



Industria y Comercio

SUPERINTENDENCIA

DELEGATURA DE PROPIEDAD INDUSTRIAL

División de Nuevas Creaciones

SOLICITUD PATENTE DE INVENCION

21. EXPEDIENTE No. _____

54. TÍTULO _____
POLYPEPTIDOS ANTICUERPOS QUE ANTAGONIZAN CD40

51. CLASIFICACIÓN INTERNACIONAL _____

71. SOLICITANTE BRISTOL MYERS SQUIBB Y
DOMANTIS LIMITED.
DOMICILIO PRINCETON Y BRENTFORD.

74. APODERADO ALVARO CORREA.

22. BOGOTÁ, D.C., 5 NOVIEMBRE 2013.



DIRECCIÓN DE NUEVAS CREACIONES
SOLICITUD FASE NACIONAL -PCT

1	TIPO DE SOLICITUD	☒ Patente de invención ☒ Capítulo I	☐ Patente de Modelo de Utilidad ☐ Capítulo II
2	DATOS SOLICITUD INTERNACIONAL PCT (86)		
Solicitud Internacional No.		PCT/US2012/034519	Fecha 20/04/2012
Publicación Internacional No.		WO/2012/145673	Fecha 26/10/2012
3	TÍTULO DE LA INVENCIÓN (200 caracteres o espacios máximos)		
POLIPEPTIDOS ANTICUERPOS QUE ANTAGONIZAN CD40			
4	CLASIFICACIÓN INTERNACIONAL (CIP)		
C07K 16/28 (2006.01), A61K 39/395 006.01)			
5	SOLICITANTE (S) ☐ Esta persona también es inventor. Para datos adicionales utilizar hoja de información complementaria		
APELLIDOS O RAZÓN SOCIAL		NOMBRE	IDENTIFICACIÓN
BRISTOL-MYERS SQUIBB COMPANY Y DOMANTIS LIMITED			
6	DATOS DEL SOLICITANTE		
DIRECCIÓN		No. TELÉFONO	
Route 206 & Province Line Road Princeton, New Jersey 08543, Estados Unidos de America y 980 Great West Road Brentford, Middlesex TW8 9GS (GB)		6341500	
CIUDAD		CORREO ELECTRÓNICO	
Princeton y Brentford		alvaro.correa@bakerm ckenzie.com	
DEPARTAMENTO/ESTADO		NACIONALIDAD O LUGAR DE CONSTITUCIÓN	
New Jersey y Middlesex		Estados Unidos de América y Reino Unido	
PAÍS DE RESIDENCIA			
Estados Unidos de América y Reino Unido			
7	INVENTOR (ES) Para datos adicionales utilizar hoja de información complementaria		
APELLIDOS		NOMBRES	NACIONALIDAD
1. SURI	Anish		US
2. SHERIFF	Steven		US
3. SUCHARD	Suzanne		US
4. YAMNIUK	Aaron		CA
5. KRYSTEK	Stanley		US
DIRECCIÓN DE CORREO ELECTRÓNICO:			
8	DATOS INVENTOR (ES)		
PAÍS RESIDENCIA	DEPARTAMENTO/ESTADO	CIUDAD	DIRECCIÓN
1. Estados Unidos de América	New Jersey	Princeton	Route 206 & Province Line Road Princeton, New Jersey 08543-4000
2. Estados Unidos de América	New Jersey	Princeton	Route 206 & Province Line Road Princeton, New Jersey 08543-4000
3. Estados Unidos de América	New Jersey	Princeton	Route 206 & Province Line Road Princeton, New Jersey 08543-4000
4. Estados Unidos de América	New Jersey	Princeton	Route 206 & Province Line Road Princeton, New Jersey 08543-4000

5. Estados Unidos de América	New Jersey	Princeton	Route 206 & Province Line Road Princeton, New Jersey 08543-4000
OTRO(S) SOLICITANTE(S) Y/O (OTRO(S)) INVENTOR(ES)			
☒ Los demás solicitantes y/o (demás) inventores se indican en una hoja a continuación.			
9	☐ REPRESENTANTE LEGAL		☒ APODERADO
APELLIDOS Correa Ordóñez		NOMBRES Álvaro	IDENTIFICACIÓN C.C. 79.143.366 T.P. 20.281
DIRECCIÓN	Av. 82 No. 10-62, Piso 5		No. TELÉFONO 6341500
CIUDAD	Bogotá		CORREO ELECTRÓNICO alvaro.correa@bakermckenzie.com
PAÍS	Colombia		No. RADICACIÓN DE PROTOCOLO DE PODER GENERAL

10	DECLARACIONES DE PRIORIDAD ☒ SI ☐ NO		
(33) PAÍS DE ORIGEN		CÓDIGO PAÍS	(31) NÚMERO
1. Estados Unidos de América		US	61/477,904
			(32) FECHA (AAAA/MM/DD) 21/04/2011

11	DECLARACIÓN SOBRE USO DE RECURSOS GENÉTICOS O BIOLÓGICOS
Declaro que el objeto de la presente solicitud de patente fue obtenido a partir de recursos genéticos o biológicos de los que cualquiera de los países miembros de la Comunidad Andina es país de origen. ☐ SI ☒ NO Nota: En caso afirmativo deberá anexar copia del contrato de acceso de recursos genéticos o productos derivados, o certificado o número de registro, expedido por la Autoridad competente.	

12	DECLARACIÓN SOBRE USO DE CONOCIMIENTOS TRADICIONALES
Declaro que el objeto de la presente solicitud de patente fue obtenido a partir de conocimientos tradicionales de comunidades indígenas, afroamericanas o locales de países miembros de la Comunidad Andina. ☐ SI ☒ NO Nota: En caso afirmativo deberá anexar la licencia o autorización de uso de conocimiento tradicional, o certificado, o número de registro expedido por la Autoridad competente.	

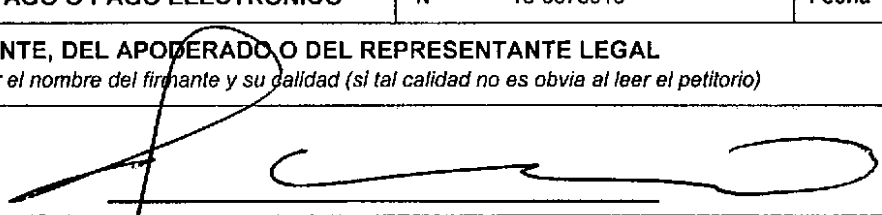
13	REDUCCIÓN DE TASAS
Declaro que carezco de medios económicos para presentar la solicitud de patente. ☐ SI ☒ NO Nota: En caso de ser persona natural y carecer de medios económicos, y por lo tanto, aplique la reducción de tasas a que se refiere la resolución vigente en tarifas, debe firmar la presente solicitud bajo la gravedad de juramento.	
Micro, pequeñas y medianas empresas ☐ Universidades públicas o privadas ☐ Entidades sin ánimo de lucro ☐	

Debe aportar los documentos que se indican en el numeral 17 de anexos

14	AUTORIZACIÓN DE NOTIFICACIÓN EN LÍNEA ☒ SI ☐ NO
Manifiesto que he leído y entendido perfectamente los términos y condiciones de uso de medios electrónicos para las notificaciones en línea a través de Internet de los actos administrativos proferidos por la Superintendencia de Industria y Comercio que deben ser notificados personalmente y, en consecuencia, autorizo el servicio de notificación a través de internet.	

15	COMPROBANTE DE PAGO O PAGO ELECTRÓNICO	N° 13-0078916	Fecha 8 de Agosto de 2013

16	FIRMA DEL SOLICITANTE, DEL APODERADO O DEL REPRESENTANTE LEGAL
Junto a cada firma, indicar el nombre del firmante y su calidad (si tal calidad no es obvia al leer el petitorio)	



17	ANEXOS
Documentación Técnica Solicitud Internacional en castellano 1. ☒ Descripción N° de folios: 2. ☒ Reivindicaciones N° Reivindicaciones: 32 3. ☒ Dibujos y/o figuras N° folios: 7 Documentación Jurídica 9. ☒ Poderes, si fuera el caso. 10. ☐ Documento que legalmente pruebe la cesión del inventor al solicitante o a su causante. 11. ☐ Copia del contrato de acceso de recursos genéticos o productos derivados, certificado o número de registro, si fuera el caso.	

4. ☒ Resumen. 5. ☐ Certificado de depósito de material biológico si fuera el caso. 6. ☒ Listado de secuencias de nucleótidos y/o aminoácidos en forma digital si fuera el caso. 7. ☐ Arte final 12 x 12. 8. ☒ Anexo formato digital.	12. ☐ Copia de la licencia o autorización de Conocimientos Tradicionales, certificado o número de registro, si fuera el caso. 13. Reducción de tasas Micro, pequeñas o medianas empresas ☐ Copia simple de la declaración de renta del año inmediatamente anterior, o en su defecto prueba documental idónea. ☐ Documento de constancia de cumplimiento con lo establecido en la ley 905 de 2004. Universidades públicas o privadas ☐ Copia acto de reconocimiento institucional emitido por el Ministerio de Educación Entidades sin ánimo de lucro ☐ Copia de registro vigente en Cámara de comercio. ☐ Hoja de información complementaria. ☐ Otros, especificar 14. ☐ Comprobante de pago de la tasa de presentación de la solicitud. 15. ☐ Comprobante de pago por reivindicación de prioridad. 16. ☐ Comprobante de pago de la tasa por concepto de excedente de palabras en la publicación. 17. ☐ Comprobante de pago por reivindicación adicional a 10.

1	(12) TIPO DE SOLICITUD		NUMERO DE RADICACIÓN	
☐ Patente de invención			FECHA DE PRESENTACIÓN	
☐ Patente de Modelo de Utilidad				
4	(71) SOLICITANTE (S)			
APELLIDOS O RAZÓN SOCIAL		NOMBRE	IDENTIFICACIÓN	TIPO
2.				
3.				
4.				
5	DATOS DEL SOLICITANTE			
PAÍS DE RESIDENCIA		DEPARTAMENTO/ESTADO	CIUDAD	DIRECCIÓN
2.				
3.				
4.				
TELÉFONO		FAX	E-MAIL	NACIONALIDAD
2.				
3.				
4.				
6	(72) INVENTOR (ES)			
APELLIDOS		NOMBRE	NACIONALIDAD	
6. TAMURA		James	US	
7. BRYSON		James	US	
8. GRANT		Steven	GB	
9. DREW		Philip	GB	
7	DATOS INVENTOR (ES)			
DIRECCIÓN		CIUDAD	DEPARTAMENTO/ESTADO	PAÍS RESIDENCIA
6. Route 206 & Province Line Road Princeton, New Jersey 08543-4000		New Jersey	Princeton	Estados Unidos de América
7. Route 206 & Province Line Road Princeton, New Jersey 08543-4000		New Jersey	Princeton	Estados Unidos de América
8. 315 Cambridge Science Park Cambridge Cambridgeshire CB4 0WG		Cambridgeshire	Cambridge	Reino Unido
9. 315 Cambridge Science Park Cambridge Cambridgeshire CB4 0WG		Cambridgeshire	Cambridge	Reino Unido
9	(30) DECLARACIONES DE PRIORIDAD			

RECIBO DE PAGO

3013/0315

SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO
NIT : 800.176.089-2
- / -

 Industria y Comercio SUPERINTENDENCIA	RECIBO DE CAJA	No. 13 - 0078916
		Bogotá D.C., Agosto 08 de 2013 - 16:36:29

RECIBIDO DE : BAKER					NI 900.532.339	
*** Soporte del Pago ***						
TIPO PAGO	BANCO	CUENTA	No. PAGO	FECHA PAGO	VR. PAGO	
CONSIGNACION	BANCO DE BOGOTA	062754387	545480563	08/08/2013	105.402.000.00	

*** Conceptos Pagados ***				
CANT.	RENTISTICO	CONCEPTO	Vr. UNDITARIO	Vr. CONCEPTO
1	50005-01-01 SOLICITUDES	1. TRAMITES DE SOL. DE PATENTE DE INVENCIÓN	500.000.00	500.000.00
				\$500.000.00
=====				

SON: **QUINIENTOS MIL PESOS MONEDA CORRIENTE**

Responsable: _____
- *-
Recibo de Caja Aplicado al Expediente No. _____

SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO

No. 13-261140- -00000-0000
Fecha: 2013-11-05 16:49:37 Dep. 2020 DIR.NUEVASCR
Tra. 11 PATENTEIYII Eve: 379 FASENACIONALI
Act. 411 PRESENTACION Folios: 8



SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO			
DIVISION DE NUEVAS CREACIONES			
TARJETA ARCHIVO TEMATICO			
PATENTE DE INVENCION		PCT	MODELO DE UTILIDAD
		X	DISEÑO INDUSTRIAL
(21) N° de solicitud:		(22) Fecha de solicitud:	
(51) Clasificación Internacional :			
(71) Solicitante(s)			
BRISTOL-MYERS SQUIBB COMPANY Y DOMANTIS LIMITED			
(72) Inventor(es)			
SURI, Anish - SHERIFF, Steven - SUCHARD, Suzanne - YAMNIUK, Aaron - KRYSTEK, Stanley - TAMURA, James - BRYSON, James - GRANT, Steven - DREW, Philip			
(74) Apoderado: ALVARO CORREA ORDOÑEZ			
(30) Prioridad	(31) No. Prioridad	(32) Fecha	(33) País
	61/477,904	21/04/2011	US
(85) Fecha límite inicio fase nacional: 21/11/2013		(87) Publicación internacional:	
(86) Datos relativos a la presentación de la solíc. PCT		Fecha: 26/10/2012	
Fecha de presentación de la solicitud: 20/04/2012		No. Publicación : WO/2012/145673	
No. de solicitud PCT/US2012/034519			
(54) Título: POLIPEPTIDOS ANTICUERPOS QUE ANTAGONIZAN CD40			
(57) Resumen:			
Se proporcionan los polipéptidos anticuerpos que se enlazan específicamente a un nuevo epítipo de CD40 humano. Los polipéptidos anticuerpos no muestran actividad agonista de CD40. Los polipéptidos anticuerpos son útiles en el tratamiento de trastornos que involucran la activación de CD40, tales como los trastornos autoinmunitarios. Los polipéptidos anticuerpos pueden ser anticuerpos de dominio (dAbs) que comprenden un dominio simple de VL o VH. La vida media de los polipéptidos anticuerpos puede ser incrementada por modificación de los polipéptidos anticuerpos para ser reactivos específicos dobles que pueden también reticularse a la albúmina sérica humana (HSA).			

SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO			
DIVISION DE NUEVAS CREACIONES			
TARJETA ARCHIVO PROPIETARIOS			
PATENTE DE INVENCION ____ PCT ☒ MODELO DE UTILIDAD ____ DISEÑO INDUSTRIAL ____			
(21) N° de solicitud:		(22) Fecha de solicitud:	
(51) Clasificación Internacional :			
(71) Solicitante(s)			
BRISTOL-MYERS SQUIBB COMPANY Y DOMANTIS LIMITED			
(72) Inventor(es)			
SURI, Anish - SHERIFF, Steven - SUCHARD, Suzanne - YAMNIUK, Aaron - KRYSTEK, Stanley - TAMURA, James BRYSON, James - GRANT, Steven - DREW, Philip			
(74) Apoderado: ALVARO CORREA ORDÓÑEZ			
(30) Prioridad	(31) No. Prioridad	(32) Fecha	(33) País
	61/477,904	21/04/2011	US
(85) Fecha inicio fase nacional: 21/11/2013		(87) Publicación internacional	
(86) Datos relativos a la presentación de la solicitud PCT		Fecha: 26/10/2012	
Fecha de presentación de la solicitud: 20/04/2012		N° publicación: WO/2012/145673	
No. de solicitud PCT/US2012/034519			
(54) Título: POLIPEPTIDOS ANTICUERPOS QUE ANTAGONIZAN CD40			

PRESENTACIÓN EN CD

		PLANILLA DE RADICACIÓN - DIGITALIZACIÓN DIARIA RELACIÓN DE ANEXOS	
Dependencia: 2020		Fecha: 13 / 11 / 05 AAAA MM DD	Recorrido: 3
Tipo de Radicación: Entrada: ☒ Salida: ☐ Traslado: ☐ Convenio: ☐			
Radicator:			Planilla:

ID	No. Radicación	Consecutivo	Item
1	13 - 261140 -	0	7
2			
3			
4			
5			
6			
7			
8			
9			
10			
11			
12			
13			
14			
15			
16			
17			

Item	Unidad de Conservación
1	Bolsa
2	Caja
3	Libro
4	Sobre
5	Tomo
6	Otro
Item	Soporte Documental
☒	CD
8	Disquete
9	DVD
10	Folleto
11	Foto
12	Periódico
13	Plano
14	Publicación Periódica
15	USB
16	Otro

Observaciones:
El C.D ANEXO CONTIENE UN TOTAL DE 6 ARCHIVOS.
6 EN FORMATO P.D.F, LOS CUALES FUERON PROCESADOS

cc



No. 13-261140- -00000-0000

Fecha: 2013-11-05 16:49:37 Dep. 2020 DIR.NUEVASCR
Tra. 11 PATENTEIYII Eve: 379 FASENACIONALI
Act. 411 PRESENTACION Folios: 8

PATENTE DE INVENCION ☐

MODELO DE UTILIDAD ☐

Art 33 Decisión 486/00

☐	Indicación que se solicita una patente.
☐	Datos de identificación del solicitante o de la persona que presenta la solicitud
☐	Descripción de la invención
☐	Dibujos de ser estos pertinentes
☐	Comprobante de pago de las tasas establecidas (De ser el caso formato de descuento)
Completa ☐	Incompleta ☐

PATENTE DE INVENCION PCT ☒

MODELO DE UTILIDAD PCT ☐

Art.33 Decisión 486/00, Circular Única

☒	Indicación que se solicita una PCT
☒	Copia de la solicitud en español, tal como fue presentada inicialmente (capítulo descriptivo, reivindicatorio, resumen)
☐	Dibujos de ser estos pertinentes
☒	Comprobante de pago de las tasas establecidas (de ser el caso formato de descuento)
Completa ☒	Incompleta ☐

DISEÑO INDUSTRIAL ☐

(Art. 119 Decisión 486/00)

☐	Indicación que se solicita Diseño industrial
☐	Datos de identificación del solicitante o de la persona que presenta la solicitud
☐	Representación gráfica y fotográfica del Diseño industrial o muestra del material que incorpora el diseño
☐	Comprobante de pago de las tasas establecidas
Completa ☐	Incompleta ☐

ESQUEMA DE TRAZADO ☐

(Art. 92 Decisión 486/00)

☐	Indicación que se solicita un esquema de trazado
☐	Datos de identificación del solicitante o de la persona que presenta la solicitud
☐	Representación gráfica de un esquema de trazado
☐	Comprobante de pago de las tasas establecidas
Completa ☐	Incompleta ☐

