Lys Val Ile Leu Arg Leu Gly Asp Tyr Gly
355 360 365

Asp Val Ser Leu Thr Cys Lys Val Ala Ser Gly Ile Asp Val Ala Gln
370 375 380

Thr Val Val Met Ser Leu Asp Ser Ser Lys Asp His Leu Pro Ser Ala
385 390 395 400

Trp Gln Val His Arg Asp Trp Phe Glu Asp Leu Ala Leu Pro Trp Lys
405 410 415

His Lys Asp Asn Gln Asp Trp Asn Ser Val Glu Lys Leu Val Glu Phe
420 425 430

Gly Pro Pro His Ala Val Lys Met Asp Val Phe Asn Leu Gly Asp Gln
435 440 445

Thr Ala Val Leu Leu Lys Ser Leu Ala Gly Val Pro Leu Ala Ser Val
450 455 460

Glu Gly Gln Lys Tyr His Leu Lys Ser Gly His Val Thr Cys Asp Val
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 Gly Leu Glu Lys Leu Lys Leu Lys Gly Thr Thr Tyr Ser Met Cys Asp
 485 490 495
 Lys Ala Lys Phe Lys Trp Lys Arg Val Pro Val Asp Ser Gly His Asp
 500 505 510
 Thr Val Val Met Glu Val Ser Tyr Thr Gly Ser Asp Lys Pro Cys Arg
 515 520 525
 Ile Pro Val Arg Ala Val Ala His Gly Val Pro Ala Val Asn Val Ala
 530 535 540
 Met Leu Ile Thr Pro Asn Pro Thr Ile Glu Thr Asn Gly Gly Gly Phe
 545 550 555 560
 Ile Glu Met Gln Leu Pro Pro Gly Asp Asn Ile Ile Tyr Val Gly Asp
 565 570 575
 Leu Ser Gln Gln Trp Phe Gln Lys Gly Ser Thr Ile Gly Arg Met Phe
 580 585 590
 Glu Lys Thr Arg Arg Gly Leu Glu Arg Leu Ser Val Val Gly Glu His
 595 600 605
 Ala Trp Asp Phe Gly Ser Val Gly Gly Val Leu Ser Ser Val Gly Lys
 610 615 620
 Ala Ile His Thr Val Leu Gly Gly Ala Phe Asn Thr Leu Phe Gly Gly
 625 630 635 640
 Val Gly Phe Ile Pro Lys Met Leu Leu Gly Val Ala Leu Val Trp Leu
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<220>

<223> Description of artificial sequence; note = synthetic construct

<220>

<221> CDS

<222> (910)..(2985)

<400> 21

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cccgccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc      420
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      Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
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Leu Ala Val Val Ile Ala Gly Thr Ser Ala Leu Gln Leu Ser Thr Tyr
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cag ggg aaa gtg tta atg tca atc aac aag act gac gct caa agc gcc      1047
Gln Gly Lys Val Leu Met Ser Ile Asn Lys Thr Asp Ala Gln Ser Ala
35             40             45

ata aac att cct agt gcc aac gga gca aac act tgc att gtg agg gct      1095
Ile Asn Ile Pro Ser Ala Asn Gly Ala Asn Thr Cys Ile Val Arg Ala
50             55             60

cta gat gtg ggg gtc atg tgc aaa gat gac atc aca tac ctg tgc cca      1143
Leu Asp Val Gly Val Met Cys Lys Asp Asp Ile Thr Tyr Leu Cys Pro
65             70             75

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tcg agg cgt agc cga cgg tca atc tct gtg cag cat cat gga gat tcc Ser Arg Arg Ser Arg Arg Ser Ile Ser Val Gln His His Gly Asp Ser 115 120 125	1287
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aaa tac ttg aca aaa gta gaa aac tgg gtt ttg cgc aat cct gga tat Lys Tyr Leu Thr Lys Val Glu Asn Trp Val Leu Arg Asn Pro Gly Tyr 145 150 155	1383
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ctttttcaat attattgaag catttatcag ggttattgtc tcatgagcgg atacatattt 5235
gaatgtattt agaaaaataa acnaataggg gttccgcgca catttccccg aaaagtgcc 5295
cctgacgtc 5304

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<210> 22
<211> 692
<212> PRT
<213> Artificial Sequence

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<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 22

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15

Val Val Ile Ala Gly Thr Ser Ala Leu Gln Leu Ser Thr Tyr Gln Gly
20 25 30

Lys Val Leu Met Ser Ile Asn Lys Thr Asp Ala Gln Ser Ala Ile Asn
35 40 45

Ile Pro Ser Ala Asn Gly Ala Asn Thr Cys Ile Val Arg Ala Leu Asp
50 55 60

Val Gly Val Met Cys Lys Asp Asp Ile Thr Tyr Leu Cys Pro Val Leu
65 70 75 80

Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Asp Val Glu
85 90 95

Glu Val Trp Val His Tyr Gly Arg Cys Thr Arg Met Gly His Ser Arg
100 105 110

Arg Ser Arg Arg Ser Ile Ser Val Gln His His Gly Asp Ser Thr Leu
115 120 125

Ala Thr Lys Asn Thr Pro Trp Leu Asp Thr Val Lys Thr Thr Lys Tyr
130 135 140

Leu Thr Lys Val Glu Asn Trp Val Leu Arg Asn Pro Gly Tyr Ala Leu
145 150 155 160

Val Ala Leu Ala Ile Gly Trp Met Leu Gly Ser Asn Asn Thr Gln Arg
165 170 175

Val Val Phe Val Ile Met Leu Met Leu Ile Ala Pro Ala Tyr Ser Phe
180 185 190

Asn Cys Leu Gly Thr Ser Asn Arg Asp Phe Val Glu Gly Ala Ser Gly
195 200 205

Ala Thr Trp Ile Asp Leu Val Leu Glu Gly Gly Ser Cys Val Thr Val
210 215 220

Met Ala Pro Glu Lys Pro Thr Leu Asp Phe Lys Val Met Lys Met Glu
 225 230 235 240

Ala Thr Glu Leu Ala Thr Val Arg Glu Tyr Cys Tyr Glu Ala Thr Leu
 245 250 255

Asp Thr Leu Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu Ala His
 260 265 270

Asn Thr Lys Arg Ser Asp Pro Thr Phe Val Cys Lys Arg Asp Val Val
 275 280 285

Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile
 290 295 300

Asp Thr Cys Ala Lys Phe Thr Cys Lys Asn Lys Ala Thr Gly Lys Thr
 305 310 315 320

Ile Leu Arg Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His Gly
 325 330 335

Ser Thr Asp Ser Thr Ser His Gly Asn Tyr Ser Glu Gln Ile Gly Lys
 340 345 350

Asn Gln Ala Ala Arg Phe Thr Ile Ser Pro Gln Ala Pro Ser Phe Thr
 355 360 365

Ala Asn Met Gly Glu Tyr Gly Thr Val Thr Ile Asp Cys Glu Ala Arg
 370 375 380

Ser Gly Ile Asn Thr Glu Asp Tyr Tyr Val Phe Thr Val Lys Glu Lys
 385 390 395 400

Ser Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Asn Leu Pro Trp
 405 410 415