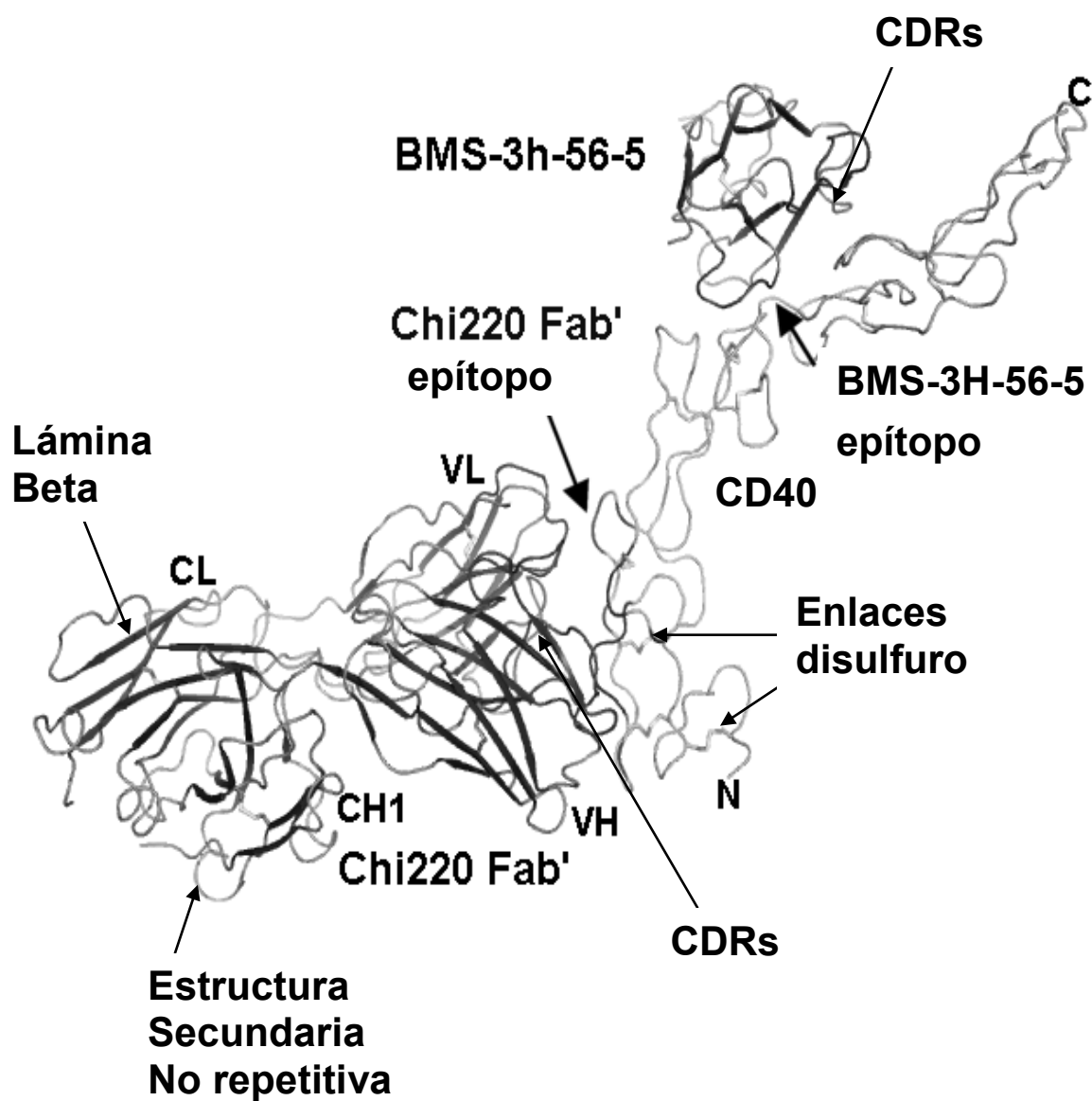
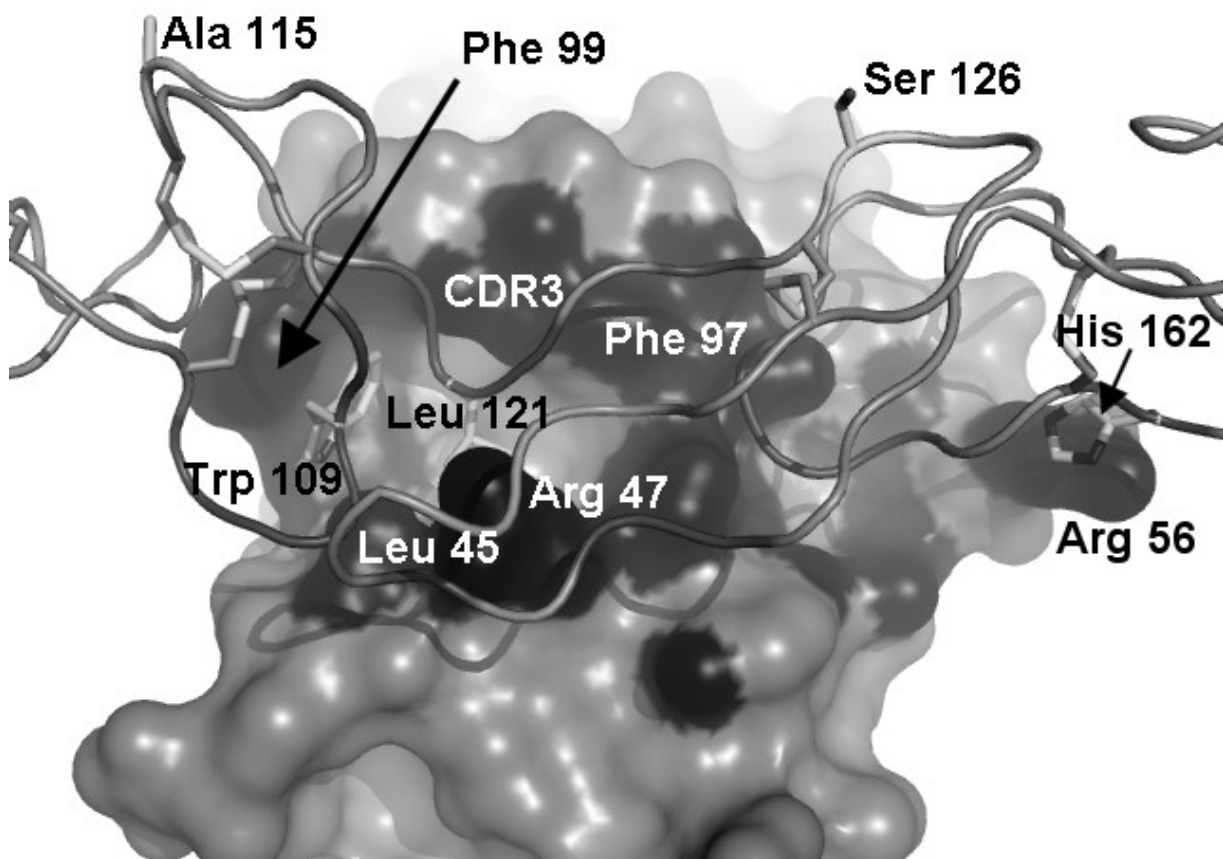
FIG. 1

FIG. 2

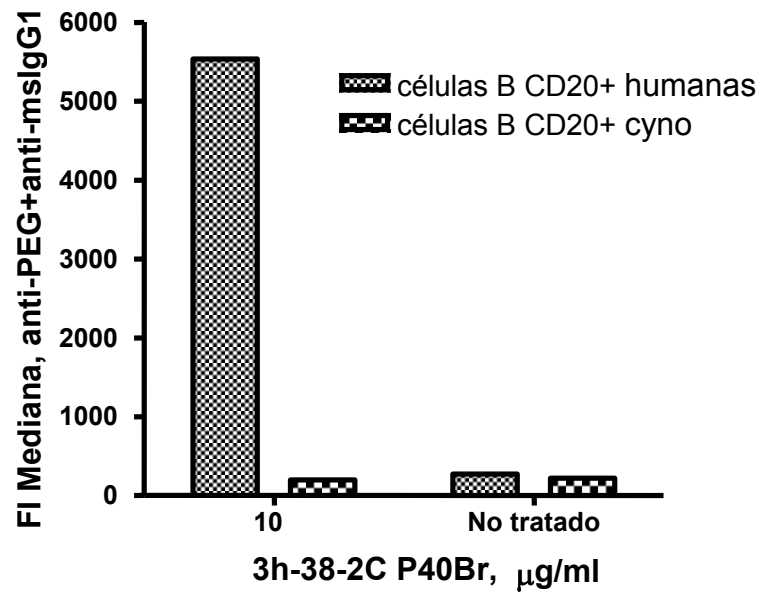
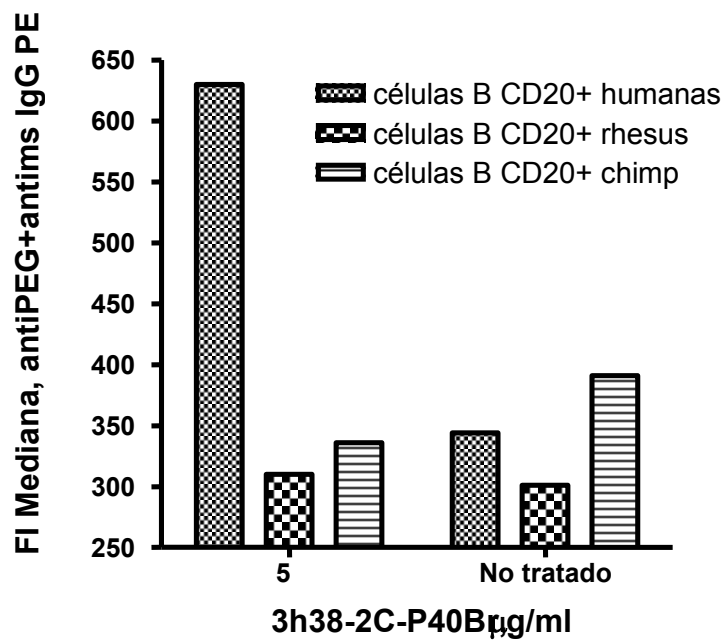
**FIG. 3A****FIG. 3B**

FIG. 4

SEQ ID NO:	CDR1	CDR2	CDR3
SEQ ID NO:9	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPQGTRITYYADSVKGRFTISRDN
SEQ ID NO:10	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPQGTRITYYADSVKGRFTISRDN
SEQ ID NO:353	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPQGTRITYYADSVKGRFTISRDN
SEQ ID NO:355	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPQGTRITYYADSVKGRFTISRDN
SEQ ID NO:410	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPQGTRITYYADSVKGRFTISRDN
SEQ ID NO:413	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPQGTRITYYADSVKGRFTISRDN
SEQ ID NO:418	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPQGTRITYYADSVKGRFTISRDN
SEQ ID NO:352	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPQGTRITYYADSVKGRFTISRDN
SEQ ID NO:324	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPQGTRITYYADSVKGRFTISRDN
SEQ ID NO:334	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPQGTRITYYADSVKGRFTISRDN
SEQ ID NO:317	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPQGTRITYYADSVKGRFTISRDN
SEQ ID NO:336	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPQGTRITYYADSVKGRFTISRDN
SEQ ID NO:337	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPQGTRITYYADSVKGRFTISRDN
SEQ ID NO:323	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPQGTRITYYADSVKGRFTISRDN
SEQ ID NO:338	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPQGTRITYYADSVKGRFTISRDN
SEQ ID NO:354	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPQGTRITYYADSVKGRFTISRDN
SEQ ID NO:335	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPQGTRITYYADSVKGRFTISRDN
SEQ ID NO:377	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPYGSLTYYADSVKGRFTISRDN
SEQ ID NO:396	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPYGNLTYYADSVKGRFTISRDN
SEQ ID NO:368	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPYGGLTYYADSVKGRFTISRDN
SEQ ID NO:371	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPPGMLTYYADSVKGRFTISRDN
SEQ ID NO:373	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPWGGYTYYADSVKGRFTISRDN
SEQ ID NO:392	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPWGGLTYYADSVKGRFTISRDN
SEQ ID NO:380	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPWGSHTYYADSVKGRFTISRDN
SEQ ID NO:387	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPWGSLTYYADSVKGRFTISRDN
SEQ ID NO:372	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPWQLTYYADSVKGRFTISRDN
SEQ ID NO:391	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPWGGFTYYADSVKGRFTISRDN
SEQ ID NO:401	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPAGGYTYYADSVKGRFTISRDN
SEQ ID NO:321	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPQGTRITYYADSVKGRFTISRDN
SEQ ID NO:341	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPQGTRITYYADSVKGRFTISRDN
SEQ ID NO:325	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPQGTRITYYADSVKGRFTISRDN
SEQ ID NO:342	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPQGTRITYYADSVKGRFTISRDN
SEQ ID NO:344	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPQGTRITYYADSVKGRFTISRDN
SEQ ID NO:345	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPQGTRITYYADSVKGRFTISRDN
SEQ ID NO:332	EVQLLESGGGLVQPGGSLRLS	CAASGFTFRDYEMWVVRQAPGKGLERVS	AINPQGTRITYYADSVKGRFTISRDN

FIG. 5

	CDR1	CDR2	
BMS3h-37-207	EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRRAPGKGLEWVSAISGDGYRTYY	60	
BMS3h-37-213	EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRRAPGKGLEWVSAISGDGYRTYY	60	
BMS3h-37-212	EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRRAPGKGLEWVSAISGDGYRTYY	60	
BMS3h-37-205	EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRRAPGKGLEWVSAISGDGYRTYY	60	
BMS3h-37-206	EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRRAPGKGLEWVSAISGDGYRTYY	60	

	CDR2	CDR3	
BMS3h-37-207	ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKELAFFDYWGRGTLVTVSS	116 (SEQ ID NO: 226)	
BMS3h-37-213	ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKELLFFDYRGRGTLVTVSS	116 (SEQ ID NO: 232)	
BMS3h-37-212	ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKELEFFDYWGRGTLVTVSS	116 (SEQ ID NO: 231)	
BMS3h-37-205	ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKELEYFDYWGRGTLVTVSS	116 (SEQ ID NO: 224)	
BMS3h-37-206	ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKLEYFDYWGRGTLVTVSS	116 (SEQ ID NO: 225)	

FIG. 6

	CDR1	CDR2	
BMS3h-38-217	EVQLLASGGGLVQPGGSLRLS	CAASGFTFE	EEEMIWVRQAPGKGLEWVSAISR
BMS3h-38-238	EVQLLASGGGLVQPGGSLRLS	CAASGFTFE	EEEMIWVRQAPGKGLEWVSAISR
BMS3h-38-228	EVQLLASGGGLVQPGGSLRLS	CAASGFTFE	EEEMIWVRQAPGKGLEWVSAISR
BMS3h-38-235	EVQLLASGGGLVQPGGSLRLS	CAASGFTFE	EEEMIWVRQAPGKGLEWVSAISR
BMS3h-38-231	EVQLLASGGGLVQPGGSLRLS	CAASGFTFE	EEEMIWVRQAPGKGLEWVSAISR
BMS3h-38-237	EVQLLASGGGLVQPGGSLRLS	CAASGFTFE	EEEMIWVRQAPGKGLEWVSAISR
BMS3h-38-218	EVQLLASGGGLVQPGGSLRLS	CAASGFTFE	EEEMIWVRQAPGKGLEWVSAISR
BMS3h-38-215	EVQLLASGGGLVQPGGSLRLS	CAASGFTFE	EEEMIWVRQAPGKGLEWVSAISR
BMS3h-38-223	EVQLLASGGGLVQPGGSLRLS	CAASGFTFE	EEEMIWVRQAPGKGLEWVSAISR
BMS3h-38-224	EVQLLASGGGLVQPGGSLRLS	CAASGFTFE	EEEMIWVRQAPGKGLEWVSAISR
BMS3h-38-225	EVQLLASGGGLVQPGGSLRLS	CAASGFTFE	EEEMIWVRQAPGKGLEWVSAISR
BMS3h-38-219	EVQLLASGGGLVQPGGSLRLS	CAASGFTFE	EEEMIWVRQAPGKGLEWVSAISR
	*****	*****	***

	CDR2	CDR3	
BMS3h-38-217	ADSVKGRFTISRDN	SKNTLYLQMN	SLRAEDTAVYYCGKEPFRYDYGQGLVTVSS 116 (SEQ ID NO: 264)
BMS3h-38-238	ADSVKGRFTISRDN	SKNTLYLQMN	SLRAEDTAVYYCGKEPFRYDYGQGLVTVSS 116 (SEQ ID NO: 285)
BMS3h-38-228	ADSVKGRFTISRDN	SKNTLYLQMN	SLRAEDTAVYYCGKEPFRYDYGQGLVTVSS 116 (SEQ ID NO: 275)
BMS3h-38-235	ADSVKGRFTISRDN	SKNTLYLQMN	SLRAEDTAVYYCGKEPFRYDYGQGLVTVSS 116 (SEQ ID NO: 282)
BMS3h-38-231	ADSVKGRFTISRDN	SKNTLYLQMN	SLRAEDTAVYYCGKEPFRYDYGQGLVTVSS 116 (SEQ ID NO: 278)
BMS3h-38-237	ADSVKGRFTISRDN	SKNTLYLQMN	SLRAEDTAVYYCGKEPFRYDYGQGLVTVSS 116 (SEQ ID NO: 284)
BMS3h-38-218	ADSVKGRFTISRDN	SKNTLYLQMN	SLRAEDTAVYYCGKEPFRYDYGQGLVTVSS 116 (SEQ ID NO: 265)
BMS3h-38-215	ADSVKGRFTISRDN	SKNTLYLQMN	SLRAEDTAVYYCGKEPFRYDYGQGLVTVSS 116 (SEQ ID NO: 262)
BMS3h-38-223	ADSVKGRFTISRDN	SKNTLYLQMN	SLRAEDTAVYYCGKEPFRYDYGQGLVTVSS 116 (SEQ ID NO: 270)
BMS3h-38-224	ADSVKGRFTISRDN	SKNTLYLQMN	SLRAEDTAVYYCGKEPFRYDYGQGLVTVSS 116 (SEQ ID NO: 271)
BMS3h-38-225	ADSVKGRFTISRDN	SKNTLYLQMN	SLRAEDTAVYYCGKEPFRYDYGQGLVTVSS 116 (SEQ ID NO: 272)
BMS3h-38-219	ADSVKGRFTISRDN	SKNTLYLQMN	SLRAEDTAVYYCGKEPFRYDYGQGLVTVSS 116 (SEQ ID NO: 266)
	*****	*****	

FIG. 7

	CDR1	CDR2	
BMS3h-198-22	EVQLLESGGGLVQPGGSLRLSCAASGFTTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYY		60
BMS3h-198-31	EVQLLESGGGLVQPGGSLRLSCAASGFTTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYY		60
BMS3h-198-33	EVQLLESGGGLVQPGGSLRLSCAASGFTTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYY		60
BMS3h-198-19	EVQLLESGGGLVQPGGSLRLSCAASGFTTFAGYELWWVRQAPGKGLERVSAISGSGGSTYY		60
BMS3h-198-38	EVQLLESGGGLVQPGGSLRLSCAASGFTTFAGYELWWVRQAPGKGLERVSAISGSGGSTYY		60
BMS3h-198-14	EVQLLESGGGLVQPGGSLRLSCAASGFTTFAGYEMWWFRQAPGKGLERVSAISGSGGSTYY		60
	***** ** *****		
	CDR2	CDR3	
BMS3h-198-22	ADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCAKEPYSYDYWGHGTLVTVSS		116 (SEQ ID NO: 523)
BMS3h-198-31	ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYHCAKEPYSYDYWGQGLVTVSS		116 (SEQ ID NO: 532)
BMS3h-198-33	ADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCAKEPYSYDYWGQGLVTVSS		116 (SEQ ID NO: 534)
BMS3h-198-19	ADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCARDPYSFDYRGQGLVTVSS		116 (SEQ ID NO: 520)
BMS3h-198-38	ADSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCARDPYSFDYWGQGLVTVSS		116 (SEQ ID NO: 539)
BMS3h-198-14	ADSVKGRFTISRDDTKNTLYLQMNSLRAEDTAVYYCAKDPYSFDYWRQGLVTVSS		116 (SEQ ID NO: 515)
	***** ** *****		

LISTADO DE SECUENCIA

<110> BRISTOL-MYERS SQUIBB COMPANY

<110> DOMANTIS LIMITED

<120> **POLIPÉPTIDOS DE ANTICUERPO QUE ANTAGONIZAN A CD40**

<130> 200896-0004-00-WO (481834)

<140>

<141>

<150> 61/477,904

<151> 2011-05-18

<160> 1287

<170> PatentIn versión 3.5

<210> 1

<211> 277

<212> PRT

<213> Homo sapiens

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Met	Val	Arg	Leu	Pro	Leu	Gln	Cys	Val	Leu	Trp	Gly	Cys	Leu	Leu	Thr
1				5					10					15	

Ala	Val	His	Pro	Glu	Pro	Pro	Thr	Ala	Cys	Arg	Glu	Lys	Gln	Tyr	Leu
			20					25					30		

Ile	Asn	Ser	Gln	Cys	Cys	Ser	Leu	Cys	Gln	Pro	Gly	Gln	Lys	Leu	Val
		35					40					45			

Ser	Asp	Cys	Thr	Glu	Phe	Thr	Glu	Thr	Glu	Cys	Leu	Pro	Cys	Gly	Glu
	50					55					60				

Ser	Glu	Phe	Leu	Asp	Thr	Trp	Asn	Arg	Glu	Thr	His	Cys	His	Gln	His
65					70					75					80

Lys	Tyr	Cys	Asp	Pro	Asn	Leu	Gly	Leu	Arg	Val	Gln	Gln	Lys	Gly	Thr
				85					90					95	

Ser	Glu	Thr	Asp	Thr	Ile	Cys	Thr	Cys	Glu	Glu	Gly	Trp	His	Cys	Thr
			100					105					110		

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

Phe	Gly	Val	Lys	Gln	Ile	Ala	Thr	Gly	Val	Ser	Asp	Thr	Ile	Cys	Glu
	130					135					140				

Pro Cys Pro Val Gly Phe Phe Ser Asn Val Ser Ser Ala Phe Glu Lys
 145 150 155 160

Cys His Pro Trp Thr Ser Cys Glu Thr Lys Asp Leu Val Val Gln Gln
 165 170 175

Ala Gly Thr Asn Lys Thr Asp Val Val Cys Gly Pro Gln Asp Arg Leu
 180 185 190

Arg Ala Leu Val Val Ile Pro Ile Ile Phe Gly Ile Leu Phe Ala Ile
 195 200 205

Leu Leu Val Leu Val Phe Ile Lys Lys Val Ala Lys Lys Pro Thr Asn
 210 215 220

Lys Ala Pro His Pro Lys Gln Glu Pro Gln Glu Ile Asn Phe Pro Asp
 225 230 235 240

Asp Leu Pro Gly Ser Asn Thr Ala Ala Pro Val Gln Glu Thr Leu His
 245 250 255

Gly Cys Gln Pro Val Thr Gln Glu Asp Gly Lys Glu Ser Arg Ile Ser
 260 265 270

Val Gln Glu Arg Gln
 275

<210> 2

<211> 278

<212> PRT

<213> *Macaca fascicularis*

<400> 2

Met Val Arg Leu Pro Leu Gln Cys Val Leu Trp Gly Cys Leu Leu Thr
 1 5 10 15

Ala Val Tyr Pro Glu Pro Pro Thr Ala Cys Arg Glu Lys Gln Tyr Leu
 20 25 30

Ile Asn Ser Gln Cys Cys Ser Leu Cys Gln Pro Gly Gln Lys Leu Val
 35 40 45

Ser Asp Cys Thr Glu Phe Thr Glu Thr Glu Cys Leu Pro Cys Gly Glu
 50 55 60

Ser Glu Phe Leu Asp Thr Trp Asn Arg Glu Thr Arg Cys His Gln His
 65 70 75 80

Lys Tyr Cys Asp Pro Asn Leu Gly Leu Arg Val Gln Gln Lys Gly Thr
85 90 95

Ser Glu Thr Asp Thr Ile Cys Thr Cys Glu Glu Gly Leu His Cys Thr
100 105 110

Ser Glu Ser Cys Glu Ser Cys Val Pro His Arg Ser Cys Leu Pro Gly
115 120 125

Phe Gly Val Lys Gln Ile Ala Thr Gly Val Ser Asp Thr Ile Cys Glu
130 135 140

Pro Cys Pro Val Gly Phe Phe Ser Asn Val Ser Ser Ala Phe Glu Lys
145 150 155 160

Cys Arg Pro Trp Thr Ser Cys Glu Thr Lys Asp Leu Val Val Gln Gln
165 170 175

Ala Gly Thr Asn Lys Thr Asp Val Val Cys Gly Pro Gln Asp Arg Gln
180 185 190

Arg Ala Leu Val Val Ile Pro Ile Cys Leu Gly Ile Leu Phe Val Ile
195 200 205

Leu Leu Leu Val Leu Val Phe Ile Lys Lys Val Ala Lys Lys Pro Asn
210 215 220

Asp Lys Val Pro His Pro Lys Gln Glu Pro Gln Glu Ile Asn Phe Pro
225 230 235 240

Asp Asp Leu Pro Gly Ser Asn Pro Ala Ala Pro Val Gln Glu Thr Leu
245 250 255

His Gly Cys Gln Pro Val Thr Gln Glu Asp Gly Lys Glu Ser Arg Ile
260 265 270

Ser Val Gln Glu Arg Gln
275

<210> 3

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido
Sintético

<400> 3

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser Ala Ala Ala
 115

<210> 4

<211> 25

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Péptido Sintético

<220>

<221> característica_miscelánea

<222> (1)..(25)

<223> Esta secuencia puede abarcar 1 hasta 5 "Gly Gly Gly Gly Ser" unidades de repetición

<400> 4

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser
 20 25

<210> 5

<211> 3

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Péptido Sintético

<400> 5

Ala Ser Thr
1

<210> 6

<211> 6

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Péptido Sintético

<400> 6

Thr Val Ala Ala Pro Ser
1 5

<210> 7

<211> 3

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Péptido Sintético

<400> 7

Thr Val Ala
1

<210> 8

<211> 7

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Péptido Sintético

<400> 8

Ala Ser Thr Ser Gly Pro Ser
1 5

<210> 9

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Poliéptido Sintético

<400> 9

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Tyr Phe Gln Glu Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 10

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 10

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 11

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 11

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Leu Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 12

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 12

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Phe Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 13

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 13

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Glu Tyr
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Gly Asn Gly Ala Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Leu Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 14

<211> 123

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 14

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asn Met Tyr
 20 25 30

Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Ser Arg Arg Gly Phe Thr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Ile Thr Tyr Ala Met Arg Tyr Ala Arg Phe Asp Tyr
 100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 15

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 15

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Ile Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 16

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 16

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

His Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Met Ile Asp Ala Asp Gly Leu Gly Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Pro Gly Pro Gln Phe Gly Gln Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 17

<211> 121

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 17

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
 20 25 30

Asp Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Ser Ala Ser Gly Val Phe Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Thr Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Tyr Pro Asn Arg Phe Ala Leu Asn Asn Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 18

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 18

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Asn Ser Ser Ile Leu Trp Ala
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Glu Ser Ser Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Asn Ala Gly Trp Pro Gly
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 19

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 19

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Ala Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 20

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 20

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 21

<211> 120

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 21

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Thr Ala
 20 25 30

Glu Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Ala Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Val Ser Tyr Val Ala Thr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 22

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 22

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

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

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 23
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 23
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Lys Asn
 20 25 30

Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Glu Ser Asp Gly Gln Ala Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asn Arg Ile Pro Asp Leu Val Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 24
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 24
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Ala Gly
 20 25 30

Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Asp Lys Glu Gly Leu Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Arg Ile Pro Gly Leu Val Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 25

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 25

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asp Ala
 20 25 30

Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Gln Pro Met Gly Asp Gly Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Arg Ile Pro Thr Leu Gln Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 26
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 26
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Asp Ser
 20 25 30

Pro Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Thr Ser Asn Gly Tyr Glu Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Arg Ile Pro Thr Leu His Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 27
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 27
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Glu His
 20 25 30

Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Gly Pro Asp Gly Phe His Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Arg Ile Pro Thr Leu His Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 28

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 28

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Glu Tyr
 20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Arg Ile Pro Ser Leu Thr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 29

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 29

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5					10					15	

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Gly	Thr	Asn
			20					25					30		

Ala	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			

Ser	Arg	Ile	Ser	Pro	Gly	Gly	Asp	Tyr	Thr	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				

Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr
65					70					75				80	

Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	

Ala	Lys	Gly	Arg	Val	Pro	Asp	Leu	Leu	Phe	Asp	Tyr	Trp	Gly	Gln	Gly
			100					105					110		

Thr	Leu	Val	Thr	Val	Ser	Ser
						115

<210> 30

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 30

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5					10					15	

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Pro	Ser	Glu
			20					25					30		

Glu	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			

Ser Arg Ile Ser Ala Asp Gly Ala Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Arg Val Pro Asp Leu Leu Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 31

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 31

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Glu Asp
 20 25 30

Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Ala Val Asp Gly Asp Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Lys Val Pro Ser Leu His Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 32

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 32

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1			5					10						15	

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Arg	Thr	Met
		20						25					30		

Asp	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			

Ser	Arg	Ile	Thr	Gly	Asp	Gly	Met	Asn	Thr	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				

Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr
65					70					75					80

Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Gly	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	

Ala	Lys	Gly	Val	Thr	Pro	Asp	Leu	Thr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly
			100					105						110	

Thr	Leu	Val	Thr	Val	Ser	Ser
						115

<210> 33

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 33

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1			5					10						15	

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Glu	Arg	Asp
			20					25					30		

Asp	Met	Thr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			

Ser Arg Ile Asn Ala Gly Gly Val His Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Val Thr Pro Asp Leu Thr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 34

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 34

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Asp
 20 25 30

Ser Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Ser Ser Asp Gly Ala Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Val Thr Pro Asp Leu Thr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 35
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 35
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Glu Glu
 20 25 30

Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Asp Ser Val Gly Glu Gly Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Val Thr Pro Asp Leu Thr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 36
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 36
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Ser
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Asp Asn Pro Gly Gln His Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Thr Val Pro Thr Leu Glu Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 37

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 37

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Gln His
 20 25 30

Ser Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Asp Gly Gly Gly Tyr Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Glu Val Pro Arg Leu His Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 38
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 38
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Gln Glu
 20 25 30

Pro Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Ala Tyr Asn Gly Gly Asp Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Ile Thr Pro Asn Leu Thr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 39
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 39
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Asn Tyr
 20 25 30

Pro Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Asn Ala Thr Gly Ser Ile Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Val Ile Pro His Leu Met Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 40

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 40

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Thr Gly Thr Gly Asn Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Gln Gly Val Val Pro Tyr Leu Ala Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 41
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 41
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Ala Asp
 20 25 30

Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Asn Val Asp Gly Asp Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Thr Val Pro Thr Leu Glu Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 42
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 42
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Arg Ala
 20 25 30

Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Met Val Pro Asn Leu Val Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 43

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 43

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe His Trp Glu
 20 25 30

Pro Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Asn Ser Ser Gly Trp Asp Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Met Val Pro Asn Leu Val Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 44

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 44

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5					10					15	

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ala	Asp	Glu
			20						25					30	

Pro	Met	Thr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
			35				40					45			

Ser	Arg	Ile	Pro	Pro	Glu	Gly	Ala	Pro	Thr	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				

Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr
65					70					75					80

Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	

Ala	Lys	Gly	Ile	Thr	Pro	Asn	Leu	Thr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly
			100					105						110	

Thr	Leu	Val	Thr	Val	Ser	Ser
						115

<210> 45

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 45

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5					10					15	

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

Asp	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			

Ser Arg Ile Ser Arg Gly Gly Leu Gln Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Ile Val Pro Asp Leu His Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 46

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 46

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Glu Tyr
 20 25 30

Pro Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Asn Gly Asp Gly Ala Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Ile Ile Pro Ala Met Gln Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 47
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 47
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asp Val
 20 25 30

Pro Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Ile Met Pro Ser Leu Thr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 48
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 48
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Tyr
 20 25 30

Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Ser Ala Leu Gly Ala Thr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Gln Leu Pro Ala Leu Glu Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 49

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 49

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Arg Tyr
 20 25 30

Tyr Met Thr Trp Val Arg Gln Ala Pro Gly Lys Asp Leu Glu Trp Val
 35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Arg Ile Pro Asp Leu His Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 50

<211> 122

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 50

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1			5					10						15	

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ala	Asp	Tyr
		20						25					30		

Asp	Met	Thr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35				40						45			

Ser	Arg	Ile	Ser	Pro	Thr	Gly	Gly	Gln	Thr	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				

Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr
65					70					75				80	

Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	

Ala	Lys	Gly	Val	Ile	Pro	Tyr	Leu	Ser	Phe	Ser	Pro	Phe	Asp	Tyr	Trp
			100					105					110		

Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
		115					120		

<210> 51

<211> 122

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 51

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1			5					10						15	

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Lys	Tyr
		20						25					30		

Trp	Met	Gly	Trp	Ala	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35				40						45			

Ser Ser Ile Asp Ser His Gly Ala Gly Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Ala Pro Lys Phe Met Thr Thr Tyr Thr Phe Asp Tyr Trp
 100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 52

<211> 117

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 52

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Leu Ser Tyr
 20 25 30

Pro Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Asp Ser Arg Gly Ser Val Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly His Ser Trp Thr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 53
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 53
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asn Ser
 20 25 30

Asn Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Glu Gly Arg Ile Pro Thr Leu His Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 54
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 54
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Pro Arg
 20 25 30

Arg Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Asp Asp Ile Gly Arg Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Glu Gly Ala Gln Gly Val Leu Leu Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 55

<211> 117

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 55

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Asp Tyr
 20 25 30

Arg Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Thr Ser Gly Glu Leu Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Glu Thr Ala Gly Gln Phe Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 56
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 56
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Glu Tyr
 20 25 30

Glu Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Arg Glu Gly Arg Ala Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Val Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 57
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 57
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
 20 25 30

Glu Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Ser Ser Gly Asn Tyr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Leu Met Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 58

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 58

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Thr Glu
 20 25 30

Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Pro Asn Gly Ala Phe Thr Phe Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Ile Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 59
 <211> 117
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 59
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly His Tyr
 20 25 30

Asp Met Val Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Asn Gly Ala Gly Leu Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Gln Ser Ala Ser Arg Ile Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 60
 <211> 117
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 60
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Tyr
 20 25 30

Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Thr Leu Gly Thr Lys Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Gln Ser Ser Thr His Ile Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 61

<211> 117

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 61

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ile Arg Tyr
 20 25 30

Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Ser Ser Gly Trp Thr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Ser Asp Ala His Ile Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 62

<211> 117

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 62

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1			5					10						15	

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Tyr	Ala	Tyr
		20						25					30		

Glu	Met	Ala	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			

Ser	Ser	Ile	Ser	Asp	Asp	Gly	Thr	Arg	Thr	Tyr	Tyr	Ala	Asp	Ser	Val
		50				55					60				

Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr
65					70					75				80	

Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	

Ala	Lys	Asp	Leu	Gly	Gln	Gly	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu
			100					105					110		

Val	Thr	Val	Ser	Ser
				115

<210> 63

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 63

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1			5					10						15	

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ala	Asp	His
		20						25					30		

Gly	Met	Thr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			

Ser Gly Ile Gly Pro Ser Gly Glu Ala Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Arg Ile Pro Asn Leu Val Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 64

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 64

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Ser Gln
 20 25 30

Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Ser Pro Asn Gly Trp Asp Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Arg Ser Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 65
 <211> 117
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 65
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asp Tyr
 20 25 30

Asp Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Arg His Pro Gly Gly Val Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Ala Val Pro Lys Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 66
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Péptido Sintético
 polypeptide

<400> 66
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Val Tyr
 20 25 30

Trp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Asp Pro Gln Gly Gly Met Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Ala Arg Ile Pro Asn Leu Glu Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 67

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 67

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Glu
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
20 25 30

Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Ala Lys Ile Pro Asn Leu Val Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 68
 <211> 121
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 68
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Ser
 20 25 30

Glu Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Ala His Asn Gly Gly His Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Ala Gly His Pro Gln Gln Thr Glu Ala Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 69
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 69
 Glu Met Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Thr Tyr
 20 25 30

Asp Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Lys Ile Ser Pro Asn Gly Trp Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Tyr Gln Thr His Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 70

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 70

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr
 20 25 30

Asp Met Arg Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Ser Ser Ser Gly Thr Tyr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Tyr Pro Lys Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 71
 <211> 117
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 71
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Glu
 20 25 30

Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Pro Asn Gly Trp Asp Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Arg Thr Arg Ser Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 72
 <211> 120
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 72
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Lys Tyr
 20 25 30

Ile Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Asp Tyr Trp Gly Gln His Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Arg Ser His Leu Ile Pro Leu Gln Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 73

<211> 123

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 73

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
 20 25 30

Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Ser Tyr Val Gly Tyr Tyr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Lys Ala Leu Arg Gly Glu Ala Phe Thr Glu Arg Phe Asp Tyr
 100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 74
 <211> 123
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 74
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Pro Tyr
 20 25 30

Met Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Glu Val Asn Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Trp Val Gly Ser Lys Thr Ser Ser Asp Lys Ser Phe Asp Tyr
 100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 75
 <211> 120
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 75
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Thr Thr
 20 25 30

Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Gly Ser Ala Gly Ala Trp Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Ile Gly Gly His Pro Gln Gly Gln Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 76

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 76

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Arg Glu
 20 25 30

Trp Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Gln Pro Met Gly Gln Thr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Tyr Ser Arg Asn Lys Gly Phe Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 77
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 77
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Ser Glu
 20 25 30

Tyr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Gln Arg Tyr Gly Ser Thr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys His Glu Ser Asn Trp Glu Thr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 78
 <211> 123
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 78
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Val Tyr
 20 25 30

Ser Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Thr Leu Gly Arg Gly Ser Tyr Pro Gly Val Asp Phe Asp Tyr
 100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 79

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 79

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Ser Tyr
 20 25 30

Ala Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Thr Ala Asp Gly Thr Val Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Ser Ile Pro Met Leu Thr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 80
 <211> 120
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 80
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
 20 25 30

Asp Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Pro Asn Gly Thr Gly Ile Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asn Gln Ser Val His His Ala Val Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 81
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 81
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Asn Tyr
 20 25 30

Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Ala Pro His Gly Arg Leu Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Gln Ile Pro Met Leu Asp Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 82

<211> 121

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 82

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr
 20 25 30

Met Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Ser His Phe Gly Asp Ile Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asn Asp Met Val Met Lys Asn Gly Gly Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 83
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 83
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Arg Tyr
 20 25 30

Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Asp Ser Arg Gly Trp Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Leu Val Pro His Leu Arg Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 84
 <211> 117
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 84
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asn Ala
 20 25 30

Gln Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Asp Ala Met Gly Asp Ala Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Lys Val Pro Ser Ile Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 85

<211> 117

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 85

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asn Ala
 20 25 30

Gln Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Asp Ala Met Gly Asp Ala Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Val Ile Pro Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 86
 <211> 118
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 86
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gln Asn Asp
 20 25 30

Arg Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Ala Thr Gly Gly Asp Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gln Thr Gly Thr Asn Arg Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 87
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 87
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Gln Pro
 20 25 30

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Asp Ala Ser Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Arg Ile Pro Asn Leu Val Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 88

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 88

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Glu
 20 25 30

Asn Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Asp Gly Gly Gly Tyr Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Gln Val Pro Glu Leu Leu Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 89
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 89
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Ser Ser
 20 25 30

Asn Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Arg Ile Pro Thr Leu Val Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 90
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 90
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Ser Ser
 20 25 30

Asn Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Arg Ile Pro Asn Leu Val Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 91

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 91

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Asp
 20 25 30

Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Asn Asp Ala Gly Ser Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Thr Ile Pro Leu Leu Glu Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 92
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 92
 Glu Met Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Ser Asp
 20 25 30

Thr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Asp Gly Thr Gly Gly Asp Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Leu Ile Pro Asp Leu Gln Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 93
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 93
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Glu Glu
 20 25 30

Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Ile Gly Gly Gly His Glu Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Thr Ile Pro Leu Leu Glu Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 94

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 94

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Glu
 20 25 30

Asn Met Thr Trp Val Arg Gln Ala Pro Gly Lys Asp Leu Glu Trp Val
 35 40 45

Ser Arg Ile Thr Glu Arg Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Thr Val Pro Thr Leu Glu Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 95
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 95
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Glu Glu
 20 25 30

Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Ile Gly Gly Gly His Glu Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Thr Val Pro Thr Leu Glu Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 96
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 96
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe His Glu Thr
 20 25 30

Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Asn Arg Leu Gly Gln Asp Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Arg Ile Pro Gly Leu Val Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 97

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 97

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Asp
 20 25 30

Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Asn Asp Ala Gly Ser Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Thr Val Pro Thr Leu Glu Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 98
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 98
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Glu
 20 25 30

Asn Met Thr Trp Val Arg Gln Ala Pro Gly Lys Asp Leu Glu Trp Val
 35 40 45

Ser Arg Ile Thr Glu Arg Gly Asp Val Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Arg Ile Pro Thr Leu Val Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 99
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 99
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Asp
 20 25 30

Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Asn Asp Ala Gly Ser Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Ile Thr Pro Asn Leu Thr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 100

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 100

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Glu
 20 25 30

Pro Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Pro Pro Glu Gly Ala Pro Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Leu Ile Pro Asp Leu Gln Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 101
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 101
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gln Asp Ser
 20 25 30

Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ala Ala Pro Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Arg Ile Pro Asn Leu Arg Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 102
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 102
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Ser Asp
 20 25 30

Thr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Asp Gly Thr Gly Gly Asp Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Gln Val Pro Glu Leu Leu Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 103

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 103

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gln Asp Ser
 20 25 30

Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ala Ala Pro Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Arg Ile Pro Asn Leu Val Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 104
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 104

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ala Gly Phe Thr Phe Asp Leu Ala
 20 25 30

Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Asp Glu Asp Gly Ala Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys
 85 90 95

Ala Glu Gly Val Ile Pro Ser Leu Thr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 105
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 105

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Asp Lys
 20 25 30

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

Ser Arg Ile Ser Pro Asp Gly Thr Tyr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys
 85 90 95

Ala Glu Gly Val Ile Pro Ser Leu Thr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 106

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 106

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Glu Asp
 20 25 30

Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Ala Val Asp Gly Asp Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Lys Thr Pro His Leu Val Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 107
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 107
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ala Gly Phe Thr Phe Asp Leu Ala
 20 25 30

Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Asp Glu Asp Gly Ala Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Gln Val Pro Ala Leu Val Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 108
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 108
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Asp Ser
 20 25 30

Met Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Asp Pro Gly Gly Ala Gln Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Val Thr Pro Asp Leu Thr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 109

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 109

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu His Ala
 20 25 30

Asp Met Ser Trp Val Arg Gln Ala Ser Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Asp Asn Ser Gly Gln Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Val Thr Pro Asp Leu Thr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 110
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 110
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Glu Ala
 20 25 30

Glu Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Thr Thr Asp Gly Asp Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Arg Ile Pro Thr Leu His Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 111
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 111
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Ser
 20 25 30

Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Ser Leu Glu Trp Val
 35 40 45

Ser Tyr Ile Arg Gly Asp Asp Asp Glu Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asn Arg Ile Pro Asp Leu Val Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 112

<211> 121

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 112

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

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

Asp Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Pro Asn Gly Trp Asp Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys His Ala Ser Thr Glu Gly Pro Thr Ala Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 113
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 113

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Pro Tyr
 20 25 30

Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Trp Ile Ser Ala His Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Trp Pro Tyr Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 114
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 114

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Ser Gly
 20 25 30

Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Gly Ser Asn Gly Ala Asp Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Met Val Pro Asn Leu Val Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 115

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 115

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Arg Phe
 20 25 30

Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Arg Ile Pro Asn Leu Val Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 116
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 116
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Glu Ser
 20 25 30

Asp Met Lys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Pro Asn Gly Trp Asp Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Ser Pro Ser Ser Arg Leu Lys Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 117
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 117
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Ser Ser
 20 25 30

Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Glu Asn Gln Gly Gly Ala Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Arg Ile Pro Asn Leu Val Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 118

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 118

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Asp Ala Tyr
 20 25 30

Pro Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Trp Ile Ala Ser Gly Gly Gly Ala Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Arg Thr Lys Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 119
 <211> 120
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 119
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Met Ser Tyr
 20 25 30

Ser Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Thr Ser Asn Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Ser Thr Gly Ala Asn Ser Arg Asn Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 120
 <211> 121
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 120
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Gly Tyr
 20 25 30

Leu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ala Ala Asn Gly Met Gln Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Lys Pro Arg Gly Ile Trp Asp Gly Asp Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 121

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 121

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe His Glu Ser
 20 25 30

Thr Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Arg His Pro Gly Glu Phe Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Leu Ile Pro Asp Leu Gln Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 122
 <211> 121
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 122
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Met Tyr
 20 25 30

Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ala Pro Pro Gly Gly Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gln Ser Leu Thr Gly Tyr Ser Arg Ser Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 123
 <211> 120
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 123
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

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

Pro Met Ser Trp Val Arg His Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Tyr Ser Gln Gln Pro Gly Arg Arg Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 124

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 124

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asn Tyr
 20 25 30

His Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Pro Asp Ser Gly Lys Gln Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Arg Ile Pro Ser Leu Leu Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 125
 <211> 120
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 125
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gln Tyr
 20 25 30

His Met Arg Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Asn Asp Ile Gly Ser Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Val Gly Gly Arg Gly Ser Phe Ser Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 126
 <211> 120
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 126
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Asp Met Lys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Ser Ala Ser Gly Val Phe Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Arg Glu His Ala Gly Gln Pro Pro Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 127

<211> 120

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 127

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Gly Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Asn Ala Asn Gly Lys Tyr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Lys Leu Thr Leu Ala Ser Asn Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 128
 <211> 121
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 128
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Met Asp Tyr
 20 25 30

Asp Met Lys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Thr Ala Leu Gly Lys Lys Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Ser Val Lys Tyr Pro Leu Asn Leu Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 129
 <211> 120
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 129
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro His Tyr
 20 25 30

Thr Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Gln Ser Pro Gly Trp Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Tyr Gly Asp Gly Leu Pro Leu Thr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 130

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 130

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Thr
 20 25 30

Pro Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Gly Asp Glu Gly Gln Glu Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Val Thr Pro Asp Leu Thr Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 131
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 131
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Ser
 20 25 30

Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Gly Ser Asp Gly Pro Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Arg Ile Pro Thr Leu His Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 132
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 132
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Pro Gly
 20 25 30

Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Asp Gly Ser Gly Ser Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Arg Ile Pro Thr Leu His Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 133

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 133

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Glu Ser
 20 25 30

Met Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Gly Tyr Pro Gly Ala Thr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Gly Ser Arg Asp Asp Asn Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 134
 <211> 124
 <212> PRT
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 134

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Gln His
 20 25 30

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

Ser Ser Ile Ser Val Pro Gly Pro Lys Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Ser Leu Arg Asp Leu Arg Pro Gly Asp Ser Lys Ser Phe Asp
 100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 135
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 135

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Ser Ala
 20 25 30

Ala Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Asn Asp Met Gly Ser Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gln Gly Gly Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 136

<211> 118

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 136

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Tyr Asp
 20 25 30

Arg Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Asp Gly Pro Gly Gly Ala Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Glu Gly Arg Arg Val Pro Asp Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 137
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 137

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Glu Tyr
 20 25 30

Glu Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Asp Pro Phe Gly Ser Glu Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Glu Gly Val Val Pro Asp Leu Asn Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 138
 <211> 120
 <212> PRT
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 138

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Lys Tyr
 20 25 30

Val Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Gly Ser Tyr Gly Gly Ala Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Arg Leu Thr Leu Ser Ala Thr Lys Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 139

<211> 120

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 139

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Asp Tyr
 20 25 30

Val Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Ala His Arg Gly Asp Ile Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Arg Arg Arg Leu Ser Asp Tyr Arg Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 140
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 140
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Gln Phe
 20 25 30

Asp Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Pro Ala Gly Thr Gly Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Ala Gly Asp Arg Ser Ser Leu Phe Asp Tyr Arg Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 141
 <211> 118
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 141
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Asp Thr
 20 25 30

Gly Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Ser Tyr Gly Arg Asp Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Asn Ala Ala Leu Gly Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 142

<211> 118

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 142

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Pro Tyr
 20 25 30

Pro Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Gln Gln Met Ser Ser Gly Val Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 143
 <211> 118
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 143
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

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

Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Asp Ser Ser Gly Gln Leu Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Val Lys Ser Leu Ala Arg Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 144
 <211> 117
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 144
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Glu Ser
 20 25 30

Asp Met Lys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Pro Asn Gly Trp Asp Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Pro Ala Gln Val Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 145

<211> 120

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 145

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Gln Tyr
 20 25 30

Val Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Gly Thr Ser Gly Lys Tyr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Gln Arg Arg Ser Leu Thr Arg Val His Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 146
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 146

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Val Glu
 20 25 30

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

Ser Ala Ile Thr Gly Asp Gly Asp Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Thr Val Ser Trp Asn Gly Arg Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 147
 <211> 117
 <212> PRT
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 147

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Trp Tyr
 20 25 30

Asn Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Ala Pro Ser Gly Ile Ile Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Leu Arg Gly Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 148

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 148

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
 20 25 30

Glu Met Arg Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Ser Ala Gly Thr Asp Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gln Ser Leu Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 149
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 149
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Asp Glu Glu
 20 25 30

Pro Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ile Ile Asp Pro Gly Gly Gly Ala Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Ser Asn Ser Met Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 150
 <211> 121
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 150
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
 20 25 30

Pro Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ala Ser Ser Gly Ile Thr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Phe Thr Arg Leu His Phe Pro Ala Gln Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 151

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 151

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Tyr
 20 25 30

Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Ser Pro Glu Gly Ser Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Arg Pro Tyr Ala Ser Lys Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 152
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 152
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Pro Tyr
 20 25 30

Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Ser His Gln Gly Asn Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Val Ser His His Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 153
 <211> 118
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 153
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
 20 25 30

Asn Met Trp Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Trp Ile Asn Ser Thr Gly Ser Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asn Trp His Arg Gly Arg Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 154

<211> 117

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 154

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Arg Tyr
 20 25 30

Arg Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Asn Arg Leu Gly Gln Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Val Lys Lys His Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 155
 <211> 117
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 155
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala His Tyr
 20 25 30

Asn Met Arg Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Thr Lys Thr Gly Phe Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Ala Gly Gln Phe Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 156
 <211> 118
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 156
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Tyr Pro Tyr
 20 25 30

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

Ser Thr Ile Asp Gly Ser Gly Met Phe Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Glu Asp Ser Leu Lys Ala Ser Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 157

<211> 117

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 157

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Leu Tyr
 20 25 30

Gly Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Tyr Ile Gly Pro Tyr Gly His Thr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Lys Arg Lys Lys Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 158
 <211> 117
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 158
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Arg Tyr
 20 25 30

Arg Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Thr Pro Tyr Gly Ala His Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Tyr Gly Lys Trp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 159
 <211> 117
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 159
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Glu Tyr
 20 25 30

Ala Met Arg Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Asp Arg Leu Gly Leu His Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Ser Gly Pro Phe Thr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 160

<211> 117

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 160

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Arg Tyr
 20 25 30

Asn Met Arg Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Asp Arg Leu Gly Leu Ala Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Ala Gly Ser Trp Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 161
 <211> 118
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 161
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Ile Tyr
 20 25 30

Asp Met Lys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Ser Ser Ser Gly Thr His Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Tyr Pro Gln Pro Tyr Pro Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 162
 <211> 118
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 162
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Trp Val Tyr
 20 25 30

Asp Met Arg Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Ser Ala Thr Gly Val His Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Tyr Pro Pro Ala Gly Arg Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 163

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 163

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
 20 25 30

Asp Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Pro Asn Gly Thr Gly Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Pro Pro Gln Val Asn Thr Glu Phe Asp Tyr Arg Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 164
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 164
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Lys Glu
 20 25 30

Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser His Ile Ser Pro Asn Gly Tyr Ala Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Ser Trp Ser Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 165
 <211> 118
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 165
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Thr
 20 25 30

Pro Met Glu Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Ser Glu Ser Gly Tyr Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Trp Asn Ser Thr Thr Gly Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 166

<211> 117

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 166

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

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

Asp Met Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Pro Asn Gly Trp Asp Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Glu Ala Pro His Arg Ala Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 167
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 167
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Asp Lys
 20 25 30

Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Asp Ala Leu Gly Asp Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Glu Gly Met Val Pro Arg Leu Lys Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 168
 <211> 114
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 168
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp His
 20 25 30

Ser Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Asp Ile Glu Pro His Gly Val His Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Asn Pro Thr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
 100 105 110

Ser Ser

<210> 169

<211> 122

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 169

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Pro His
 20 25 30

Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Pro Asp Gly Thr Thr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Arg Ser Tyr Ser Trp Asp Arg Gly Trp Thr Phe Asp Tyr Trp
 100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 170
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 170
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Tyr Ala Ser
 20 25 30

Asp Met Lys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Pro Asn Gly Trp Asp Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Ala Asp Tyr Thr Tyr His Ser Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 171
 <211> 117
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 171
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala His Tyr
 20 25 30

Asn Met Arg Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Thr Lys Thr Gly Phe Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Ala Gly Gln Phe Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 172

<211> 118

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 172

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr
 20 25 30

His Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Val Ile Gly Pro Arg Gly Ile Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Ser Pro Ser Arg His Arg Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 173
 <211> 117
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 173
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Glu Tyr
 20 25 30

Ala Met Arg Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Asp Arg Leu Gly Leu His Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Ser Gly Pro Phe Thr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 174
 <211> 123
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 174
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asn Tyr
 20 25 30

Ser Met Lys Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Thr Pro Asp Gly Trp Tyr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Val Gly Asp Ala Val Trp Gly Trp Ile Gly Gly Phe Asp Tyr
 100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 175

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 175

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asp Tyr
 20 25 30

Gly Met Lys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Thr Ser Asn Gly Asp Phe Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Ser Leu Tyr Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 176
 <211> 123
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 176
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Gly Ser Gly Phe Thr Phe Pro Thr Tyr
 20 25 30

Lys Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Phe Ile Asp Tyr Trp Gly Trp Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Ser Pro Tyr Ser Trp Thr His Asp Ser Pro His Phe Asp Tyr
 100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 177
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 177
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Pro Tyr
 20 25 30

Thr Met Cys Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Cys Ile Ser Asp Ala Gly Ser Phe Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Arg Met Ser Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 178

<211> 122

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 178

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gln Asn Tyr
 20 25 30

Gln Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Ser Gly Thr Gly Lys Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Thr Pro Gln Asn Tyr Phe Ser Val Arg Arg Phe Asp Tyr Trp
 100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 179
 <211> 118
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 179
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Ala Tyr
 20 25 30

Thr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Lys Ile Ser Thr Ser Gly Gly Gln Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Pro Leu Asn Trp Trp Ala Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 180
 <211> 117
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 180
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Ala Tyr
 20 25 30

Pro Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Arg Ile Asp Gly Tyr Gly Arg His Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Ile Ile Pro Asn Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 181

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 181

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Ala Val
 20 25 30

Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Pro Ser Gly Ser Ala Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Arg Val Pro Asp Leu Gly Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 182
 <211> 117
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 182
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Ser Tyr
 20 25 30

Ala Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Gly Ala Lys Gly Leu Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Ala Ala Arg Gly Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 183
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 183
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Arg Tyr
 20 25 30

Gln Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Val Ile Asn Val Trp Gly Ser Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Met Ser Gly Lys Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 184

<211> 117

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 184

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asn Tyr
 20 25 30

Ser Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Ile Pro Ala Gly Thr Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Pro Ser Ile Arg Leu Phe Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser
 115

<210> 185
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 185
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Ala Tyr
 20 25 30

Asp Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Trp Ile Ser Pro Asn Gly Tyr Asp Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Gly Val Lys Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 186
 <211> 123
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 186
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Trp Tyr
 20 25 30

Glu Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Gln Ala Asp Gly Glu Gln Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Ala Ser Tyr Ala Leu Val Tyr Pro Pro Glu Glu Phe Asp Tyr
 100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 187

<211> 122

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 187

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Asn Tyr
 20 25 30

Arg Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Asp Asp Leu Gly Val Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Trp Arg Leu Lys Asn Ser Gln Pro Thr Asp Phe Asp Tyr Trp
 100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 188
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 188
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Gln Ala
 20 25 30

His Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Phe Ile Asn Pro Ser Gly Tyr Tyr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Pro Ser Leu Ser Pro Ser Ser Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 189
 <211> 118
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 189
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Thr Gly
 20 25 30

Gln Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Asn Ile Asp Gly Ser Gly Thr Tyr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Ser Thr Gln Asn Tyr Arg Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 190

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 190

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Ala Tyr
 20 25 30

Pro Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile His Lys Asp Gly Arg Ile Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gln Gly Thr Pro Val Asp Gly Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 191
 <211> 121
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 191
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Asp Glu
 20 25 30

Gly Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Glu Thr Gly Gly Thr Val Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Met Asp Gly Ser Gly Thr Trp Gln Thr Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 192
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 192
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Ser Leu
 20 25 30

Gly Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Tyr Ile Arg Ala Glu Gly Ala Tyr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Tyr Leu Ala Asp Ser Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 193

<211> 120

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 193

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Glu Ser
 20 25 30

Tyr Met Glu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Asp His Ile Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Asp Gly Arg Gly Gly Ser Met Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 194
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 194
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Gly
 20 25 30

Tyr Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Gly Ala Ser Gly Ala Tyr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Thr Gly Gly Arg Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 195
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 195
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Glu Gly
 20 25 30

His Met Gly Trp Val Arg Gln Ala Pro Gly Lys Asp Leu Glu Trp Val
 35 40 45

Ser Tyr Ile Gly Ser Leu Gly Leu His Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Arg Glu Phe Ser Asn Gly Gly Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 196

<211> 121

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 196

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Lys Thr Ser
 20 25 30

Pro Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Asp Arg Thr Gly Gly His Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gln Ala Leu Leu Thr Asp Ala Lys Arg Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 197
 <211> 120
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 197
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Gly Arg
 20 25 30

Asp Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Pro Ser Gly Leu Asp Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Glu Arg Pro Gln Met Leu Val Thr Asn Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 198
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 198
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Asn Asp
 20 25 30

Pro Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Arg Glu Gly Asp Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Ser Met Arg His Gln Pro Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 199

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 199

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Glu Thr
 20 25 30

Tyr Met Lys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Gly Ala Ser Gly Ala Asp Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Phe Thr His Leu Asn Gly Arg Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 200
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 200
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Gly Trp
 20 25 30

Pro Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Asp Ile Asp Gly Ala Pro Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Glu Ala Gly Ser Trp Ser Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 201
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 201
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Gln
 20 25 30

Ala Met Trp Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Phe Ile Gln Gly Asp Gly Gly Phe Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Pro Ser Lys Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 202

<211> 118

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 202

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Thr Gly
 20 25 30

Gln Met Gly Trp Ala Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Asn Ile Asp Gly Ser Gly Thr Tyr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Ala Val Arg Asn Phe Ala Phe Asp Tyr Trp Gly Gln Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 203
 <211> 124
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 203
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly His
 20 25 30

Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Pro His Gly Thr His Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Ile Arg Gly Trp Ile Gly His Asp Thr Gln Pro Phe Asp
 100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 204
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 204
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Ser Lys
 20 25 30

Asp Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Ser Asp Gly Thr His Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Gln Glu Leu Gly Gly Ser Trp Gln Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 205

<211> 122

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 205

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Arg
 20 25 30

Asp Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Gly Ala Ser Gly Thr Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Gly Thr Gly Pro Thr Asp Leu Trp Asp Phe Asp Tyr Trp
 100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 206
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 206
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Glu
 20 25 30

Lys Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Val Ser Gly Leu His Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Glu Ala Gly Ser Trp Ser Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 207
 <211> 119
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 207
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Gln Glu
 20 25 30

Arg Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Asp Ile Ser Ala Ser Gly Gly Thr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Glu Ala Gly Ser Trp Ser Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 208