Thr Ser Pro Ala Thr Thr Asp Trp Arg Asn Arg Glu Thr Leu Val Glu
 420 425 430

Phe Glu Glu Pro His Ala Thr Lys Gln Thr Val Val Ala Leu Gly Ser
 435 440 445

Gln Glu Gly Ala Leu His Thr Ala Leu Ala Gly Ala Ile Pro Ala Thr
 450 455 460

Val Ser Ser Ser Thr Leu Thr Leu Gln Ser Gly His Leu Lys Cys Arg
465 470 475 480

Ala Lys Leu Asp Lys Val Lys Ile Lys Gly Thr Thr Tyr Gly Met Cys
485 490 495

Asp Ser Ala Phe Thr Phe Ser Lys Asn Pro Thr Asp Thr Gly His Gly
500 505 510

Thr Val Ile Val Glu Leu Gln Tyr Thr Gly Ser Asn Gly Pro Cys Arg
515 520 525

Val Pro Ile Ser Val Thr Ala Asn Leu Met Asp Leu Thr Pro Val Gly
530 535 540

Arg Leu Val Thr Val Asn Pro Phe Ile Ser Thr Gly Gly Ala Asn Asn
545 550 555 560

Lys Val Met Ile Glu Val Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val
565 570 575

Val Gly Arg Gly Thr Thr Gln Ile Asn Tyr His Trp His Lys Glu Gly
580 585 590

Ser Ser Ile Gly Lys Ala Leu Ala Thr Thr Trp Lys Gly Ala Gln Arg
595 600 605

Leu Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly
610 615 620

Val Phe Asn Ser Ile Gly Lys Ala Val His Gln Val Phe Gly Gly Ala
625 630 635 640

Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu
645 650 655

Gly Ala Leu Leu Leu Trp Met Gly Leu Gln Ala Arg Asp Arg Ser Ile
660 665 670

Ser Leu Thr Leu Leu Ala Val Gly Gly Ile Leu Ile Phe Leu Ala Thr
675 680 685

Ser Val Gln Ala
690

<210> 23
<211> 5271
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> CDS
<222> (910)..(2952)

<400> 23
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cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180
ttagggtag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt 240
gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata 300
tggagttccg cgttacataa cttacggtaa atggcccgcg tggctgaccg cccaacgacc 360
cccgccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420
attgacgtca atgggtggac tatttacggg aaactgcccc cttggcagta catcaagtgt 480
atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540
atgccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca 600
tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg 660
actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc 720
aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg 780
gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca 840
ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa gcttgggtacc 900
gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc 951
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
1 5 10
ttg gca gtt gtc ata gct ggt aca agc gct gtg acc ttg gtg cgg aaa 999
Leu Ala Val Val Ile Ala Gly Thr Ser Ala Val Thr Leu Val Arg Lys
15 20 25 30
aac aga tgg ttg ctc cta aat gtg aca tct gag gac ctc ggg aaa aca 1047
Asn Arg Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr
35 40 45
ttc tct gtg ggc aca ggc aac tgc aca aca aac att ttg gaa gcc aag 1095
Phe Ser Val Gly Thr Gly Asn Cys Thr Thr Asn Ile Leu Glu Ala Lys
50 55 60

tac tgg tgc cca gac tca atg gaa tac aac tgt ccc aat ctc agt cca Tyr Trp Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro 65 70 75	1143
aga gag gag cca gat gac att gat tgc tgg tgc tat ggg gtg gaa aac Arg Glu Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn 80 85 90	1191
gtt aga gtc gca tat ggt aag tgt gac tca gca ggc agg tct agg agg Val Arg Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg 95 100 105 110	1239
tca aga agg gcc att gac ttg cct acg cat gaa aac cat ggt ttg aag Ser Arg Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys 115 120 125	1287
acc cgg caa gaa aaa tgg atg act gga aga atg ggt gaa agg caa ctc Thr Arg Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Gln Leu 130 135 140	1335
caa aag att gag aga tgg ttc gtg agg aac ccc ttt ttt gca gtg acg Gln Lys Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr 145 150 155	1383
gct ctg acc att gcc tac ctt gtg gga agc aac atg acg caa cga gtc Ala Leu Thr Ile Ala Tyr Leu Val Gly Ser Asn Met Thr Gln Arg Val 160 165 170	1431
gtg att gcc cta ctg gtc ttg gct gtt ggt ccg gcc tac tca gct cac Val Ile Ala Leu Leu Val Leu Ala Val Gly Pro Ala Tyr Ser Ala His 175 180 185 190	1479
tgc att gga att act gac agg gat ttc att gag ggg gtg cat gga gga Cys Ile Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly 195 200 205	1527
act tgg gtt tca gct acc ctg gag caa gac aag tgt gtc act gtt atg Thr Trp Val Ser Ala Thr Leu Glu Gln Asp Lys Cys Val Thr Val Met 210 215 220	1575
gcc cct gac aag cct tca ttg gac atc tca cta gag aca gta gcc att Ala Pro Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile 225 230 235	1623
gat aga cct gct gag gtg agg aaa gtg tgt tac aat gca gtt ctc act Asp Arg Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr 240 245 250	1671
cat gtg aag att aat gac aag tgc ccc agc act gga gag gcc cac cta His Val Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu 255 260 265 270	1719
gct gaa gag aac gaa ggg gac aat gcg tgc aag cgc act tat tct gat Ala Glu Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp 275 280 285	1767
aga ggc tgg ggc aat ggc tgt ggc cta ttt ggg aaa ggg agc att gtg Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val 290 295 300	1815

gca tgc gcc aaa ttc act tgt gcc aaa tcc atg agt ttg ttt gag gtt Ala Cys Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val 305 310 315	1863
gat cag acc aaa att cag tat gtc atc aga gca caa ttg cat gta ggg Asp Gln Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly 320 325 330	1911
gcc aag cag gaa aat tgg act acc gac att aag act ctc aag ttt gat Ala Lys Gln Glu Asn Trp Thr Thr Asp Ile Lys Thr Leu Lys Phe Asp 335 340 345 350	1959
gcc ctg tca ggc tcc cag gaa gtc gag ttc att ggg tat gga aaa gct Ala Leu Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala 355 360 365	2007
aca ctg gaa tgc cag gtg caa act gcg gtg gac ttt ggt aac agt tac Thr Leu Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr 370 375 380	2055
atc gct gag atg gaa aca gag agc tgg ata gtg gac aga cag tgg gcc Ile Ala Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala 385 390 395	2103
cag gac ttg acc ctg cca tgg cag agt gga agt ggc ggg gtg tgg aga Gln Asp Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Gly Val Trp Arg 400 405 410	2151
gag atg cat cat ctt gtc gaa ttt gaa cct ccg cat gcc gcc act atc Glu Met His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile 415 420 425 430	2199
aga gta ctg gcc ctg gga aac cag gaa ggc tcc ttg aaa aca gct ctt Arg Val Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu 435 440 445	2247
act ggc gca atg agg gtt aca aag gac aca aat gac aac aac ctt tac Thr Gly Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr 450 455 460	2295
aaa cta cat ggt gga cat gtt tct tgc aga gtg aaa ttg tca gct ttg Lys Leu His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu 465 470 475	2343
aca ctc aag ggg aca tcc tac aaa ata tgc act gac aaa atg ttt ttt Thr Leu Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe 480 485 490	2391
gtc aag aac cca act gac act ggc cat ggc act gtt gtg atg cag gtg Val Lys Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val 495 500 505 510	2439
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gat ctt aca gcg gca atc aat aaa ggc att ttg gtt aca gtt aac ccc Asp Leu Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro 530 535 540	2535

atc gcc tca acc aat gat gat gaa gtg ctg att gag gtg aac cca cct Ile Ala Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro 545 550 555	2583
ttt gga gac agc tac att atc gtt ggg aga gga gat tca cgt ctc act Phe Gly Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr 560 565 570	2631
tac cag tgg cac aaa gag gga agc tca ata gga aag ttg ttc act cag Tyr Gln Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln 575 580 585 590	2679
acc atg aaa ggc gtg gaa cgc ctg gcc gtc atg gga gac acc gcc tgg Thr Met Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp 595 600 605	2727
gat ttc agc tcc gct gga ggg ttc ttc act tcg gtt ggg aaa gga att Asp Phe Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile 610 615 620	2775
cat acg gtg ttt ggc tct gcc ttt cag ggg cta ttt ggc ggc ttg aac His Thr Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn 625 630 635	2823
tgg ata aca aag gtc atc atg ggg gcg gta ctt ata tgg gtt ggc atc Trp Ile Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile 640 645 650	2871
aac aca aga aac atg aca atg tcc atg agc atg atc ttg gta gga gtg Asn Thr Arg Asn Met Thr Met Ser Met Ser Met Ile Leu Val Gly Val 655 660 665 670	2919
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catactcttc ctttttcaat attattgaag catttatcag ggttattgtc tcatgagcgg 5192
atacatattt gaatgtattt agaaaaataa acaaataggg gttccgcgca catttccccg 5252
aaaagtgcc cctgacgtc 5271

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<210> 24
<211> 681
<212> PRT
<213> Artificial Sequence

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<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 24

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15

Val Val Ile Ala Gly Thr Ser Ala Val Thr Leu Val Arg Lys Asn Arg
20 25 30

Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr Phe Ser
35 40 45

Val Gly Thr Gly Asn Cys Thr Thr Asn Ile Leu Glu Ala Lys Tyr Trp
50 55 60

Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro Arg Glu
65 70 75 80

Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn Val Arg
85 90 95

Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg Ser Arg
100 105 110

Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys Thr Arg
115 120 125

Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Gln Leu Gln Lys
130 135 140

Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr Ala Leu
145 150 155 160

Thr Ile Ala Tyr Leu Val Gly Ser Asn Met Thr Gln Arg Val Val Ile
165 170 175

Ala Leu Leu Val Leu Ala Val Gly Pro Ala Tyr Ser Ala His Cys Ile
180 185 190

Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly Thr Trp
195 200 205

Val Ser Ala Thr Leu Glu Gln Asp Lys Cys Val Thr Val Met Ala Pro
210 215 220

Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile Asp Arg
225 230 235 240

Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr His Val
245 250 255

Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu Ala Glu
260 265 270

Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp Arg Gly
275 280 285

Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val Ala Cys
290 295 300

Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val Asp Gln
305 310 315 320

Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly Ala Lys
325 330 335

Gln Glu Asn Trp Thr Thr Asp Ile Lys Thr Leu Lys Phe Asp Ala Leu
340 345 350

Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala Thr Leu
355 360 365

Glu Cys Gln Val Gln Thr Ala Val Asp Phe Gly Asn Ser Tyr Ile Ala
370 375 380

Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala Gln Asp
385 390 395 400

Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Gly Val Trp Arg Glu Met
405 410 415

His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile Arg Val
420 425 430

Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu Thr Gly
435 440 445

Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr Lys Leu
450 455 460

His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu Thr Leu
 465 470 475 480

 Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe Val Lys
 485 490 495

 Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val Lys Val
 500 505 510

 Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp Asp Leu
 515 520 525

 Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro Ile Ala
 530 535 540

 Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro Phe Gly
 545 550 555 560

 Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr Tyr Gln
 565 570 575

 Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln Thr Met
 580 585 590

 Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp Asp Phe
 595 600 605

 Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile His Thr
 610 615 620

 Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn Trp Ile
 625 630 635 640

 Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile Asn Thr
 645 650 655

 Arg Asn Met Thr Met Ser Met Ser Met Ile Leu Val Gly Val Ile Met
 660 665 670

 Met Phe Leu Ser Leu Gly Val Gly Ala
 675 680

<210> 25
 <211> 35

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> misc_feature
<222> (1)..(35)
<223> POW 454

<400> 25
aaaagaaaaa gcgctaccac catccaccgg gacag 35

<210> 26
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> misc_feature
<222> (1)..(41)
<223> CPOW 2417

<400> 26
actgttacc c tcaaccccg t actcgccggc gaaaaagaaa a 41

<210> 27
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> misc_feature
<223> Modified JE Signal

<400> 27

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15

Val Val Ile Ala Gly Thr Ser Ala
20

<210> 28
<211> 36
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<220>

<221> misc_feature

<222> (1)..(36)

<223> YF 482

<400> 28

aaaagaaaaa gcgctgtgac cttggtgcgg aaaaac

36

<210> 29

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<220>

<221> misc_feature

<222> (1)..(41)

<223> CYF 2433

<400> 29

acagagatcc tcaacccgcg actcgccggc gaaaaagaaa a

41

<210> 30

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<220>

<221> misc_feature

<222> (1)..(41)

<223> SLE 463

<400> 30

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41

<210> 31

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<220>
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 <222> (1)..(40)
 <223> CSLE 2477

<400> 31
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40

<210> 32
 <211> 39
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note = synthetic construct

<400> 32

Leu Asp Thr Ile Asn Arg Arg Pro Ser Lys Lys Arg Gly Gly Thr Arg
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Ser Leu Leu Gly Leu Ala Ala Leu Ile Gly Leu Ala Ser Ser Leu Gln
 20 25 30

Leu Leu Ser Thr Tyr Gln Gly
 35

<210> 33
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note = synthetic construct

<400> 33

Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met
 1 5 10 15

Lys Leu Ser Asn Phe Gln Gly Lys
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<210> 34
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 <212> PRT
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<220>
 <223> Description of artificial sequence; note = synthetic construct