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 208

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Met Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Leu Gly Tyr Phe Asp Tyr Arg Gly Arg Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 209
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 209
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Leu Gly Tyr Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 210
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 210
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Leu Gly Tyr Phe Asp Tyr Arg Val Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 211

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 211

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Leu Gly Tyr Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 212
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 212
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Leu Gly Tyr Phe Asp Tyr Arg Val Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 213
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 213
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Glu Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Leu Gly Tyr Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 214

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 214

Glu Val Gln Leu Leu Glu Thr Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asp Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Leu Gly Tyr Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
 100 105 110

Thr Val Thr Ser
 115

<210> 215
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 215
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Leu Gly Tyr Phe His Tyr Trp Gly Arg Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 216
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 216
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Gln Ala Pro Gly Asn Gly Leu Glu Trp Ile
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Leu Gly Tyr Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 217

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 217

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Leu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Leu Gly Tyr Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 218
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 218
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Leu Gly Tyr Phe Asp Tyr Arg Gly Arg Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 219
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 219
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Met Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Leu Gly Tyr Phe Asp Tyr Arg Gly Arg Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 220

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 220

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Met Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Leu Gly Tyr Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 221
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 221
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Trp Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Leu Gly Tyr Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 222
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 222
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Leu Leu Tyr Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 223

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 223

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Leu Gly Phe Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 224
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 224
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Leu Glu Tyr Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 225
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 225
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Gly Leu Glu Tyr Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 226

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 226

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Leu Ala Phe Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 227
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 227
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Leu Leu Tyr Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 228
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 228
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Leu Glu Phe Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 229

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 229

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Leu Gln Phe Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 230
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 230
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Leu Leu Phe Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 231
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 231
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Arg Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Leu Glu Phe Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 232

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 232

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Leu Leu Phe Phe Asp Tyr Arg Gly Arg Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 233
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 233
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Glu Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asn Leu Glu Tyr Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 234
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 234
 Glu Val Arg Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Leu Gln Phe Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 235

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 235

Glu Val Gln Leu Leu Gly Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ser Lys Glu Pro Phe Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 236
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 236
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 237
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 237
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 238

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 238

Glu Val Gln Leu Leu Asp Pro Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Lys Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 239
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 239
 Glu Val Gln Leu Leu Gly Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 240
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 240
 Glu Val Gln Leu Leu Glu Pro Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Leu Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ser Lys Glu Pro Phe Arg Phe Asp Tyr Trp Gly Gln Gly Ala Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 241

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 241

Glu Val Gln Leu Leu Asp Pro Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Lys Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Leu Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 242
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 242
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile His Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ser Lys Glu Pro Phe Arg Phe Asp Tyr Arg Gly Leu Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 243
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 243
 Glu Val Gln Leu Leu Asp Pro Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Lys Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Leu Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 244

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 244

Glu Val Gln Leu Leu Asp Ser Gly Gly Gly Phe Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Phe Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 245
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 245
 Glu Val Gln Leu Leu Asp Pro Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Asn Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Arg Glu Pro Phe Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 246
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 246
 Glu Val Arg Leu Leu Glu Ser Gly Glu Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 247

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 247

Glu Val Gln Gln Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 248
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 248
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Tyr Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 249
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 249
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 250

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 250

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Lys
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Phe Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 251
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 251
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Gln Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 252
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 252
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Phe Ala Ala
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 253

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 253

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Arg Pro Gly Thr Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 254
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 254
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Arg Met Gly Phe Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 255
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 255
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Arg Trp Gly His Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 256

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 256

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Arg Leu Gly Trp Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 257
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 257
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Arg Trp Gly Ala Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 258
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 258
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Arg Gln Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 259

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 259

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Val Ser Gly Trp Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 260
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 260
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Arg Trp Gly Trp Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 261
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 261
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 262

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 262

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Leu Gly Trp Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 263
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 263
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Ala Leu Gly Trp Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 264
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 264
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Arg Arg Gly Tyr Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 265

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 265

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Arg His Gly Trp Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 266
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 266
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Arg Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 267
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 267
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Arg Ile Gly Asn Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 268

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 268

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly His Gly Trp Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 269
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 269
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Arg Trp Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 270
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 270
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Met Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 271

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 271

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Pro Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 272
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 272
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 273
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 273
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Leu Tyr Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 274

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 274

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Met Tyr Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 275
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 275
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Arg Asn Gly Phe Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 276
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 276
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Arg Thr Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 277

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 277

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Arg Glu Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 278
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 278
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Pro Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Arg Gln Gly Trp Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 279
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 279
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Arg Gly Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 280

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 280

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Arg Thr Gly Tyr Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 281
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 281
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Arg Asn Gly Arg Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 282
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 282
 Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Arg Asn Gly Tyr Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 283

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 283

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Arg Lys Gly Ser Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 284
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 284

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Arg Gly Gly Trp Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 285
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 285

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Arg Ser Gly Tyr Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 286

<211> 116

<212> PRT

<213> Secuencia Artificial

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<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 286

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Arg Asn Gly Met Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 287

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 287

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Arg Asn Gly Tyr Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 288

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 288

Glu Val Gln Leu Leu Glu Ser Gly Glu Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Glu His
20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Gly Asn Gly Ala Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Leu Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 289

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 289

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Thr Phe Thr Glu Tyr
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

Ser Ser Ile Ser Gly Asn Gly Ala Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
 85 90 95

Ala Lys Glu Pro Leu Arg Phe Asp Tyr Arg Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
115

<210> 290

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 290

Glu Val Gln Leu Leu Glu Pro Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Glu Tyr
20 25 30

Glu Met Ile Trp Val Arg Lys Ala Pro Gly Lys Gly Met Glu Trp Val
35 40 45

Ser Ser Ile Ser Gly Asn Gly Ala Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Leu Arg Phe Gly Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 291

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 291

Glu Val Gln Leu Leu Asp Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Glu Tyr
20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Gly Asn Gly Ala Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Leu Arg Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 292

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 292

Glu Val Gln Leu Leu Gly Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Glu Tyr
 20 25 30

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

Ser Ser Ile Ser Gly Asn Gly Ala Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Leu Arg Tyr Asp Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
115

<210> 293

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 293

Glu Val Gln Pro Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Asn Glu Tyr
20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Gly Asn Gly Ala Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Leu Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 294

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 294

Glu Val Gln Leu Leu Glu Ser Gly Glu Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Glu Tyr
20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Gly Asn Gly Ala Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Leu Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 295

<211> 116

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 295

Glu Val Gln Leu Leu Asp Pro Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Glu Ser
20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Gly Asn Gly Ala Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Leu Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 296

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 296

Glu Val Gln Leu Leu Glu Pro Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Glu Tyr
20 25 30

Glu Met Ile Trp Val Arg Lys Ala Pro Gly Lys Gly Met Glu Trp Val
35 40 45

Ser Ser Ile Ser Gly Asn Gly Ala Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Leu Arg Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 297

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 297

Glu Val Gln Leu Leu Glu Ser Gly Val Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Glu Tyr
20 25 30

Glu Met Ile Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Gly Asn Gly Ala Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Leu Arg Phe Asp Asn Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 298

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 298

Glu Val Gln Leu Leu Glu Ser Arg Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Glu His
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Gly Asn Gly Ala Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Ser Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Leu Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
115

<210> 299

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 299

Glu Val Gln Pro Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Glu Tyr
20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Gly Asn Gly Ala Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Leu Arg Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 300

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 300

Glu Val Gln Leu Leu Glu Ser Ala Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Glu Tyr
20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Gly Asn Gly Ala Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Leu Arg Phe Asp Tyr Trp Gly Gln Gly Ala Leu Val
100 105 110

Thr Val Ser Ser
115

$\langle 210 \rangle$ 301

<211> 116

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 301

Glu Val Gln Leu Leu Glu Pro Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr Glu Tyr
20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Gly Asn Gly Ala Asn Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Leu Arg Phe Asp Asn Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 302

<211> 123

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 302

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asn Met Tyr
20 25 30

Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Arg Arg Gly Phe Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Ile Thr Tyr Asp Leu Arg Tyr Ala Arg Phe Asp Tyr
100 105 110

Ser Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 303

<211> 123

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 303

Glu Glu Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asn Met Tyr
20 25 30

Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Arg Arg Gly Phe Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Ile Thr Tyr Ala Thr Arg Tyr Ala Arg Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 304

$\langle 211 \rangle$ 123

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 304

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asn Met Tyr
20 25 30

Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Arg Arg Gly Phe Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Phe Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Ile Thr Tyr Asp Met Arg Tyr Ala Arg Phe Asp Tyr
100 105 110

Gly Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 305

<211> 123

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 305

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asn Met Tyr
20 25 30

Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Arg Arg Gly Phe Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Ile Thr Tyr Asp Met Arg Tyr Ala Arg Phe Asp Asn
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Asn
115 120

<210> 306

 $\langle 211 \rangle$ 123

<212> PRT

<213> Secuencia Artificial

$\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 306

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asn Thr Tyr
20 25 30

Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Gly Arg Arg Gly Phe Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Ile Thr Tyr Asp Leu Arg Tyr Ala Arg Phe Asp Tyr
100 105 110

Ser Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 307

$\langle 211 \rangle$ 123

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 307

Glu Val Gln Leu Met Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Asn Met Tyr
20 25 30

Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Arg Arg Gly Tyr Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Ile Thr Tyr Asp Met Arg Tyr Ala Arg Phe Asp Tyr
100 105 110

Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 308

$\langle 211 \rangle$ 123

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 308

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ala Phe Asn Met Tyr
20 25 30

Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Arg His Gly Phe Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Ile Thr Tyr Asp Met Arg Tyr Ala Arg Ser Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 309

 $\langle 211 \rangle$ 123

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 309

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asn Met Tyr
20 25 30

Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Arg Arg Gly Phe Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

Ala Lys Glu Pro Ile Thr Tyr Asp Met Arg Tyr Ala Arg Ser Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

$\langle 210 \rangle$ 310

$\langle 211 \rangle$ 123

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

 $\langle 400 \rangle$ 310

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asn Met Tyr
20 25 30

Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Arg Arg Gly Phe Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Ile Thr Tyr Ser Met Arg Tyr Ala Arg Phe Asp Tyr
100 105 110

Ser Gly Leu Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 311

 $\langle 211 \rangle$ 123

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 311

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asn Met Tyr
20 25 30

Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Arg Arg Gly Phe Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Ile Thr Tyr Asp Met Arg Tyr Ala Arg Phe Asp Tyr
100 105 110

Ser Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 312

 $\langle 211 \rangle$ 123

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 312

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asn Met Tyr
20 25 30

Glu Met Ser Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Ser Arg His Gly Phe Thr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Ile Thr Tyr Asp Met Arg Tyr Ala Arg Phe Asp Tyr
 100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 313

<211> 123

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 313

Glu Val Gln Leu Phe Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asn Met Tyr
 20 25 30

Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Ser Arg Arg Gly Phe Thr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Ile Thr Tyr Asp Met Arg Tyr Ala Arg Phe Asp Tyr
 100 105 110

Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 314

<211> 123

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 314

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asn Met Tyr
 20 25 30

Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Ser Arg Arg Gly Phe Thr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Ile Thr Tyr Asp Met Arg Tyr Ala Arg Phe Asp Tyr
 100 105 110

Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 315

<211> 123

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 315

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Ser Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Ser Phe Asn Met Tyr
 20 25 30

Glu Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Arg Arg Gly Phe Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Ile Thr Tyr Asp Met Arg Tyr Ala Arg Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Gly
115 120

<210> 316

$\langle 211 \rangle$ 123

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 316

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asn Met Tyr
20 25 30

Glu Met Ser Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Arg Arg Gly Phe Thr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Ile Thr Tyr Asp Met Arg Tyr Ala Arg Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 317

<211> 116

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 317

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 318

$\langle 211 \rangle$ 116

<212> PRT

<213> Secuencia Artificial

$\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 318

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 319

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 319

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Thr Lys Leu Pro Phe Ile Phe Glu Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
115

<210> 320

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 320

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Met Phe Asp Asp Arg Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 321

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 321

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 322

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 322

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Tyr Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Ile Phe Asp Asn Arg Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
115

<210> 323

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 323

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ser Val Tyr His Cys
85 90 95

Ala Lys Pro Pro Phe Ile Phe Gly Asp Trp Gly Pro Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 324

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 324

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Arg Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 325

<211> 116

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 325

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Met Phe Asp Asp Arg Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 326

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 326

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Val Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Met Phe Asp Asp Arg Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 327

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 327

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Met Phe Asp Asp Arg Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 328

<211> 116

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 328

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Ile Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Leu Lys Leu Pro Phe Ile Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 329

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 329

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr His Cys
85 90 95

Thr Lys Leu Pro Phe Ile Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 330

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 330

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Met Val Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Phe Phe Asp Ser Arg Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 331

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 331

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
115

<210> 332

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 332

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 333

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 333

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Tyr Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 334

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 334

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Val Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
115

<210> 335

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 335

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 336

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 336

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Thr Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 337

<211> 116

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 337

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Leu Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 338

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 338

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr His Cys
85 90 95

Thr Lys Leu Pro Phe Ile Phe Glu Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 339

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 339

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Tyr Ser Phe Asp Ser Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 340

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 340

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys
 85 90 95

Ala Lys Glu Pro Tyr Ser Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
115

<210> 341

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 341

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 342

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 342

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Met Phe Asp Asp Arg Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 343

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 343

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Met Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
115

<210> 344

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 344

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
20 25 30

Glu Leu Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 345

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 345

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
20 25 30

Glu Leu Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Met Phe Asp Asp Arg Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 346

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 346

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
115

<210> 347

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 347

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
20 25 30

Glu Met Trp Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Met Phe Asp Asp Arg Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 348

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 348

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 349

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 349

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Met Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Met Phe Asp Asp Arg Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
115

<210> 350

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 350

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Thr Tyr Phe Ser Asp Arg Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 351

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 351

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Phe Phe Glu Glu Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 352

<211> 116

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 352

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Thr Tyr Phe Lys Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 353

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 353

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Tyr Phe Ser Glu Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 354

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 354

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys
 85 90 95

Ala Lys Leu Pro Met Phe Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Asn
 115

<210> 355

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 355

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Pro Phe Ser Glu Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
115

<210> 356

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 356

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asp Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Tyr Phe Ser Glu Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 357

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 357

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 358

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 358

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Arg Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
115

<210> 359

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 359

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Leu Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 360

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 360

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Met Gly Gly Phe Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 361

<211> 116

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 361

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Trp Gly Ser His Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 362

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 362

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Arg Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 363

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 363

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro His Gly Ser Leu Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 364

<211> 116

<212> PRT

<213> Secuencia Artificial

$\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 364

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 365

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 365

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Trp Gly Ser Leu Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 366

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 366

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 367

<211> 116

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 367

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Asp Ser Gly Phe Thr Phe Pro Pro Val
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 368

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 368

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 369

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 369

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Trp Gly Asn His Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 370

<211> 116

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 370

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro His Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 371

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 371

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Pro Gly Met Leu Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 372

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 372

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Trp Gly Gln Leu Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 373

<211> 116

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 373

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 374

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 374

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 375

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 375

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 376

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 376

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
115

<210> 377

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 377

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 378

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 378

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 379

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 379

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Gly Leu Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
115

<210> 380

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 380

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Trp Gly Ser His Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 381

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 381

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Trp Gly Thr Leu Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Arg Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 382

<211> 116

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 382

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Ala Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 383

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 383

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Trp Gly Gln Leu Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 384

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 384

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro His Gly Gly Leu Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 385

<211> 116

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 385

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Ala Gly Met Leu Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 386

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 386

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro His Gly Thr Leu Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 387

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 387

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Trp Gly Ser Leu Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 388

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 388

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
115

<210> 389

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 389

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Ala Gly Phe Leu Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 390

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 390

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Arg Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 391

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 391

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Phe Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
115

<210> 392

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 392

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Leu Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 393

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 393

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asp Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 394

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 394

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Trp Gly Thr Leu Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
115

<210> 395

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 395

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Arg Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 396

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 396

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 397

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 397

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro His Gly Gly Phe Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
115

<210> 398

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 398

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Ala Gly Phe Tyr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 399

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 399

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Asp Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

$\langle 210 \rangle$ 400

<211> 116

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

 $\langle 400 \rangle$ 400

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro His Gly Ser Leu Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 401

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 401

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Ala Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys
85 90 95

Ala Lys Leu Pro Phe Thr Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 402

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 402

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Trp Phe Thr Glu Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 403

<211> 116

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 403

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Met Phe Ser Asp Arg Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 404

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 404

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Leu Phe Gln Glu Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 405

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 405

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Thr Arg Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 406

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 406

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
115

<210> 407

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 407

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 408

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 408

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Thr Phe Phe Lys Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 409

<211> 116

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 409

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Phe Phe Gln Glu Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 410

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 410

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Gln Leu Phe His Asp Arg Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 411

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 411

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Gln Leu Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 412

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 412

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys
 85 90 95

Ala Lys Leu Pro Phe Gly Phe Ser Glu Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
115

<210> 413

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 413

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Gln Leu Phe Gln Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 414

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 414

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Phe Phe His Glu Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 415

<211> 116

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 415

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro His Tyr Phe Lys Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 416

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 416

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Ser Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Tyr Phe Glu Glu Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 417

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 417

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Arg Phe Ser Asp Arg Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 418

<211> 116

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 418

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Thr Leu Phe Gln Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 419

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 419

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Tyr Phe Ser Glu Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Asn
115

<210> 420

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 420

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Trp Phe Gln Glu Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 421

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 421

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Trp Gly Ser Leu Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Tyr Phe Gln Glu Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
115

<210> 422

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 422

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Trp Gly Ser Leu Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys
85 90 95

Ala Lys Leu Pro Met Phe Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Asn
115

<210> 423

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 423

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Trp Gly Ser Leu Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 424

<211> 116

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 424

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Trp Gly Ser Leu Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Phe Phe Gln Glu Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 425

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 425

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Trp Gly Ser Leu Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Phe Phe His Glu Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 426

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 426

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Phe Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Tyr Phe Gln Glu Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 427

<211> 116

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 427

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Phe Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys
85 90 95

Ala Lys Leu Pro Met Phe Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Asn
115

<210> 428

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 428

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Phe Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 429

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 429

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Phe Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Phe Phe Gln Glu Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 430

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 430

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Phe Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Phe Phe His Glu Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 431

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 431

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Leu Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Tyr Phe Gln Glu Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 432

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 432

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Leu Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys
 85 90 95

Ala Lys Leu Pro Met Phe Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Asn
 115

<210> 433

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 433

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Leu Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 434

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 434

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Leu Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Phe Phe Gln Glu Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 435

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 435

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Trp Gly Gly Leu Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Phe Phe His Glu Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 436

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 436

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys
 85 90 95

Ala Lys Leu Pro Met Phe Phe Glu Asp Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 437

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 437

Glu Val Gln Leu Leu Glu Thr Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
 20 25 30

His Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Met Ile Asp Ala Asp Gly Leu Gly Thr Tyr Tyr Ala Asp Pro Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Lys Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Pro Gly Pro Gln Phe Gly Gln Phe Asp Tyr Leu Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 438

<211> 119

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 438

Glu Val Gln Leu Phe Glu Ser Gly Gly Gly Leu Val Gln Thr Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

His Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Met Ile Asp Ala Asp Gly Leu Gly Lys Tyr Tyr Ala Asp Pro Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Lys Pro Gly Pro Gln Phe Gly Gln Tyr Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 439

<211> 121

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 439

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Ser Gly Tyr
20 25 30

Asp Met Gln Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Thr Ile Ser Ala Ser Gly Val Tyr Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Tyr Pro Asn Arg Phe Ala Leu Asn Ser Phe Asp Tyr Arg Gly
 100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 440

<211> 121

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 440

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
 20 25 30

Asp Met Gln Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
 35 40 45

Ser Thr Ile Ser Ala Ser Gly Val Tyr Thr Tyr Tyr Thr Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Thr Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Thr Lys Tyr Pro Asn Arg Phe Ala Arg Asn Asn Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 441

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 441

Asp Ile Leu Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Asn Ser Ser Ile Leu Trp Ala
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Glu Ala Pro Lys Leu Leu Ile
 35 40 45

Glu Ser Ser Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Asn Ala Val Trp Pro Gly
 85 90 95