<400> 34

Met Asn Glu Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile

1 5 10 15

Ala Cys Ala Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys
20 25 30

<210> 35
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 35

Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu Gly Ser Ile Met
1 5 10 15

Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met Lys
20 25 30

Leu Ser Asn Phe Gln Gly Lys
35

<210> 36
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 36

Met Ser Lys Lys Arg Gly Gly Ser Glu Thr Ser Val Leu Met Val Ile
1 5 10 15

Phe Met Leu Ile Gly Phe Ala Ala Ala Leu Lys Leu Ser Asn Phe Gln
20 25 30

Gly Lys

<210> 37
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 37

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15

Val Val Ile Ala Cys Ala Gly Ala Val Thr Leu Ser Asn Phe Gln Gly
20 25 30

Lys

<210> 38

<211> 46

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 38

Met Asn Val Leu Arg Gly Phe Arg Lys Glu Ile Gly Arg Met Leu Asn
1 5 10 15

Ile Leu Asn Arg Arg Arg Arg Thr Ala Gly Met Ile Ile Met Leu Ile
20 25 30

Pro Thr Val Met Ala Phe His Leu Thr Thr Arg Asn Gly Glu
35 40 45

<210> 39

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 39

Met Val Gly Leu Gln Lys Arg Gly Lys Arg Arg Ser Ala Thr Asp Trp
1 5 10 15

Met Ser Trp Leu Leu Val Ile Thr Leu Leu Gly Met Thr Leu Ala Ala
20 25 30

Thr Val Arg Lys Glu Arg Gly Asp
35 40

<210> 40

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 40

Met Gly Trp Leu Leu Val Val Val Leu Leu Gly Val Thr Leu Ala Ala
1 5 10 15

Thr Val Arg Lys Glu Arg Gly Asp
20

<210> 41

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 41

Met Ser Trp Leu Leu Val Ile Thr Leu Leu Gly Met Thr Ile Ala Ala
1 5 10 15

Thr Val Arg Lys Glu Arg Gly Asp
20

<210> 42

<211> 5292

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<220>

<221> CDS

<222> (910)..(2964)

<400> 42

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cgagcaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180
ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatagc cgttgacatt 240
gattattgac tagttattaa tagtaantcaa ttacggggtc attagttcat agcccatata 300
tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc 360
cccgccatt gacgtcaata atgacgtatg ttcccatagt aacgccataa gggactttcc 420

attgacgtca atgggtggag tatttacggt aaactgcccc cttggcagta catcaagtgt 480
 atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540
 atgcccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca 600
 tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg 660
 actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc 720
 aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg 780
 gtaggcgtgt acgggtgggag gtctatataa gcagagctct ctggctaact agagaaccca 840
 ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa gcttgggtacc 900
 gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc 951
 Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
 1 5 10
 ttg gca gtt gtc ata gct tgt gca ggc gcc ttc cat tta acc aca cgt 999
 Leu Ala Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg
 15 20 25 30
 aac gga gaa cca cac atg atc gtc agc aga caa gag aaa ggg aaa agt 1047
 Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser
 35 40 45
 ctt ctg ttt aaa aca gag gat ggc gtg aac atg tgt acc ctc atg gcc 1095
 Leu Leu Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala
 50 55 60
 atg gac ctt ggt gaa ttg tgt gaa gac aca atc acg tac aag tgt ccc 1143
 Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro
 65 70 75
 ctt ctc agg cag aat gag cca gaa gac ata gac tgt tgg tgc aac tct 1191
 Leu Leu Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser
 80 85 90
 acg tcc acg tgg gta act tat ggg acg tgt acc acc atg gga gaa cat 1239
 Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His
 95 100 105 110
 aga aga gaa aaa aga tca gtg gca ctc gtt cca cat gtg gga atg gga 1287
 Arg Arg Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly
 115 120 125
 ctg gag aca cga act gaa aca tgg atg tca tca gaa ggg gcc tgg aaa 1335
 Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys
 130 135 140
 cat gtc cag aga att gaa act tgg atc ttg aga cat cca ggc ttc acc 1383
 His Val Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr
 145 150 155
 atg atg gca gca atc ctg gca tac acc ata gga acg aca cat ttc caa 1431
 Met Met Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln
 160 165 170

aga gcc ctg att ttc atc tta ctg aca gct gtc act cct tca atg aca Arg Ala Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr 175 180 185 190	1479
atg cgt tgc ata gga atg tca aat aga gac ttt gtg gaa ggg gtt tca Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser 195 200 205	1527
gga gga agc tgg gtt gac ata gtc tta gaa cat gga agc tgt gtg acg Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr 210 215 220	1575
acg atg gca aaa aac aaa cca aca ttg gat ttt gaa ctg ata aaa aca Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr 225 230 235	1623
gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys 240 245 250	1671
cta acc aac aca aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc Leu Thr Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro 255 260 265 270	1719
agc cta aat gaa gag cag gac aaa agg ttc gtc tgc aaa cac tcc atg Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met 275 280 285	1767
gta gac aga gga tgg gga aat gga tgt gga cta ttt gga aag gga ggc Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly 290 295 300	1815
att gtg acc tgt gct atg ttc aga tgc aaa aag aac atg gaa gga aaa Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys 305 310 315	1863
gtt gtg caa cca gaa aac ttg gaa tac acc att gtg ata aca cct cac Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His 320 325 330	1911
tca ggg gaa gag cat gca gtc gga aat gac aca gga aaa cat ggc aag Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys 335 340 345 350	1959
gaa atc aaa ata aca cca cag agt tcc atc aca gaa gca gaa ttg aca Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr 355 360 365	2007
ggg tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp 370 375 380	2055
ttc aat gag atg gtg ttg ttg cag atg gaa aat aaa gct tgg ctg gtg Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val 385 390 395	2103
cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala 400 405 410	2151

gac aca caa ggg tca aat tgg ata cag aaa gag aca ttg gtc act ttc Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe 415 420 425 430	2199
aaa aat ccc cat gcg aag aaa cag gat gtt gtt gtt tta gga tcc caa Lys Asn Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln 435 440 445	2247
gaa ggg gcc atg cac aca gca ctt aca ggg gcc aca gaa atc caa atg Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met 450 455 460	2295
tca tca gga aac tta ctc ttc aca gga cat ctc aag tgc agg ctg aga Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg 465 470 475	2343
atg gac aag cta cag ctc aaa gga atg tca tac tct atg tgc aca gga Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly 480 485 490	2391
aag ttt aaa gtt gtg aag gaa ata gca gaa aca caa cat gga aca ata Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile 495 500 505 510	2439
gtt atc aga gtg caa tat gaa ggg gac ggc tct cca tgc aag atc cct Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro 515 520 525	2487
ttt gag ata atg gat ttg gaa aaa aga cat gtc tta ggt cgc ctg att Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile 530 535 540	2535
aca gtc aac cca att gtg aca gaa aaa gat agc cca gtc aac ata gaa Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu 545 550 555	2583
gca gaa cct cca ttc gga gac agc tac atc atc ata gga gta gag cgc Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro 560 565 570	2631
gga caa ctg aag ctc aac tgg ttt aag aaa gga agt tct atc ggc caa Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Ser Ile Gly Gln 575 580 585 590	2679
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gac aca gcc tgg gat ttt gga tcc ttg gga gga gtg ttt aca tct ata Asp Thr Ala Trp Asp Phe Gly Ser Leu Gly Gly Val Phe Thr Ser Ile 610 615 620	2775
gga aag gct ctc cac caa gtc ttt gga gca atc tat gga gct gcc ttc Gly Lys Ala Leu His Gln Val Phe Gly Ala Ile Tyr Gly Ala Ala Phe 625 630 635	2823
agt ggg gtt tca tgg act atg aaa atc ctc ata gga gtc att atc aca Ser Gly Val Ser Trp Thr Met Lys Ile Leu Ile Gly Val Ile Ile Thr 640 645 650	2871

tgg ata gga atg aat tca cgc agc acc tca ctg tct gtg aca cta gta	2919
Trp Ile Gly Met Asn Ser Arg Ser Thr Ser Leu Ser Val Thr Leu Val	
655 660 665 670	
ttg gtg gga att gtg aca ctg tat ttg gga gtc atg gtg cag gcc	2964
Leu Val Gly Ile Val Thr Leu Tyr Leu Gly Val Met Val Gln Ala	
675 680 685	
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ccatctggcc ccagtgtgc aatgataccg cgagaccac gtcaccggc tccagattta	4464
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atttatcagg gttattgtct catgagcgga tacatatctg aatgtattta gaaaaataaa 5244
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<210> 43
<211> 685
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of artificial sequence; note = synthetic construct
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<400> 43
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```

```
Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg Asn Gly
20          25          30
```

```
Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser Leu Leu
35          40          45
```

```
Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala Met Asp
50          55          60
```

```
Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro Leu Leu
65          70          75          80
```

```
Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser Thr Ser
85          90          95
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Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His Arg Arg
 100 105 110

Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly Leu Glu
 115 120 125

Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys His Val
 130 135 140

Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr Met Met
 145 150 155 160

Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln Arg Ala
 165 170 175

Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr Met Arg
 180 185 190

Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser Gly Gly
 195 200 205

Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr Thr Met
 210 215 220

Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr Glu Ala
 225 230 235 240

Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys Leu Thr
 245 250 255

Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro Ser Leu
 260 265 270

Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met Val Asp
 275 280 285

Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly Ile Val
 290 295 300

Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys Val Val
 305 310 315 320

Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His Ser Gly
 325 330 335

Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys Glu Ile
340 345 350

Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr Gly Tyr
355 360 365

Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp Phe Asn
370 375 380

Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val His Arg
385 390 395 400

Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala Asp Thr
405 410 415

Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe Lys Asn
420 425 430

Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln Glu Gly
435 440 445

Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met Ser Ser
450 455 460

Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg Met Asp
465 470 475 480

Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly Lys Phe
485 490 495

Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile Val Ile
500 505 510

Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro Phe Glu
515 520 525

Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile Thr Val
530 535 540

Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu Ala Glu
545 550 555 560

Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro Gly Gln
565 570 575

Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Ser Ile Gly Gln Met Phe
580 585 590

Glu Thr Thr Met Arg Gly Ala Lys Arg Met Ala Ile Leu Gly Asp Thr
595 600 605

Ala Trp Asp Phe Gly Ser Leu Gly Gly Val Phe Thr Ser Ile Gly Lys
610 615 620

Ala Leu His Gln Val Phe Gly Ala Ile Tyr Gly Ala Ala Phe Ser Gly
625 630 635 640

Val Ser Trp Thr Met Lys Ile Leu Ile Gly Val Ile Ile Thr Trp Ile
645 650 655

Gly Met Asn Ser Arg Ser Thr Ser Leu Ser Val Thr Leu Val Leu Val
660 665 670

Gly Ile Val Thr Leu Tyr Leu Gly Val Met Val Gln Ala
675 680 685

<210> 44
<211> 5293
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> CDS
<222> (910)..(2964)

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cgagcaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180
ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatatc cgttgacatt 240
gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata 300
tggagttccg cgttacataa cttacggtaa atggcccgcc tggctgaccg cccaacgacc 360
cccgccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420
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 gccgcgccc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc 951
 Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser
 1 5 10
 ttg gca gtt gtc ata gct tgt gca ggc gcc ttc cat tta acc aca cgt 999
 Leu Ala Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg
 15 20 25 30
 aac gga gaa cca cac atg atc gtc agc aga caa gag aaa ggg aaa agt 1047
 Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser
 35 40 45
 ctt ctg ttt aaa aca gag gat ggc gtg aac atg tgt acc ctc atg gcc 1095
 Leu Leu Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala
 50 55 60
 atg gac ctt ggt gaa ttg tgt gaa gac aca atc acg tac aag tgt ccc 1143
 Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro
 65 70 75
 ctt ctc agg cag aat gag cca gaa gac ata gac tgt tgg tgc aac tct 1191
 Leu Leu Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser
 80 85 90
 acg tcc acg tgg gta act tat ggg acg tgt acc acc atg gga gaa cat 1239
 Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His
 95 100 105 110
 aga aga gaa aaa aga tca gtg gca ctc gtt cca cat gtg gga atg gga 1287
 Arg Arg Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly
 115 120 125
 ctg gag aca cga act gaa aca tgg atg tca tca gaa ggg gcc tgg aaa 1335
 Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys
 130 135 140
 cat gtc cag aga att gaa act tgg atc ttg aga cat cca ggc ttc acc 1383
 His Val Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr
 145 150 155
 atg atg gca gca atc ctg gca tac acc ata gga acg aca cat ttc caa 1431
 Met Met Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln
 160 165 170
 aga gcc ctg att ttc atc tta ctg aca gct gtc act cct tca atg aca 1479
 Arg Ala Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr

175	180	185	190	
atg cgt tgc ata gga atg tca aat aga gac ttt gtg gaa ggg gtt tca Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser 195 200 205				1527
gga gga agc tgg gtt gac ata gtc tta gaa cat gga agc tgt gtg acg Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr 210 215 220				1575
acg atg gca aaa aac aaa cca aca ttg gat ttt gaa ctg ata aaa aca Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr 225 230 235				1623
gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys 240 245 250				1671
cta acc aac aca aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc Leu Thr Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro 255 260 265 270				1719
agc cta aat gaa gag cag gac aaa agg ttc gtc tgc aaa cac tcc atg Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met 275 280 285				1767
gta gac aga gga tgg gga aat gga tgt gga cta ttt gga aag gga ggc Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly 290 295 300				1815
att gtg acc tgt gct atg ttc aga tgc aaa aag aac atg gaa gga aaa Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys 305 310 315				1863
gtt gtg caa cca gaa aac ttg gaa tac acc att gtg ata aca cct cac Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His 320 325 330				1911