Thr Phe Ser Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 442

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 442

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Asp Ser Ser Ile Leu Trp Ala
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Glu Ser Ser Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Asn Ala Val Trp Pro Gly
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 443
 <211> 108
 <212> PRT
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 443

Asp Ile Gln Met Thr Val Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Asp Ser Ser Ile Leu Trp Ala
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Glu Ser Ser Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Asn Ala Val Trp Pro Gly
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 444
 <211> 108
 <212> PRT
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 444

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Asn Ser Ser Ile Leu Trp Ala
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Glu Ser Ser Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Asn Ala Val Trp Pro Gly
85 90 95

Thr Phe Asp Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 445

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 445

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Asn Ser Ser Ile Leu Trp Ala
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Glu Ser Ser Thr Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Asn Ala Val Trp Pro Gly
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 446

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 446

Asp Ile Gln Met Thr Val Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Asn Ser Ser Ile Leu Trp Ala
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Glu Ser Ser Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Asn Ala Val Trp Pro Gly
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 447

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 447

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Asp Ser Ser Ile Leu Trp Ala
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Glu Ser Ser Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Asn Ala Val Trp Pro Gly
 85 90 95

Thr Phe Asp Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 448

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 448

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10					15		

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Asn	Ser	Ser	Ile	Leu	Trp	Ala
			20					25					30		

Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Glu	Leu	Leu	Ile
		35					40					45			

Glu	Ser	Ser	Ser	Gly	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75				80	

Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Val	Gln	Asn	Ala	Val	Trp	Pro	Gly
				85					90					95	

Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg
			100					105			

<210> 449

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 449

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10					15		

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Asn	Ser	Ser	Ile	Leu	Trp	Ala
			20					25					30		

Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Glu	Ser	Ser	Ser	Gly	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Asn Ala Val Trp Pro Gly
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Asn Lys Arg
100 105

<210> 450

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 450

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Asn Ser Ser Ile Leu Trp Ala
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Glu Ser Ser Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Asn Ala Val Trp Pro Gly
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 451

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 451

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Asn Ser Ser Ile Leu Trp Ala
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Glu Ser Ser Ser Gly Leu Gln Ser Gly Ile Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Asn Ala Val Trp Pro Gly
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 452

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 452

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Asn Ser Ser Ile Leu Trp Ala
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Glu Ser Ser Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Asn Ala Val Trp Pro Gly
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 453

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 453

Asp	Ile	Leu	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10					15		

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Asn	Ser	Ser	Ile	Leu	Trp	Ala
			20					25					30		

Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Glu	Ser	Ser	Ser	Gly	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75				80	

Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Val	Gln	Asn	Ala	Val	Trp	Pro	Gly
				85					90					95	

Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg
			100					105			

<210> 454

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 454

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10					15		

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Asn	Ser	Ser	Ile	Leu	Trp	Ala
			20					25					30		

Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Glu	Ser	Ser	Ser	Gly	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

Ser Gly Thr Gly Thr Asp Phe Thr Leu Thr Ile Ser Gly Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Asn Ala Val Trp Pro Gly
85 90 95

Thr Phe Asp Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 455

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 455

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Pro Cys Arg Ala Asn Ser Ser Ile Leu Trp Ala
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Glu Ser Ser Ser Gly Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Ala Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Asn Ala Val Trp Pro Gly
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 456

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 456

Asp Ile Gln Met Ala Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Ala Ser Pro Pro Leu
 85 90 95

Thr Leu Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 457

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 457

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Ser Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Glu Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Ala Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Asn Val Glu Ile Lys Arg
 100 105

<210> 458

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 458

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10					15		

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Thr	Ile	Glu	Arg	Arg
		20						25					30		

Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Tyr	Leu	Ala	Ser	Arg	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75					80

Glu	Asp	Phe	Ala	Ala	Tyr	Tyr	Cys	His	Gln	Tyr	Glu	Ser	Pro	Pro	Leu
				85					90					95	

Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg
			100					105			

<210> 459

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 459

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10					15		

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Arg	Thr	Ile	Glu	Arg	Arg
		20						25					30		

Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Tyr	Leu	Ala	Ser	Arg	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 460

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 460

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Glu Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro
65 70 75 80

Glu Asp Ser Ala Thr Tyr Tyr Cys His Gln Tyr Ala Ser Pro Pro Leu
85 90 95

Thr Leu Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 461

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 461

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Ala Ser Pro Pro Leu
 85 90 95

Thr Leu Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 462

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 462

Asp Ile Gln Ile Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Asp Pro Lys Leu Leu Ile
 35 40 45

Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 463

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 463

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10					15		

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Thr	Ile	Glu	Arg	Arg
			20					25					30		

Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Glu	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Tyr	Leu	Ala	Ser	Arg	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75					80

Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	His	Gln	Tyr	Glu	Ser	Pro	Pro	Leu
				85					90					95	

Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Trp
			100					105			

<210> 464

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 464

Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10					15		

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Thr	Ile	Glu	Arg	Arg
			20					25					30		

Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Tyr	Leu	Ala	Ser	Arg	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 465

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 465

Asp Ile Gln Met Ser Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
85 90 95

Met Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 466

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 466

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Asp Pro Lys Leu Leu Ile
 35 40 45

Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 467

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 467

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 468

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 468

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Phe	Ala	Ser	Val	Gly
1				5				10					15		

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Thr	Ile	Glu	Arg	Arg
		20						25					30		

Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Tyr	Leu	Ala	Ser	Arg	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75					80

Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	His	Gln	Tyr	Glu	Ser	Pro	Pro	Leu
				85					90					95	

Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg
				100					105		

<210> 469

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 469

Asp	Ile	Gln	Met	Thr	Gln	Tyr	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10					15		

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Glu	Arg	Arg
		20						25					30		

Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Glu	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Tyr	Leu	Ala	Ser	Arg	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 470

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 470

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Thr Ile Glu Arg Arg
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Pro Tyr Glu Ser Pro Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 471

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 471

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ala Ile Glu Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Ala Ser Pro Pro Leu
 85 90 95

Thr Leu Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 472

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 472

Asn Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ala Ile Glu Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 473
 <211> 108
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 473
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Gly Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Ser Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 474
 <211> 108
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 474
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 475

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 475

Asp Ile Gln Met Thr Gln Thr Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Glu Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Lys Ile Lys Arg
100 105

<210> 476

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 476

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Ser Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 477

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 477

His Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 478
 <211> 108
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 478
 Asp Val Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Glu Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Leu Thr Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Ala Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 479
 <211> 108
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 479
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Val Ile Lys Arg
100 105

<210> 480

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 480

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 481

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 481

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Glu Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 482

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 482

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Gly Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 483

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 483

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Glu Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Ile Arg
 100 105

<210> 484

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 484

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 485

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 485

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Glu Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Leu Ala Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 486

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 486

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Phe Glu His Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 487

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 487

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Phe Pro Ile Asp Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 488

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 488

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Thr Ile Gly Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 489

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 489

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Gln Ile Gly Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 490

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 490

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Arg Ile Gly Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 491

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 491

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gln Ile Gly Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 492

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 492

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Pro Ile Ala Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 493

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 493

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile Gly Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 494

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 494

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Asn Ile Asp Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 495

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 495

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 496

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 496

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Gly Thr Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 497

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 497

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Val Ile Gly Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 498

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 498

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Ala Ile Gly Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 499

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 499

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Thr Ser Ile Ala Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 500

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 500

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

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

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Leu Ala Thr Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 501

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 501

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Glu Arg Arg
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Leu Ser Ser Lys Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Glu Ser Pro Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 502

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 502

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Thr Ile Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 503

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 503

Glu Val Gln Pro Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Ile
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 504

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 504

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Ser Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Thr Gly Ser Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Pro Tyr Ser Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Ser Val Ser Ser
 115

<210> 505

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 505

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys
 85 90 95

Ala Arg Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 506

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 506

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys
 85 90 95

Ala Lys Glu Pro Tyr Ser Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 507

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 507

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Thr Phe Ala Gly Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Lys Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 508

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 508

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Thr Ile Ala Gly Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Pro Val
 100 105 110

Thr Val Ser Ser
 115

<210> 509

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 509

Glu Val Gln Leu Met Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Tyr Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Arg Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 510

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 510

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 511

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 511

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Thr Ile Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 512
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 512
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Ser Val Ser Ser
 115

<210> 513
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 513
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Ile Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 514

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 514

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Thr Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 515
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 515
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Thr Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Pro Tyr Ser Phe Asp Tyr Trp Arg Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 516
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 516
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Thr Phe Ala Gly Tyr
 20 25 30

Glu Val Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 517

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 517

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Ile
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Lys Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 518

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 518

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 519

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 519

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ala Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 520

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 520

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
 20 25 30

Glu Leu Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Pro Tyr Ser Phe Asp Tyr Arg Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 521
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 521
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Pro Gly Phe Thr Leu Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 522
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 522
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Thr Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Arg Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 523

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 523

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Tyr Ser Tyr Asp Tyr Trp Gly His Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 524

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 524

Glu Val Gln Pro Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Gly Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 525

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 525

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Tyr Ser Phe Asp Ser Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 526

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 526

Glu Ala Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
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<211> 116

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<213> Secuencia Artificial

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<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 527

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Ser Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Tyr Ser Phe Asp His Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

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<211> 116

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<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 528

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
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<211> 116

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<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 529

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Pro Tyr Ser Phe Asp Asn Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

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<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 530
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Glu Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Tyr Ser Phe Asp His Arg Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

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<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 531
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Phe Ala Gly Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Tyr Ser Phe Asp His Arg Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 532

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 532

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys
85 90 95

Ala Lys Glu Pro Tyr Ser Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 533

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<212> PRT

<213> Secuencia Artificial

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<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 533

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Pro Tyr Ser Phe Asp Asn Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

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<211> 116

<212> PRT

<213> Secuencia Artificial

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<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 534

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Tyr Ser Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

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<211> 116

<212> PRT

<213> Secuencia Artificial

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<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 535

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Pro Tyr Ser Phe Asp Asn Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
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<211> 116

<212> PRT

<213> Secuencia Artificial

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<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 536

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr His Cys
 85 90 95

Ala Lys Glu Pro Tyr Ser Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 537

<211> 116

<212> PRT

<213> Secuencia Artificial

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<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 537

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
 20 25 30

Glu Met Trp Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Pro Tyr Ser Phe Asp Asn Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 538

<211> 116

<212> PRT

<213> Secuencia Artificial

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<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 538

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
 20 25 30

Glu Leu Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Asp Pro Tyr Ser Phe Asp Tyr Arg Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

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 <211> 116
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<400> 539
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Tyr
 20 25 30

Glu Leu Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Pro Tyr Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 540
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<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 540
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Thr Ala
 20 25 30

Glu Met Leu Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Ala Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Val Ser Tyr Val Ala Thr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 541

<211> 120

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 541

Glu Val Gln Leu Leu Val Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Thr Ala
 20 25 30

Glu Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Pro Glu Trp Val
 35 40 45

Ser Ser Ile Ser Ala Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Val Ser Tyr Val Ala Thr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 542

<211> 120

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 542

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Thr Ala
 20 25 30

Glu Met Val Trp Val Arg Lys Ala Pro Gly Met Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Ala Ser Gly Gly Tyr Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Met Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Val Ser Tyr Val Ala Thr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Ala Leu Val Thr Val Thr Ser
 115 120

<210> 543

<211> 120

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 543

Glu Val Gln Leu Leu Val Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Thr Ala
20 25 30

Glu Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Ala Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Ser Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Val Ser Tyr Val Ala Thr Phe Asp Tyr Trp Gly His
100 105 110

Gly Ala Leu Val Thr Val Ser Ser
115 120

<210> 544

<211> 120

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 544

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Thr Ala
20 25 30

Glu Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Ala Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Val Ser Tyr Val Ala Thr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 545

<211> 120

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 545

Glu Ala Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Thr Ala
 20 25 30

Glu Met Val Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

Ser Ser Ile Ser Ala Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Leu Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Val Ser Tyr Val Ala Thr Phe Asp Tyr Trp Gly Arg
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 546

<211> 120

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 546

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Thr Ala
 20 25 30

Glu Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Ala Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Ser Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Val Ser Tyr Val Ala Thr Phe Asp Tyr Trp Gly Pro
 100 105 110

Gly Ala Leu Val Thr Val Ser Ser
 115 120

<210> 547

<211> 120

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<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 547

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Thr Ala
 20 25 30

Glu Met Leu Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Ala Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Val Ser Tyr Val Ala Thr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 548

<211> 120

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 548

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Thr Ala
 20 25 30

Glu Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ser Ile Ser Ala Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Glu Pro Val Ser Tyr Val Ala Thr Phe Asp Tyr Trp Gly Pro
 100 105 110

Gly Ala Leu Val Thr Val Ser Ser
 115 120

<210> 549

<211> 120

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 549

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Thr Ala
20 25 30

Glu Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Ala Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Val Tyr Tyr Val Ala Thr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 550

<211> 120

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 550

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Pro Thr Ala
20 25 30

Glu Met Leu Trp Val Arg Lys Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Ala Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Ala Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Glu Pro Val Ser Tyr Val Ala Thr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 551

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 551

Asn Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

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

Leu Thr Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 552

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 552

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

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

Leu Ser Trp Tyr Gln Gln Lys Pro Arg Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu His Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Pro
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 553

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 553

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Thr Ala Ser Val Gly
 1 5 10 15

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

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Val
 35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Pro
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Asn Ile Arg
 100 105

<210> 554

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 554

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10						15	

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	His	Phe	Ile	Ala	Thr	Leu
			20					25					30		

Leu	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Thr	Tyr	Gly	Ser	Leu	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75				80	

Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gly	Gln	Gly	Val	Leu	Trp	Pro	Pro
				85					90					95	

Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg
			100					105			

<210> 555

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 555

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Phe	Leu	Ser	Ala	Ser	Val	Gly
1				5				10						15	

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	His	Phe	Ile	Ala	Thr	Leu
			20					25					30		

Leu	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Thr	Tyr	Gly	Ser	Leu	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75				80	

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 556

$\langle 211 \rangle$ 108

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 556

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Thr Lys Leu Leu Ile
35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 557

<211> 108

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 557

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

Leu Ser Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 558

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 558

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

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

Leu Ser Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 559

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 559

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10						15	

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

Leu	Ser	Trp	Tyr	Gln	His	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Thr	Tyr	Gly	Ser	Met	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75				80	

Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gly	Gln	Gly	Val	Leu	Trp	Pro	Ala
				85					90					95	

Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg
			100					105			

<210> 560

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 560

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10						15	

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

Leu	Ser	Trp	Tyr	Gln	His	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Thr	Tyr	Gly	Ser	Leu	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

Ser	Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75				80	

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 561

$\langle 211 \rangle$ 108

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 561

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Thr Ala Ser Val Gly
1 5 10 15

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

Leu Ser Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 562

<211> 108

<212> PRT

<213> Secuencia Artificial

$\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 562

Asn Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

Leu Ser Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 563

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 563

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

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

Leu Ser Trp Tyr Gln His Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 564

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 564

Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10						15	

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

Leu	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Thr	Lys	Leu	Leu	Ile
		35					40					45			

Thr	Tyr	Gly	Ser	Leu	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75				80	

Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gly	Gln	Gly	Val	Leu	Trp	Pro	Pro
				85					90					95	

Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg
			100					105			

<210> 565

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 565

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Tyr	Ala	Ser	Val	Gly
1				5				10						15	

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Val	Ser	His	Phe	Ile	Gly	Thr	Leu
			20					25					30		

Leu	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Thr	Tyr	Gly	Ser	Leu	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Ser	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75				80	

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gln
100 105

<210> 566

$\langle 211 \rangle$ 108

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 566

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

Leu Ser Trp Tyr Gln Gln Lys Pro Arg Lys Ala Pro Lys Leu Leu Ile
35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 567

<211> 108

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 567

Asp Ile Gln Ile Ile Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Pro
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 568

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 568

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

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

Leu Ser Trp Tyr Gln Leu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 569

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 569

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10						15	

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

Leu	Ser	Trp	Tyr	Gln	Leu	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Thr	Tyr	Gly	Ser	Trp	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75					80

Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gly	Gln	Gly	Val	Leu	Trp	Pro	Ala
				85					90						95

Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Asn	Lys	Arg
			100					105			

<210> 570

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 570

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10						15	

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

Leu	Ser	Trp	Tyr	Gln	Leu	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Thr	Tyr	Gly	Ser	Leu	Leu	Gln	Arg	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75					80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 571

<211> 108

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 571

Asp Ile Gln Met Thr Gln Ala Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

Leu Ser Trp Tyr Gln Leu Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Asn Lys Arg
100 105

<210> 572

<211> 108

<212> PRT

<213> Secuencia Artificial

 $\langle 220 \rangle$

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 572

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Ala Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 573

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 573

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

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

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
 100 105

<210> 574

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 574

Asp	Ile	Leu	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10						15	

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

Leu	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Thr	Tyr	Gly	Ser	Leu	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75					80

Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gly	Gln	Gly	Val	Leu	Trp	Pro	Ala
				85					90						95

Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg
			100					105			

<210> 575

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 575

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10						15	

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

Val	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Thr	Tyr	Gly	Ser	Leu	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75					80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Tyr Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 576

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 576

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

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

Val Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Asn Lys Arg
 100 105

<210> 577

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 577

Asp Ile Lys Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

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

Val Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Tyr Gly Ser Met Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 578

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 578

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser His Phe Ile Gly Thr Leu
 20 25 30

Val Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 579

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 579

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10					15		

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

Leu	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Thr	Tyr	Gly	Ser	Trp	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55				60					

Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75				80	

Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gly	Gln	Gly	Val	Leu	Trp	Pro	Ala
				85					90					95	

Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg
			100					105			

<210> 580

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 580

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10					15		

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

Leu	Ser	Trp	Tyr	Gln	Leu	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Thr	Tyr	Gly	Ser	Trp	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55				60					

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 581

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 581

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Phe Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Glu Val Leu Trp Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 582

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 582

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Phe Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Leu Ala Thr Tyr Tyr Cys Gly Gln Glu Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 583

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 583

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser His Phe Ile Gly Thr Leu
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Phe Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Glu Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 584
 <211> 108
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 584
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu
 20 25 30
 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Phe Gly Thr Glu Phe Thr Leu Thr Ile Gly Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100 105

<210> 585
 <211> 108
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 585
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Thr Leu
 20 25 30
 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Thr Lys Leu Leu Ile
 35 40 45
 Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 586

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 586

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Ala Ser Leu
20 25 30

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
100 105

<210> 587

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 587

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Ala Gln Leu
 20 25 30

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
 100 105

<210> 588

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 588

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Ala Gln Leu
 20 25 30

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Arg Arg
 100 105

<210> 589

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 589

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10					15		

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	His	Tyr	Ile	Ala	Ser	Leu
			20					25					30		

Leu	Ser	Trp	Tyr	Gln	Val	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Thr	Tyr	Gly	Ser	Leu	Leu	Gln	Ser	Gly	Ala	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro
65					70					75				80	

Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gly	Gln	Gly	Val	Leu	Trp	Pro	Ala
				85					90					95	

Thr	Phe	Gly	Gln	Gly	Thr	Thr	Val	Glu	Ile	Lys	Arg
			100					105			

<210> 590

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 590

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10					15		

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

Leu	Ser	Trp	Tyr	Gln	Val	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Thr	Trp	Ala	Ser	Tyr	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
100 105

<210> 591

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 591

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Thr Trp Thr Ser Tyr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
100 105

<210> 592

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 592

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Trp Ser Ser Tyr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
 100 105

<210> 593

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 593

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

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

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Trp Gly Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
 100 105

<210> 594
 <211> 108
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 594
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Ser Leu
 20 25 30
 Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Thr Trp Ala Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95
 Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
 100 105

<210> 595
 <211> 108
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 595
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Gly Ser Leu
 20 25 30
 Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Thr Trp Ser Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
100 105

<210> 596

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 596

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Trp Ile Ala Gln Leu
20 25 30

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
100 105

<210> 597

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 597

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

Leu Arg Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
 100 105

<210> 598

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 598

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Arg Ile Ala Gln Leu
 20 25 30

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
 100 105

<210> 599
 <211> 108
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 599
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Tyr Ile Ala Ser Leu
 20 25 30