tca ggg gaa gag cat gca gtc gga aat gac aca gga aaa cat ggc aag Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys 335 340 345 350				1959
gaa atc aaa ata aca cca cag agt tcc atc aca gaa gca gaa ttg aca Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr 355 360 365				2007
ggc tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp 370 375 380				2055
ttc aat gag atg gtg ttg ttg cag atg gaa aat aaa gct tgg ctg gtg Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val 385 390 395				2103
cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala 400 405 410				2151
gac aca caa ggg tca aat tgg ata cag aaa gag aca ttg gtc act ttc Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe 415 420 425 430				2199

52
476

415	420	425	430	
aaa aat ccc cat gcg aag aaa cag gat gtt gtt gtt tta gga tcc caa				2247
Lys Asn Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln	435	440	445	
gaa ggg gcc atg cac aca gca ctt aca ggg gcc aca gaa atc caa atg				2295
Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met	450	455	460	
tca tca gga aac tta ctc ttc aca gga cat ctc aag tgc agg ctg aga				2343
Ser Ser Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg	465	470	475	
atg gac aag cta cag ctc aaa gga atg tca tac tct atg tgc aca gga				2391
Met Asp Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly	480	485	490	
aag ttt aaa gtt gtg aag gaa ata gca gaa aca caa cat gga aca ata				2439
Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile	495	500	505	510
gtt atc aga gtg caa tat gaa ggg gac ggc tct cca tgc aag atc cct				2487
Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro	515	520	525	
ttt gag ata atg gat ttg gaa aaa aga cat gtc tta ggt cgc ctg att				2535
Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile	530	535	540	
aca gtc aac cca att gtg aca gaa aaa gat agc cca gtc aac ata gaa				2583
Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu	545	550	555	
gca gaa cct cca ttc gga gac agc cac atc atc ata gga gta gag ccg				2631
Ala Glu Pro Pro Phe Gly Asp Ser His Ile Ile Ile Gly Val Glu Pro	560	565	570	
gga caa ctg aag ctc aac tgg ttt aag aaa gga agt tct atc ggc caa				2679
Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Ser Ile Gly Gln	575	580	585	590
atg ttt gag aca aca atg agg ggg gcg aag aga atg gcc att tta ggt				2727
Met Phe Glu Thr Thr Met Arg Gly Ala Lys Arg Met Ala Ile Leu Gly	595	600	605	
gac aca gcc tgg gat ttt gga tcc ttg gga gga gtg ttt aca tct ata				2775
Asp Thr Ala Trp Asp Phe Gly Ser Leu Gly Gly Val Phe Thr Ser Ile	610	615	620	
gga aag gct ctc cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt				2823
Gly Lys Ala Leu His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe	625	630	635	
ggg gga atg tct tgg atc aca caa ggg cta atg ggt gcc cta ctg ctc				2871
Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu	640	645	650	
tgg atg ggc gtc aac gca cga gac cga tca att gct ttg gcc ttc tta				2919
Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu				

655	660	665	670	
gcc aca ggg ggt gtg ctc gtg ttc tta gcg acc aat gtg cat gct				2964
Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala				
	675	680	685	
taattagttt gggcgggcgc tcgagcatgc atctagaggg ccctattcta tagtgtcacc				3024
taaatgctag agctcgtga tcagcctcga ctgtgccttc tagttgccag ccctctgttg				3084
tttgccctc ccccggtgct tccttgacct tggaaaggtgc cactcccaact gtcctttcct				3144
aataaaatga ggaaattgca tcgcattgtc tgagtaggtg tcattctatt ctgggggggtg				3204
gggtggggca ggacagcaag ggggaggatt ggggaagaca tagcaggcat gctggggatg				3264
cgggtgggctc tatggcttct gaggcggaag gaaccagctg cattaatgaa tcggccaacg				3324
cgcggggaga ggcgggttgc gtattgggcg ctcttcgctt tcctcgctca ctgactcgt				3384
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caggaaccgt aaaaaggccg cgttgctggc gtttttccat aggtccgcc cccctgacga				3564
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ccaggcggtt cccctggaa gctccctcgt gcgctctcct gttccgacct tgccgcttac				3684
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atccggcaaa caaaccaccg ctggtagcgg tgggtttttt gtttgcaagc agcagattac				4104
gcgcagaaaa aaaggatctc aagaagatcc tttgatcttt tctacggggc ctgacgctca				4164
gtggaacgaa aactcacgtt aagggtattt ggtcatgaga ttatcaaaaa ggatcttcac				4224
ctagatcctt ttaaattaaa aatgaagttt taantcaatc taaagtatat atgagtaaac				4284
ttggtctgac agttaccaat gcttaatcag tgaggcacct atctcagcga tctgtctatt				4344
tcgttcatcc atagttgcct gactccccgt cgtgtagata actacgatac gggagggcct				4404
accatctggc ccagtgctg caatgatacc gcgagacca cgctcaccgg ctccagattt				4464
atcagcaata aaccagccag ccggaagggc cgagcgcaga agtggtcctg caactttatc				4524
cgctccatc cagtctatta attgttgccg ggaagctaga gtaagtagtt cgccagttaa				4584

57
477

tagtttgccg aacgttggtg ccattgctac aggcacgtg gtgtcacgct cgtcgtttgg 4644
tatggcttca ttcagctccg gttcccaacg atcaaggcga gttacatgat ccccatgtt 4704
gtgcaaaaaa gcggttagct ctttcggtec tccgatcgtt gtcagaagta agttggccgc 4764
agtgttatca ctcatggta tggcagcact gcataattct cttactgtca tgccatccgt 4824
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gcgaccgagt tgetcttgcc cggcgtaaat acgggataat accgcgccac atagcagaac 4944
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gctgttgaga tccagttcga tgtaacccac tctgtcaccc aactgatctt cagcatcttt 5064
tactttcacc agcgtttctg ggtgagcaaa aacaggaagg caaaatgccg caaaaaaggg 5124
aataagggcg acacggaaat gttgaatact catactcttc ctttttcaat attattgaag 5184
catttatcag gggtattgtc tcatgagcgg atacatattt gaatgtattt agaaaaataa 5244
acaaataggg gttccgcgca catttccccg aaaagtgcc a cctgacgtc 5293

<210> 45
<211> 685
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 45

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
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Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg Asn Gly
20 25 30

Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser Leu Leu
35 40 45

Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala Met Asp
50 55 60

Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro Leu Leu
65 70 75 80

Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser Thr Ser
85 90 95

Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His Arg Arg
73

100	105	110
Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly Leu Glu 115 120 125		
Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys His Val 130 135 140		
Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr Met Met 145 150 155 160		
Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln Arg Ala 165 170 175		
Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr Met Arg 180 185 190		
Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser Gly Gly 195 200 205		
Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr Thr Met 210 215 220		
Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr Glu Ala 225 230 235 240		
Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys Leu Thr 245 250 255		
Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro Ser Leu 260 265 270		
Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met Val Asp 275 280 285		
Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly Ile Val 290 295 300		
Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys Val Val 305 310 315 320		
Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His Ser Gly 325 330 335		
Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys Glu Ile		

478 54

340

345

350

Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr Gly Tyr
355 360 365

Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp Phe Asn
370 375 380

Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val His Arg
385 390 395 400

Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala Asp Thr
405 410 415

Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe Lys Asn
420 425 430

Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln Glu Gly
435 440 445

Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met Ser Ser
450 455 460

Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg Met Asp
465 470 475 480

Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly Lys Phe
485 490 495

Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile Val Ile
500 505 510

Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro Phe Glu
515 520 525

Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile Thr Val
530 535 540

Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu Ala Glu
545 550 555 560

Pro Pro Phe Gly Asp Ser His Ile Ile Ile Gly Val Glu Pro Gly Gln
565 570 575

Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Ser Ile Gly Gln Met Phe

580

585

590

Glu Thr Thr Met Arg Gly Ala Lys Arg Met Ala Ile Leu Gly Asp Thr
595 600 605

Ala Trp Asp Phe Gly Ser Leu Gly Gly Val Phe Thr Ser Ile Gly Lys
610 615 620

Ala Leu His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly
625 630 635 640

Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met
645 650 655

Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr
660 665 670

Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
675 680 685

<210> 46
<211> 5293
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<220>
<221> CDS
<222> (910)..(2964)

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cgagcaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180
ttagggtttag gcgttttgcg ctgcttcgcy atgtacgggc cagatatacg cgttgacatt 240
gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata 300
tggagttccg cgttacataa cttacggtaa atggcccgcg tggctgaccg cccaacgacc 360
cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420
attgacgtca atgggtggac tatttacggt aaactgcca cttggcagta catcaagtgt 480
atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540
atgccagta catgacctta tgggactttc ctacttggca gtacatctac gtattagtca 600

tcgctattac catggtgatg cgggttttggc agtacatcaa tgggcgtgga tagcgggtttg	660
actcacggggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc	720
aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggag	780
gtaggcgtgt acgggtgggag gtctatataa gcagagctct ctggctaact agagaaccca	840
ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa gcttgggtacc	900
gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser	951
1 5 10	
ttg gca gtt gtc ata gct tgt gca ggc gcc ttc cat tta acc aca cgt Leu Ala Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg	999
15 20 25 30	
aac gga gaa cca cac atg atc gtc agc aga caa gag aaa ggg aaa agt Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser	1047
35 40 45	
ctt ctg ttt aaa aca gag gat ggc gtg aac atg tgt acc ctc atg gcc Leu Leu Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala	1095
50 55 60	
atg gac ctt ggt gaa ttg tgt gaa gac aca atc acg tac aag tgt ccc Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro	1143
65 70 75	
ctt ctc agg cag aat gag cca gaa gac ata gac tgt tgg tgc aac tct Leu Leu Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser	1191
80 85 90	
acg tcc acg tgg gta act tat ggg acg tgt acc acc atg gga gaa cat Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His	1239
95 100 105 110	
aga aga gaa aaa aga tca gtg gca ctc gtt cca cat gtg gga atg gga Arg Arg Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly	1287
115 120 125	
ctg gag aca cga act gaa aca tgg atg tca tca gaa ggg gcc tgg aaa Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys	1335
130 135 140	
cat gtc cag aga att gaa act tgg atc ttg aga cat cca ggc ttc acc His Val Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr	1383
145 150 155	
atg atg gca gca atc ctg gca tac acc ata gga acg aca cat ttc caa Met Met Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln	1431
160 165 170	
aga gcc ctg att ttc atc tta ctg aca gct gtc act cct tca atg aca Arg Ala Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr	1479
175 180 185 190	
atg cgt tgc ata gga atg tca aat aga gac ttt gtg gaa ggg gtt tca	1527

Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser	
195 200 205	
gga gga agc tgg gtt gac ata gtc tta gaa cat ggg agc tgt gtg acg	1575
Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr	
210 215 220	
acg atg gca aaa aac aaa cca aca ttg gat ttt gaa ctg ata aaa aca	1623
Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr	
225 230 235	
gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag	1671
Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys	
240 245 250	
cta acc aac aca aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc	1719
Leu Thr Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro	
255 260 265 270	
agc cta aat gaa gag cag gac aaa agg ttc gtc tgc aaa cac tcc atg	1767
Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met	
275 280 285	
gta gac aga gga tgg gga aat gga tgt gga cta ttt gga aag gga ggc	1815
Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly	
290 295 300	
att gtg acc tgt gct atg ttc aga tgc aaa aag aac atg gaa gga aaa	1863
Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys	
305 310 315	
gtt gtg caa cca gaa aac ttg gaa tac acc att gtg ata aca cct cac	1911
Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His	
320 325 330	
tca ggg gaa gag cat gca gtc gga aat gac aca gga aaa cat ggc aag	1959
Ser Gly Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys	
335 340 345 350	
gaa atc aaa ata aca cca cag agt tcc atc aca gaa gca gaa ttg aca	2007
Glu Ile Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr	
355 360 365	
ggt tat ggc act gtc aca atg gag tgc tct cca aga acg ggc ctc gac	2055
Gly Tyr Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp	
370 375 380	
ttc aat gag atg gtg ttg ttg cag atg gaa aat aaa gct tgg ctg gtg	2103
Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val	
385 390 395	
cac agg caa tgg ttc cta gac ctg ccg tta cca tgg ttg ccc gga gcg	2151
His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala	
400 405 410	
gac aca caa ggg tca aat tgg ata cag aaa gag aca ttg gtc act ttc	2199
Asp Thr Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe	
415 420 425 430	
aaa aat ccc cat gcg aag aaa cag gat gtt gtt gtt tta gga tcc caa	2247

Lys	Asn	Pro	His	Ala	Lys	Lys	Gln	Asp	Val	Val	Val	Leu	Gly	Ser	Gln	
				435					440					445		
gaa	ggg	gcc	atg	cac	aca	gca	ctt	aca	ggg	gcc	aca	gaa	atc	caa	atg	2295
Glu	Gly	Ala	Met	His	Thr	Ala	Leu	Thr	Gly	Ala	Thr	Glu	Ile	Gln	Met	
				450				455					460			
tca	tca	gga	aac	tta	ctc	ttc	aca	gga	cat	ctc	aag	tgc	agg	ctg	aga	2343
Ser	Ser	Gly	Asn	Leu	Leu	Phe	Thr	Gly	His	Leu	Lys	Cys	Arg	Leu	Arg	
		465					470					475				
atg	gac	aag	cta	cag	ctc	aaa	gga	atg	tca	tac	tct	atg	tgc	aca	gga	2391
Met	Asp	Lys	Leu	Gln	Leu	Lys	Gly	Met	Ser	Tyr	Ser	Met	Cys	Thr	Gly	
	480					485					490					
aag	ttt	aaa	gtt	gtg	aag	gaa	ata	gca	gaa	aca	caa	cat	gga	aca	ata	2439
Lys	Phe	Lys	Val	Val	Lys	Glu	Ile	Ala	Glu	Thr	Gln	His	Gly	Thr	Ile	
495					500					505					510	
gtt	atc	aga	gtg	caa	tat	gaa	ggg	gac	ggc	tct	cca	tgc	aag	atc	cct	2487
Val	Ile	Arg	Val	Gln	Tyr	Glu	Gly	Asp	Gly	Ser	Pro	Cys	Lys	Ile	Pro	
				515					520					525		
ttt	gag	ata	atg	gat	ttg	gaa	aaa	aga	cat	gtc	tta	ggt	cgc	ctg	att	2535
Phe	Glu	Ile	Met	Asp	Leu	Glu	Lys	Arg	His	Val	Leu	Gly	Arg	Leu	Ile	
			530					535					540			
aca	gtc	aac	cca	att	gtg	aca	gaa	aaa	gat	agc	cca	gtc	aac	ata	gaa	2583
Thr	Val	Asn	Pro	Ile	Val	Thr	Glu	Lys	Asp	Ser	Pro	Val	Asn	Ile	Glu	
		545						550				555				
gca	gaa	cct	cca	ttc	gga	gac	agc	tac	atc	atc	ata	gga	gta	gag	ccg	2631
Ala	Glu	Pro	Pro	Phe	Gly	Asp	Ser	Tyr	Ile	Ile	Ile	Gly	Val	Glu	Pro	
	560					565					570					
gga	caa	ctg	aag	ctc	aac	tgg	ttt	aag	aaa	gga	agc	acg	ctg	ggc	aag	2679
Gly	Gln	Leu	Lys	Leu	Asn	Trp	Phe	Lys	Lys	Gly	Ser	Thr	Leu	Gly	Lys	
575					580					585					590	
gcc	ttt	tca	aca	act	ttg	aag	gga	gct	caa	aga	ctg	gca	gcg	ttg	ggc	2727
Ala	Phe	Ser	Thr	Thr	Leu	Lys	Gly	Ala	Gln	Arg	Leu	Ala	Ala	Leu	Gly	