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
 100 105

<210> 600
 <211> 108
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 600
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

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

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Arg Phe Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
100 105

<210> 601

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 601

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Thr Tyr Lys Ser Tyr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
100 105

<210> 602

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 602

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Trp Gly Ser Tyr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
 100 105

<210> 603

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 603

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Trp Gly Pro
 20 25 30

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Ser Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
 100 105

<210> 604
 <211> 108
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 604
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Trp Ile Ala Thr Leu
 20 25 30

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
 100 105

<210> 605
 <211> 108
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 605
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser His Phe Ile Trp Gly Pro
 20 25 30

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
100 105

<210> 606

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 606

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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

Leu Asn Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Thr Tyr Gly Ser Leu Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
100 105

<210> 607

<211> 108

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 607

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

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

Leu Ser Trp Tyr Gln Val Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Thr Tyr Gly Ser Trp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gly Gln Gly Val Leu Trp Pro Ala
 85 90 95

Thr Phe Gly Gln Gly Thr Thr Val Glu Ile Lys Arg
 100 105

<210> 608

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 608

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tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cgcagcaggt 120

ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaata acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300

ttttactttc aggagtgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 609

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 609

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tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cgcagcaggt 120

ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300
 ttttactttc acgagtgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 610
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 610
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 tcctgtgcag cctccggatt cacctttgag tggtatgaga tgcagtgggt ccgccaggct 120
 ccaggaagg gtctagagtg ggtctcagc atttctggtg atggttatcg tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt 300
 gggatatttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 611
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccaggaagg gtctagagtg ggtctcagc attagtggta gtggtgtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagccg 300
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<210> 612
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggaaggt gtctggagtg ggtctcatct atttcgggta atggtgctaa tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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cttaggtttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 613
<211> 369
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggaaggt gtctagagtg ggtctcaggt attagtaggc gtggttttac tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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attacgtatg ctatgaggtg tgcgcgtttt gactactggg gtcaggaac cctggtcacc 360
gtctcgagc 369

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<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggaaggt gtctagagcg ggtctcagct attaatccgc agggtagcgc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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tttatttttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

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 <211> 357
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgggt 300
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<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccaggaagg gtctagagtg ggtctcaacg attagtgcgt cgggtgtttt tacatactac 180
 gcagactccg tgaagggccg gttcaccacc tcccgcgaca attccaagaa cacgctgtat 240
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<210> 617
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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gggaaagccc ctaagctcct gatcgagagt tcttccggtt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
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 gggaccaagg tggaaatcaa acgg 324

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 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 gggaaagccc ctaagctcct gatctatctt gcttcccggtt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
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 gggaccaaag tggaaatcaa acgg 324

<210> 619
 <211> 348
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 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccagggaagg gtctagagcg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatcct 300
 tatagttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 620
 <211> 360
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccagggaagg gtctagagtg ggtctcatct atttcggcta gtggtgggtc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg 300
gtgagttatg tggcgacgtt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc 360

<210> 621
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
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gggaccaagg tggaaatcaa acgg 324

<210> 622
<211> 357
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccagggaagg gtctagagtg ggtctcagcg attgagtcgg atggtcaggc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tgctgaggac accgcggtat attactgtgc gaaaaatcgg 300
attcctgac ttgtgtttga ctactggggg cagggaaccc tggtcaccgt ctcgagc 357

<210> 623
<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccagggaagg gtctagagtg ggtctcatct attgataagg agggctctgtc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaggtagg	300
attcctgggc tggtttttga ctactggggc cagggaaccc tggtcaccgt ctcgagc	357

<210> 624

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccagggaagg gtctagagtg ggtctcagcg attcagccta tgggtgatgg tacatactac	180
gcagactccg tgaagggccg gttcaccgtc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggcgt	300
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<210> 625

<211> 357

<212> ADN

<213> Secuencia Artificial

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<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 625

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ccagggaagg gtctagagtg ggtctcagct attacttcga atgggtatga gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggcgt 300
 attcctactc ttcattttga ctactgggggt caggggaaccc tggtcaccgt ctcgagc 357

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<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggcgt 300
 attcctactc ttcattttga ctactgggggt caggggaaccc tggtcaccgt ctcgagc 357

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<220>
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 ccaggaaggt gtctagagtg ggtctcaagg attactctc ttggtacgct tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggcgt 300
 attccttcgc ttacgtttga ctactgggggt caggggaaccc tggtcaccgt ctcgagc 357

<210> 628
 <211> 357
 <212> ADN
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<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggaagg gtctggagtg ggtctcaagg atttcgccgg gtggtgatta tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtgt attactgtgc gaaagggcgt      300
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<210> 629

<211> 357

<212> ADN

<213> Secuencia Artificial

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<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggaagg gtctagagtg ggtctcaagg atttcggctg atggtgctaa tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac gccgcggtat attactgtgc gaaagggcgt      300
gttccggatc tgctttttga ctactgggggt caggaacccc tggtcaccgt ctcgagc      357

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<210> 630

<211> 357

<212> ADN

<213> Secuencia Artificial

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<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggaagg gtctagagtg ggtctcacgt attgcggttg atggtgatcg gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtaag      300
gttccgtctc ttcattttga ctactgggggt caggaacccc tggtcaccgt ctcgagc      357

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<211> 357

<212> ADN

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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccggggac accgcggtat attactgtgc gaaaggggtg	300
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<210> 632

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggaagg gtctagagtg ggtctcacgt attaatgctg ggggtgtgca tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaggggtg	300
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<210> 633

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

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ccaggaagg gtctagagtg ggtctcacg atttcgagtg atggtgcgag tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggggtg	300
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<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggggag 300
 gttcctcgtc ttcattttga ctactgggggt caggggaacc tggtcaccgt ctcgagc 357

<210> 637
 <211> 357
 <212> ADN
 <213> Secuencia Artificial

<220>
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 ccaggaagg gtctagagt ggtctcacg attgcgtata atggtggtga tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggatt 300
 actcctaatt tgacttttga ctactgggggt caggggaacc tggtcaccgt ctcgagc 357

<210> 638
 <211> 357
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccaggaagg gtctagagt ggtctcacgt attaatgcta cgggttctat tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggggtt 300
 attcctcatt tgatgtttga ctactgggggt caggggaacc tggtcaccgt ctcgagc 357

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 <213> Secuencia Artificial

<220>
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ccaggaaggt gtctagagtg ggtctcacgt attactggta ctggtaatag tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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gtgccgtatc ttgcttttga ctactgggggt caggaaccc ttgtcaccgt ctcgagc 357

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<400> 640
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tcctgtgcag cctccggatt cacctttgag gctgatgcga tgacgtgggt cgcgcaggt 120
ccaggaaggt gtctagagtg ggtctcaagg attaatgtgg atggtgatcg gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggtat 300
gttcctacgc ttgagtttga ctactgggggt caggaaccc ttgtcaccgt ctcgagc 357

<210> 641
<211> 357
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 641
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgat cgggcggata tgacgtgggt cgcgcaggt 120
ccaggaaggt gtctagagtg ggtctcaagg atttcggggg agggtaagtg tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggatg 300
gttcctaatt ttggttttga ctactgggggt caggaaccc ttgtcaccgt ctcgagc 357

<210> 642
<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 642

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gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcat tgggagccga tgtcttgggt ccgccaggct      120
ccggggaagg gtctagagtg ggtctcacgt attaattctt ctggttggga tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggatg      300
gttcctaatt tggtttttga ctactggggg caggggaaccc tggtcaccgt ctcgagc      357
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<210> 643

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 643

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gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgct gatgagccga tgacttgggt ccgccaggct      120
ccaggggaagg gtctagagtg ggtctcacgt attcctcctg aggggtgctcc gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggatt      300
actcctaatt tgacttttga ctactggggg caggggaaccc tggtcaccgt ctcgagc      357
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<210> 644

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 644

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tcctgtgcag cctccggatt cacctttcat aatcatgata tgtcttgggt ccgccaggct      120
ccaggggaagg gtctagagtg ggtctcacgt attagtcggg gtggtcttca gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
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ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggatt 300

gtgccggatc tgcattttga ctactgggggt caggggaaccc tggtcaccgt ctcgagc 357

<210> 645

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 645

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttaat gagtatccta tgtcgtgggt ccgccaggct 120

ccaggaaggt gtctagagtg ggtctcacgt attaatgggg atgggtgctaa tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggatt 300

attccggcta tgcagtttga ctactgggggt caggggaaccc tggtcaccgt ctcgagc 357

<210> 646

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 646

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttggg gatgtgccta tgtcgtgggt ccgccaggct 120

ccaggaaggt gtctagagtg ggtctcaagg attgatcctt atggttctaa tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtatt 300

atgcctagtc ttacttttga ctactgggggt caggggaaccc tggtcaccgt ctcgagc 357

<210> 647

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 647

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tctgtgcag cctccggatt cacctttgcg gattatgata tgtcttgggt ccgccaggct	120
ccaggaagg gtctagagtg ggtctcacgt atttcggcgc ttggtgctac tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggctag	300
cttcggcgt tggagtttga ctactggggt caggaaccc tggtcaccgt ctcgagc	357

<210> 648

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 648

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tctgtgcag cctccggatt cacctttaag cggtattata tgacttgggt ccgccaggct	120
ccaggaagg atctagagtg ggtctcaggt attgttcctt ctggtaatag gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtagg	300
attccggatc tgcattttga ctactggggt caggaaccc tggtcaccgt ctcgagc	357

<210> 649

<211> 366

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 649

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tctgtgcag cctccggatt cacctttgct gattatgata tgacttgggt ccgccaggct	120
ccaggaagg gtctagagtg ggtctcaagg atttctccga cgggtgggca gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggtgtt	300
attccgtatt tgtctttttc tccgtttgac tactgggggtc aggaaccct ggtcaccgtc	360
tcgagc	366

<210> 650

<211> 366

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 650

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gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt caccttttct aagtattgga tgggttgggc cgcagggt      120
ccagggaagg gtctagagtg ggtctcatcg attgattcgc atggtgctgg tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatac acagcctgcg tgtcgaggac accgcggtat attactgtgc gaaagggtgc      300
cctaagttaa tgactacgta tacgtttgac tactgggggc agggaaacct ggtcaccgtc      360
tcgagc                                           366
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<210> 651

<211> 351

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 651

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gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttttg tcttatccga tgcattgggt cgcagggt      120
ccagggaagg gtctagagtg ggtctcatcg attgattcga ggggttcggt tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggtcat      300
agttggacgt ttgactactg gggtcaggga accctgggtc cgtctcgag c                351
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<210> 652

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 652

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gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttgcg aatagtaata tgacttgggt cgcagggt      120
ccagggaagg gtctagagtg ggtctcacgt attaatccgg atggtgggtc tacatactac      180
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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagggcgt 300
 attcctactc ttcattttga ctactgggggt caggggaacc tggtcaccgt ctcgagc 357

<210> 653
 <211> 357
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 653
 gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttggg ccgaggagga tgggttgggt ccgccaggct 120
 ccaggaagg gtctagagt ggtctcatcg attgatgata ttggtcgtag gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagggcgt 300
 caggggtgtgt tgttggttga ctactgggggt caggggaacc tggtcaccgt ctcgagc 357

<210> 654
 <211> 351
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 654
 gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgag gattatagga tgggttgggt ccgccaggct 120
 ccaggaagg gtctagagt ggtctcatcg atttctactt ctggtgagct gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaacggcg 300
 ggtcagtttt ttgactactg gggtcaggga accctggtca ccgtctcgag c 351

<210> 655
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 655
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttccg gagtatgaga tggtttgggt cgcgcaggt 120
 ccaggaaggt gtctggagtg ggtctcagcg atttcgcgtg agggtcgggc tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acaacctgcg tgccgaggat accgcggtat attactgtgc gaaagagcct 300
 gttcggtttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 656
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 656
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt caccttttcg acttatgaga tgctttgggt cgcgcaggt 120
 ccaggaaggt gtctagagtg ggtctcatct atttcttctt ctggtaatta tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg 300
 ctgatgtttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 657
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 657
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgat actgaggaga tgagttgggt cgcgcaggt 120
 ccaggaaggt gtctagagtg ggtctcagcg attagtccta atggtgcttt tacattctac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagcct 300
 attctgtttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 658
 <211> 351

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 658

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gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttggt cattatgata tggtttggt cgcgcaggct      120
ccagggaggg gtctagagtg ggtctcaact attaatggtg ctggtctgaa tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gcaaagtgtc      300
agtcgtatct ttgactactg gggtcaggga accctgggtc ccgtctcgag c              351
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<210> 659

<211> 351

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 659

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gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttagg agttatgaga tggcgtgggt cgcgcaggct      120
ccagggaaag gtctagagtg ggtctcatct attagtactc tgggtacgaa gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gcaatcttct      300
actcatatct ttgactactg gggtcaggga accctgggtc ccgtctcgag c              351
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<210> 660

<211> 351

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 660

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gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttatt aggtatgaga tggcttggt cgcgcaggct      120
ccagggaaag gtctagagtg ggtctcaagt atttcgtcgt ctggttggt gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
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ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaagtgat 300
 gtcataatgt ttgactactg gggtcaggga accctgggtca ccgtctcgag c 351

<210> 661
 <211> 351
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 661
 gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt caccttttat gcttatgaga tggcttgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcatct atttcggatg atggtacgcy gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcy tgccgaggac accgcggtat attactgtgc gaaagatctg 300
 gggcaggggt ttgactactg gggtcaggga accctgggtca ccgtctcgag c 351

<210> 662
 <211> 357
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 662
 gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgct gatcatggga tgacgtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaggg attggtccgt ctggtgaggc gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcy tgccgaggac accgcggtat attactgtgc gaaagatcgt 300
 attoctaatc ttgtgtttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 663
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 663
 gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

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tctgtgcag cctccggatt cacctttgag tctcaggata tgtcttgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcagggt attagtccga atggttggga tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatagg      300
tctgattttg actactgggg tcaggaacc ctggtcaccg tctcgagc                    348

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<210> 664
 <211> 351
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 664
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tctgtgcag cctccggatt cacctttggg gattatgata tgtggtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcaagg attcgtcatc cgggtggtgt tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagctggt      300
cctaagggtt ttgactactg gggtcaggga accctgggtca ccgtctcgag c                351

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<210> 665
 <211> 357
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 665
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tctgtgcag cctccggatt cacctttcgg gtttattgga tgacttgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcatct attgatccgc aggggtgggat gacatactac      180
gcagactccg tgaagggccg gttcaccatc tctcgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagcgcgt      300
attcctaatt tggagtttga ctactgggggt caggaacccc tggtcaccgt ctcgagc        357

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<210> 666
 <211> 357
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 666

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggagtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttagt gcttatgata tgacgtgggt ccgccaggct	120
ccaggaagg gtcttagtg ggtctcacgt attaatccga cgggttctta tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagctaag	300
attccgaatt tggtttttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc	357

<210> 667

<211> 363

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 667

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgcg gatagtgaga tgatgtgggt ccgccaggct	120
ccaggaagg gtctagagtg ggtctcaggt attgcgcata atgggtgggca tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagctggt	300
catcctcagc agactgaggc ttttgactac tggggtcagg gaaccctggt caccgtctcg	360
agc	363

<210> 668

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 668

gagatgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgct acttatgata tgtattgggt ccgccaggct	120
ccaggaagg gtctagagtg ggtctcaaag atttctccga atggttggag tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatcag	300

acgcattttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 669

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 669

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tcctgtgcag cctccggatt cacctttagt gtttatgata tgaggtgggt cgcgcaggt 120

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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaata acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatcct 300

aagaattttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 670

<211> 351

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 670

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tcctgtgcag cctccggatt caccttttct catgaggata tgacttgggt cgcgcaggt 120

ccaggaagg gtctagagtg ggtctcaagt attagtcga atggttggga tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaata acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacgtact 300

aggagtaagt ttgactactg gggtcagga accctgggtc cgtctcgag c 351

<210> 671

<211> 360

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 671

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tctgtgcag cctccggatt cacctttgag aagtatatta tgggttgggc cgcaggct	120
ccaggaagg gtctagagt ggtctcaacg attgattatt ggggtcagca tacatactac	180
gcagactccg tgaagggccg gttcactatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacgtagt	300
catcttattc ctctgcagtt tgactactgg ggtcaggga cctggtcac cgtctcgagc	360

<210> 672

<211> 369

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 672

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tctgtgcag cctccggatt caccttttct gattatgcga tgggtgggt cgcaggct	120
ccaggaagg gtctggagt ggtctcaacg atttcgtatg tgggttatta tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaaaggct	300
ctgccccggg aggcgtttac ggagcgtttt gactactggg gtcagggaac cctggtcacc	360
gtctcgagc	369

<210> 673

<211> 369

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 673

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tctgtgcag cctccggatt cacctttggt ccgtatatga tgcattgggt cgcaggct	120
ccaggaagg gtctagagt ggtctcaacg attgaggtta atggtaatag gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatgggtt	300
ggttcgaaga cgtcgtcgga taagagtttt gactactggg gtcagggaac cctggtcacc	360
gtctcgagc	369

<210> 674

<211> 360
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 674
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 tcctgtgcag cctccggatt cacctttggt acgacggaga tggcttgggt ccgccaggct 120
 ccaggaaggt gtctagagtg ggtctcaagt attggtagtg ctgggtgcttg gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaattggt 300
 gggcatcctc agggtcagtt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc 360

<210> 675
 <211> 357
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 675
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 ccaggaaggt gtctagagtg ggtctcaagt attcagccta tgggtcagac tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatattct 300
 cggaataagg ggttttttga ctactggggt caggggaacc tggtcacctg ctcgagc 357

<210> 676
 <211> 357
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 676
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 tcctgtgcag cctccggatt cacctttacg agtgagtata tggggtgggt ccgccaggct 120
 ccaggaaggt gtctagagtg ggtctcatct attcagaggt atggtagtac gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacatgag 300
tctaattggg agacttttga ctactggggt cagggaaacc ttgtcaccgt ctcgagc 357

<210> 677
<211> 369
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 677
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tcctgtgcag cctccggatt caccttttcg gtgtatagta tgcagtgggt ccgccaggct 120
ccaggaaggt gtctagagtg ggtctcagcg attactccta atggtactcg gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaactctt 300
ggtcgggggt cttatcctgg tggtgatttt gactactggg gtcagggaac cctggtcacc 360
gtctcgagc 369

<210> 678
<211> 357
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 678
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tcctgtgcag cctccggatt cacctttccg agttatgcta tgacgtgggt ccgccaggct 120
ccaggaaggt gtctggagtg ggtctcacgt attacggcgg atggtactgt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggttct 300
attccgatgc ttacgtttga ctactggggt cagggaaacc ttgtcaccgt ctcgagc 357

<210> 679
<211> 360
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 679
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60

tctgtgcag cctccggatt caccttttcg acttatgata tgatttgggt cgcagggt	120
ccaggaagg gtctagagtg ggtctcagct atttctccta atggtagtg tatatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaaatcag	300
agtgttcac atgctgtttt tgactactgg ggtcaggga cctggtcac cgtctcgagc	360

<210> 680

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 680

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc	60
tctgtgcag cctccggatt cacctttgag aattatgaga tgacgtgggt cgcagggt	120
ccaggaagg gtctagagtg ggtctcacgt attgcgccgc atggtagtg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaggtcag	300
attccgatgc ttgattttga ctactggggg cagggaaccc tggtcaccgt ctcgagc	357