				595				600						605		
gac	aca	gcc	tgg	gac	ttt	ggc	tct	att	gga	ggg	gtc	ttc	aac	tcc	ata	2775
Asp	Thr	Ala	Trp	Asp	Phe	Gly	Ser	Ile	Gly	Gly	Val	Phe	Asn	Ser	Ile	
		610						615					620			
gga	aaa	gcc	gtt	cac	caa	gtg	ttt	ggt	ggt	gcc	ttc	aga	aca	ctc	ttt	2823
Gly	Lys	Ala	Val	His	Gln	Val	Phe	Gly	Gly	Ala	Phe	Arg	Thr	Leu	Phe	
		625					630				635					
ggg	gga	atg	tct	tgg	atc	aca	caa	ggg	cta	atg	ggt	gcc	cta	ctg	ctc	2871
Gly	Gly	Met	Ser	Trp	Ile	Thr	Gln	Gly	Leu	Met	Gly	Ala	Leu	Leu	Leu	
	640					645					650					
tgg	atg	ggc	gtc	aac	gca	cga	gac	cga	tca	att	gct	ttg	gcc	ttc	tta	2919
Trp	Met	Gly	Val	Asn	Ala	Arg	Asp	Arg	Ser	Ile	Ala	Leu	Ala	Phe	Leu	
	655				660					665					670	
gcc	aca	ggg	ggt	gtg	ctc	gtg	ttc	tta	gcg	acc	aat	gtg	cat	gct		2964

Ala Thr Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
675 680 685

taattagttt gageggccgc tcgagcatgc atctagaggg ccctattcta tagtgcacc	3024
taaatgctag agctcgctga tcagcctcga ctgtgccttc tagttgccag ccatctgttg	3084
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gggtggggca ggacagcaag ggggaggatt ggggaagaca tagcaggcat gctggggatg	3264
cggtgggctc tatggcttct gaggcggaaa gaaccagctg cattaatgaa tcggccaacg	3324
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gcgctcggtc gttcggctgc ggcgagcggc atcagctcac tcaaaggcgg taatacggtt	3444
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caggaaccgt aaaaaggccg cgttgctggc gtttttccat aggctccgc cccctgacga	3564
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cgttcagccc gaccgctgcg ccttatccgg taactatcgt cttgagtcca acccggtatg	3864
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gcgcagaaaa aaaggatctc aagaagatcc ttgatcttt tctacggggt ctgacgctca	4164
gtggaacgaa aactcacgtt aagggtttt ggtcatgaga ttatcaaaaa ggatcttcac	4224
ctagatcctt ttaaattaa aatgaagttt taaatcaatc taaagtatat atgagtaaac	4284
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tcgttcaccc atagttgcct gactccccgt cgtgtagata actacgatac gggagggctt	4404
accatctggc ccagtgctg caatgatacc gcgagacca cgctcaccgg ctccagattt	4464
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cgctccatc cagtctatta attgttgccg ggaagctaga gtaagtagtt cgccagttaa	4584
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tatggcttca ttcagctccg gttcccaacg atcaaggcga gttacatgat ccccatgtt	4704

gtgcaaaaaa gcggttagct ccttcgggtc tccgatcggt gtcagaagta agttggccgc 4764
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 gctgttgaga tccagttcga tgtaaccac tctgtcaccc aactgatctt cagcatcttt 5064
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 aataagggcg acacggaaat gttgaatact catactcttc ctttttcaat attattgaag 5184
 catttatcag ggttattgtc tcatgagcgg atacatattt gaatgtattt agaaaaataa 5244
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<210> 47

<211> 685

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note = synthetic construct

<400> 47

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15

Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg Asn Gly
20 25 30

Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser Leu Leu
35 40 45

Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala Met Asp
50 55 60

Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro Leu Leu
65 70 75 80

Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser Thr Ser
85 90 95

Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His Arg Arg
100 105 110

Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly Leu Glu
 115 120 125

Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys His Val
 130 135 140

Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr Met Met
 145 150 155 160

Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln Arg Ala
 165 170 175

Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr Met Arg
 180 185 190

Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser Gly Gly
 195 200 205

Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr Thr Met
 210 215 220

Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr Glu Ala
 225 230 235 240

Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys Leu Thr
 245 250 255

Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro Ser Leu
 260 265 270

Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met Val Asp
 275 280 285

Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly Ile Val
 290 295 300

Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys Val Val
 305 310 315 320

Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His Ser Gly
 325 330 335

Glu Glu His Ala Val Gly Asn Asp Thr Gly Lys His Gly Lys Glu Ile
 340 345 350

Lys Ile Thr Pro Gln Ser Ser Ile Thr Glu Ala Glu Leu Thr Gly Tyr
 355 360 365

Gly Thr Val Thr Met Glu Cys Ser Pro Arg Thr Gly Leu Asp Phe Asn
 370 375 380

Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val His Arg
 385 390 395 400

Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala Asp Thr
 405 410 415

Gln Gly Ser Asn Trp Ile Gln Lys Glu Thr Leu Val Thr Phe Lys Asn
 420 425 430

Pro His Ala Lys Lys Gln Asp Val Val Val Leu Gly Ser Gln Glu Gly
 435 440 445

Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Met Ser Ser
 450 455 460

Gly Asn Leu Leu Phe Thr Gly His Leu Lys Cys Arg Leu Arg Met Asp
 465 470 475 480

Lys Leu Gln Leu Lys Gly Met Ser Tyr Ser Met Cys Thr Gly Lys Phe
 485 490 495

Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile Val Ile
 500 505 510

Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro Phe Glu
 515 520 525

Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile Thr Val
 530 535 540

Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu Ala Glu
 545 550 555 560

Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro Gly Gln
 565 570 575

Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys Ala Phe
 580 585 590

Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr
595 600 605

Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys
610 615 620

Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly
625 630 635 640

Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met
645 650 655

Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr
660 665 670

Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
675 680 685

<210> 48
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 48
tgtgcaggcg ccttcattt aaccacacgt aacg 34

<210> 49
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 49
tcgagcggcc gctcaactaa ttaggcctgc accatgactc 40

<210> 50
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 50
cttatcgaaa ttaatacgac tcactatagg 30

<210> 51
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 51
atagattgct ccaaacactt ggtgg 25

<210> 52
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 52
actccatagg aaaagccgtt cacc 24

<210> 53
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 53
gcgagctcta gcatttaggt gacactatag 30

<210> 54
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 54
ctccaccaag tgtttggtgg tgccttcaga aca 33

<210> 55
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct

<400> 55
Leu His Gln Val Phe Gly Gly Ala Phe Arg Thr
1 5 10

<210> 56
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <400> 56
 cttatcgaaa ttaatacgac tcactatagg 30

 <210> 57
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <400> 57
 gaattcgtct cacttccttt cttaaaccag ttgagcttc 39

 <210> 58
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <400> 58
 ggaattcgtc tcggaagcac gctgggcaag g 31

 <210> 59
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <400> 59
 gcgagctcta gcatttaggt gacactatag 30

 <210> 60
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of artificial sequence; note = synthetic construct

 <400> 60
 aactggttta agaaaggaag cacgctgggc gcc 33

484 ~~60~~
LJB

<210> 61
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note = synthetic construct
<400> 61

Asn	Trp	Lys	Lys	Gly	Ser	Thr	Leu	Gly	Lys	Ala
1			5						10	