<210> 681

<211> 363

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 681

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tctgtgcag cctccggatt caccttttcg cattatatga tgatgtgggt cgcagggt	120
ccaggaagg gtctagagtg ggtctcaacg atttctcatt ttggtgatat tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaaatgat	300
atggtgatga agaattgggg gtttgactac tggggtcagg gaaccctggg caccgtctcg	360
agc	363

<210> 682

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 682

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tcctgtgcag cctccggatt cacctttgag aggtatgata tgagttgggt cgcgcaggct	120
ccaggaagg gtctagagtg ggtctcacgt attgattcgc ggggttggtc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggttg	300
gtgccgcac tgcagtttga ctactggggt caggaaccc tggtcaccgt ctcgagc	357

<210> 683

<211> 351

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 683

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tcctgtgcag cctccggatt cacctttgcg aatgcgcaga tgacttgggt cgcgcaggct	120
ccaggaagg gtctagagtg ggtctcaagg attgatgcta tgggtgatgc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtaag	300
gttccgagta ttgactactg gggtcaggga accctgggtc cgtctcgag c	351

<210> 684

<211> 351

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 684

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tcctgtgcag cctccggatt cacctttgcg aatgcgcaga tgacttgggt cgcgcaggct	120
ccaggaagg gtctagagtg ggtctcaagg attgatgcta tgggtgatgc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagggtt	300

attccggcgt ttgactactg gggtcagga accctgggtca ccgtctcgag c 351

<210> 685
 <211> 354
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 685
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 tcctgtgcag cctccggatt cacctttcag aatgatcgga tgcattgggt ccgccaggct 120
 ccaggaaggt gtctagagtg ggtctcatcg atttctgcta ctggtggtga tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacagacg 300
 ggtacgaatc gttttgacta ctggggtcag ggaaccctgg tcaccgtctc gaggc 354

<210> 686
 <211> 357
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 686
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 ccaggaaggt gtctggagtg ggtctcatct attgatgctt cgggtggtac tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac gccgcggtat attactgtgc gaaagatcgt 300
 attcctaatac ttgtgtttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 687
 <211> 357
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 tcctgtgcag cctccggatt cacctttgat aatgagaata tgacttgggt ccgccaggct 120

ccaggggaagg gtctagagtg ggtctcacgt attgatgggtg ggggttataa tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggcag 300
gttcctgagc tgctgtttga ctactgggggt caggggaaccc tggtcaccgt ctcgagc 357

<210> 688
<211> 357
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 688
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tcctgtgcag cctccggatt cacctttgtt tcgtcgaata tgacttgggt ccgccaggct 120
ccaggggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactat 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtcgg 300
attcctacgt tgggtgtttga ctactgggggt caggggaaccc tggtcaccgt ctcgagc 357

<210> 689
<211> 357
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 689
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tcctgtgcag cctccggatt cacctttgtt tcgtcgaata tgacttgggt ccgccaggct 120
ccaggggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactat 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagatcgt 300
attcctaatac ttgtgtttga ctactgggggt caggggaaccc tggtcaccgt ctcgagc 357

<210> 690
<211> 357
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 690
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tcctgtgcag cctccggatt caccttttct gatgattcga tgagttgggt cgcgcaggt 120
ccagggaagg gtctagagtg ggtctcacgt attaatgatg ctggtagttc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtact 300
attcctcttc tggagtttga ctactggggg cagggaaccc tggtcaccgt ctcgagc 357

<210> 691
<211> 357
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 691
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ccagggaagg gtctagagtg ggtctcacgt attgatggga ctgggtgtga tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tgccgggggac accgcggtat attactgtgc gaaagggctt 300
attcctgatac ttcagtttga ctactggggg cagggaaccc tggtcaccgt ctcgagc 357

<210> 692
<211> 357
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 692
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ccagggaagg gtctagagtg ggtctcacgt attattggtg gtggatcatga gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtact 300
attcctcttc tggagtttga ctactggggg cagggaaccc tggtcaccgt ctcgagc 357

<210> 693
<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 693

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tcctgtgcag cctccggatt cacctttgat aatgagaata tgacttgggt ccgccaggct	120
ccagggaagg atctagagtg ggtctcacgg attactgaga ggggtgatgt gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggact	300
gttcctacgc tggagtttga ctactggggc cagggaaccc tggtcaccgt ctcgagc	357

<210> 694

<211> 357

<212> ADN

<213> Secuencia Artificial

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<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 694

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tcctgtgcag cctccggatt cacctttgat gaggaggaga tgacgtgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcacgt attattggtg gtggatcatga gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggact	300
gttcctacgc tggagtttga ctactggggc cagggaaccc tggtcaccgt ctcgagc	357

<210> 695

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 695

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tcctgtgcag cctccggatt cacctttcat gagacggaga tgacgtgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcagct attaatcggc tgggtcagga tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtagg 300

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<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggaaggt gtctagagtg ggtctcacgt attaatgatg ctggtagtgc tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtact 300

gttcctacgc tggagtttga ctactgggggt caggggaaccc tggtcaccgt ctcgagc 357

<210> 697

<211> 357

<212> ADN

<213> Secuencia Artificial

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<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 697

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttgat aatgagaata tgacttgggt ccgccaggct 120

ccaggaaggt atctagagtg ggtctcacgt attactgaga ggggtgatgt gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtcgg 300

attcctacgt tgggtgttga ctactgggggt caggggaaccc tggtcaccgt ctcgagc 357

<210> 698

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 698

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ccaggaagg gtctagagtg ggtctcacgt attaagtgatg ctggtagttc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggatt	300
actcctaatt tgacttttga ctactgggggt caggaaccc tggtcaccgt ctcgagc	357

<210> 699

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 699

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ccaggaagg gtctagagtg ggtctcacgt attcctcctg aggggtgctcc gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggctt	300
attcctgatc ttcagtttga ctactgggggt caggaaccc tggtcaccgt ctcgagc	357

<210> 700

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 700

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tctgtgcag cctccggatt cacctttcag gatagtgata tgacgtgggt cgcagggt	120
ccaggaagg gtctagagtg ggtctcagct attgctgcgc ctggtggtag tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagatcgt	300
attcctaadc ttaggtttga ctactgggggt caggaaccc tggtcaccgt ctcgagc	357

<210> 701

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 701
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tcctgtgcag cctccggatt cacctttgtt tcggatacta tgagttgggt cgcgcaggt 120
ccagggaagg gtctagagtg ggtctcacgt attgatggga ctggtggtga tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggcag 300
gttcctgagc tgctgtttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 702
<211> 357
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 702
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttcag gatagtata tgacgtgggt cgcgcaggt 120
ccagggaagg gtctagagtg ggtctcagct attgctgcgc ctggtggtag tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatcgt 300
attcctaatac ttgtgtttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 703
<211> 357
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 703
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tcctgtgcag cgcgcggatt cacctttgat ctggcggaga tgacttgggt cgcgcaggt 120
ccagggaagg gtctagagtg ggtctcacgt attgatgagg atggtgcttc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tgccgaggac gccgcggtat attactgtgc ggaaggtgtt 300
attccgtctc tgacttttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 704
<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 704

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ccagggaagg gtctagagtg ggtctcacgg atttcgcctg atggtacgta tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatac acagcctgcg tgccgaggac gccgcggtat attactgtgc ggaaggtgtt      300
attccgtctc tgacttttga ctactggggg cagggaaccc tggtcaccgt ctcgagc      357
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<210> 705

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 705

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tcctgtgcag cctccggatt cacctttgct gaggatgata tgacttgggt cgcgcaggct      120
ccagggaagg gtctagagtg ggtctcacgt attgcggttg atggtgatcg gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatac acagcctgcg taccgaggac accgcggtat attactgtgc gaaagggag      300
acgccgcatac ttgtgtttga ctactggggg cagggaaccc tggtcaccgt ctcgagc      357
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<210> 706

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 706

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gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag ccgccggatt cacctttgat ctggcgagga tgacttgggt cgcgcaggct      120
ccagggaagg gtctagagtg ggtctcacgt attgatgagg atggtgcttc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
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ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggtcag 300
gttcctgctt tggtttttga ctactgggggt caggggaaccc tggtcaccgt ctcgagc 357

<210> 707
<211> 357
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 707
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tcctgtgcag cctccggatt cacctttgag gattcgatga tgcgtgggt ccgccaggcg 120
ccaggaagg gtctagagtg ggtctcacgg attgatcctg ggggtgctca gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggggtg 300
actccggatt tgacttttga ctactgggggt caggggaaccc tggtcaccgt ctcgagc 357

<210> 708
<211> 357
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 708
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgag catgcggata tgagttgggt ccgccaggct 120
tcaggaagg gtctagagtg ggtctcacgt attgataata gtggtcagtc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggggtg 300
actccggatt tgacgtttga ctactgggggt caggggaaccc tggtcaccgt ctcgagc 357

<210> 709
<211> 357
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 709
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tctgtgcag cctccggatt cacctttagt gaggcggaga tgaattgggt cgcagggt	120
ccaggaagg gtctagagtg ggtctcacgt attacgacgg atggtgattc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggcgt	300
attcctactc ttcattttga ctactggggt caggaaccc tggtcaccgt ctcgagc	357

<210> 710

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 710

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tctgtgcag cctcaggatt cacctttgat gatagtata tgacttgggt cgcagggt	120
ccaggaaga gtctagagtg ggtctcatat attcgggtg atgatgatga gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaaatcgg	300
attcctgata ttgtgtttga ctactggggt caggaaccc tggtcaccgt ctcgagc	357

<210> 711

<211> 363

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 711

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tctgtgcag cctccggatt cacctttaat gtggcgata tgagtggt cgcagggt	120
ccaggaagg gtctagagtg ggtctcaagt attagtccga atggttgga tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacatgct	300
tctacggagg ggccgactgc ttttgactac tggggtcagg gaaccctggt caccgtctcg	360
agc	363

<210> 712

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 712

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ccaggaaggt gtctggagtg ggtctcatgg atttctgctc atggttcgtt tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatggcct      300
tataagtttg actactgggg tcaggaacc ctggtcaccg tctcgagc      348
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<210> 713

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 713

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgctctc      60
tcctgtgcag cctccggatt cacctttggg agtgggtcta tgagttgggt ccgccaggct      120
ccaggaaggt gtctagagtg ggtctcacgg attggtagta atgggtcgga tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggatg      300
gttcctaatt tggtttttga ctactggggg caggaaccc tggtcaccgt ctcgagc      357
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<210> 714

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 714

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ccaggaaggt gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagatcgt      300
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attcctaatac ttgtgtttga ctactgggggt caggggaaccc tggtcaccgt ctcgagc 357

<210> 715
 <211> 357
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 715
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 tcctgtgcag cctccggatt cacctttggg gagagtgata tgaagtgggt ccgccaggct 120
 ccaggggaagg gtctagagtg ggtctcaagt attagtccga atggttggga tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatctcct 300
 tcttctcgtc ttaagtttga ctactgggggt caggggaaccc tggtcaccgt ctcgagc 357

<210> 716
 <211> 357
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 716
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 tcctgtgcag cctccggatt cacctttgat agtagtgaga tgagttgggt ccgccaggct 120
 ccaggggaagg gtctagagtg ggtctcatcg attgagaatc aggggtggtgc gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatcgt 300
 attcctaatac ttgtgtttga ctactgggggt caggggaaccc tggtcaccgt ctcgagc 357

<210> 717
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 717
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 tcctgtgcag cctccggatt cacccttgat gcgtatccta tgtattgggt ccgccaggct 120

ccaggggaagg gtctagagtg ggtctcatgg attgcttcgg gtggtggtgc gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacgtacg 300
aagaatthttg actactgggg tcaggggaacc ctgggtcaccg tctcgagc 348

<210> 718
<211> 360
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 718
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tcctgtgcag cctccggatt cacctttatg agttattcta tggcttgggt ccgccaggct 120
ccaggggaagg gtctagagtg ggtctcaggg attacttcta atggtaatcg gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatcgact 300
ggggctaata gtaggaattt tgactactgg ggtcaggga cctggtcac cgtctcgagc 360

<210> 719
<211> 363
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 719
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tcctgtgcag cctccggatt cacctttgag gggtatctga tgtcgtgggt ccgccaggct 120
ccaggggaagg gtctagagtg ggtctcaagt attgcggcta atggatatgca gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaaagccg 300
aggggtattht gggtatgggga ttttgactac tggggtcagg gaaccctggg caccgtctcg 360
agc 363

<210> 720
<211> 357
<212> ADN
<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 720

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tcctgtgcag cctccggatt cacctttcat gagtctacga tgacgtgggt ccgccaggct	120
ccaggaagg gtctagagtg ggtctcaact attcggcatc cgggtgagtt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccggggac accgcggtat attactgtgc gaaagggctt	300
attcctgata ttcagtttga ctactggggc cagggaaccc tggtcaccgt ctcgagc	357

<210> 721

<211> 363

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 721

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tcctgtgcag cctccggatt cacctttgcg atgtatagta tgagttgggt ccgccaggct	120
ccaggaagg gtctagagtg ggtctcatcg attgcgccgc cgggtggtag gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacagtcg	300
ctgacggggc atagtaggtc ttttgactac tggggtcagg gaaccctggt caccgtctcg	360
agc	363

<210> 722

<211> 360

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 722

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt caccttttcg cagaatccga tgctgtgggt ccgccacgct	120
ccaggaagg gtctagagtg ggtctcaacg attcctgcga atggctgtcc tacatcctac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatatagt	300
cagcagccgg gtcgtcggtt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc	360

<210> 723
 <211> 357
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 723
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 tcctgtgcag cctccggatt cacctttgct aattatcata tgacgtgggt ccgccaggct 120
 ccaggaagg gtctagagtg ggtctcatcg attcctgata gtggttaagca gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctacaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggtagg 300
 attcctctc ttctttttga ctactgggggt caggaaccc tggtcaccgt ctcgagc 357

<210> 724
 <211> 360
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 724
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 tcctgtgcag cctccggatt cacctttgcg cagtatcata tgcgttgggt ccgccaggct 120
 ccaggaagg gtctagagtg ggtctcaacg attaatagata ttggtagtaa tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttggg 300
 gggcggggga gtttttcttt tgactactgg ggtcagggaa cctggtcac cgtctcgagc 360

<210> 725
 <211> 360
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 725
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 tcctgtgcag cctccggatt caccttttct tcgtatgata tgaagtgggt ccgccaggct 120
 ccaggaagg gtctagagtg ggtctcaacg attagtgcgt ctggtgtgtt tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacgggag 300
 catgcgggtc agccgccttt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc 360

<210> 726
 <211> 360
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 726
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttaat ggttatgcta tgagttgggt ccgccaggct 120
 ccaggaaggt gtctagagtg ggtctcaact attaatgcta atggtaagta tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaaagttg 300
 actcttgctt ctaattattt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc 360

<210> 727
 <211> 363
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 727
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 tcctgtgcag cctccggatt cacctttatg gattatgata tgaagtgggt ccgccaggct 120
 ccaggaaggt gtctagagtg ggtctcaagt attactgcgc ttggtaagaa gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagatagt 300
 gttaagtatc ctcttaatct ttttgactac tggggtcagg gaaccctggt caccgtctcg 360
 agc 363

<210> 728
 <211> 360
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 728
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tcctgtgcag cctccggatt cacctttccg cattatacga tggcgtgggt cgcgcaggt 120
ccagggaagg gtctggagtg ggtctcatct attcagtcgc ctggttggcg gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatatggg 300
gatggctctc ctttgacttt tgactactgg ggtcaggga cctggtcac cgtctcgagc 360

<210> 729
<211> 357
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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tcctgtgcag cctccggatt caccttttagt ggtacgccga tgtcttgggt cgcgcaggt 120
ccagggaagg gtctagagtg ggtctcacgt attggggatg agggtcagga gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaggggtg 300
actccggatt tgacttttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 730
<211> 357
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccagggaagg gtctagagtg ggtctcagcg attgggtctg atggtcagag tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggcgt 300
attcctactc ttcatTTTTga ctactgggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 731
<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 731

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tcctgtgcag cctccggatt cacctttaat cctggtgaga tgacgtgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaagt attgatgggt ctggttcttc gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatac acagcctgcg tgccgatgac accgcggtat attactgtgc gaaagggcgt	300
attcctactc ttcattttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc	357

<210> 732

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 732

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tcctgtgcag cctccggatt cacctttcct gagtctatga tgggggtgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcatcg attgggtatc ctggtgctac tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaggtggg	300
agtcgggatg ataattttga ctactgggggt cagggaaccc tggtcaccgt ctcgagc	357

<210> 733

<211> 372

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 733

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tcctgtgcag cctccggatt cacctttggg cagcatagta tgcattgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaagt attagtgttc cgggtccgaa gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaagtctt 300
 agggatttgc gtccgggtga tagtaagagt tttgactact ggggtcaggg aaccctggtc 360
 accgtctcga gc 372

<210> 734
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 tcctgtgcag cctccggatt caccttttgt tctgctgcta tggattgggt ccgccaggct 120
 ccaggaaggt gtctagagtg ggtctcatct attaatgata tgggttctaa tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacagggt 300
 ggtcgttttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 735
 <211> 354
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 735
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 ccaggaaggt gtctagagtg ggtctcatcg attgatggtc ctggtggggc tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaggagg 300
 agggttcctg attttgacta ctggggtcag ggaaccctgg tcaccgtctc gage 354

<210> 736
 <211> 357
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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tcctgtgcag cctccggatt cacctttggt gagtatgaga tgacttgggt cgcgcaggt 120
ccaggaaggt gtctagagtg ggtctcaagg attgatccgt ttggttctga gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaaggtgtg 300
gttcctgatt tgaattttga ctactggggt caggaaccc ttgtcaccgt ctcgagc 357

<210> 737
<211> 360
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 737
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tcctgtgcag cctccggatt cacctttgat aagtatgtta tggggtgggt cgcgcaggt 120
ccaggaaggt gtctagagtg ggtctcaact attggtagtt atggtggggc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaaggctt 300
actcttagtg cgactaagtt tgactactgg ggtcaggga ccctggtcac cgtctcgagc 360

<210> 738
<211> 360
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 738
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tcctgtgcag cctccggatt cacctttgag gattatgtga tgggttgggt cgcgcaggt 120
ccaggaaggt gtctagagtg ggtctcaact attgcgcac ggggtgatat tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacgtagg 300
cgtcttagtg attatcggtt tgactactgg ggtcaggga ccctggtcac cgtctcgagc 360

<210> 739
<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 739

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tcctgtgcag cctccggatt cacctttggg cagtttgata tgtattgggt cgcgcaggct      120
ccagggaagg gtctagagtg ggtctcagcg attagtccgg ctggtactgg tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaataa acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgggg      300
gatcgggtcta gtctttttga ctacaggggt cagggaaccc tggtcaccgt ctcgagc      357
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<210> 740

<211> 354

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 740

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tcctgtgcag cctccggatt cacctttaag gatacgggta tgacgtgggt cgcgcaggct      120
ccagggaagg gtctagagtg ggtctcaagt atttctagtt atggtcgtga tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaataa acagcctgcg tgccgaggac gccgcggtat attactgtgc gaaattgaat      300
gcggcgctgg gttttgacta ctggggtcag ggaaccctgg tcaccgtctc gaggc      354
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<210> 741

<211> 354

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 741

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tcctgtgcag cctccggatt cacctttggt ccgtatccga tgagttgggt cgcgcaggct      120
ccagggaagg gtctagagtg ggtctcaggt attaatacgc cgggtacgag gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
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ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gcaacagatg 300
 tctagtgggg tttttgacta ctgggggtcag ggaaccctgg tcaccgtctc gagg 354

<210> 742
 <211> 354
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 742
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 tcctgtgcag cctccggatt caccttttcg aatcaggata tgacttgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaagt attgatagtt ctggtcagct tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagttaag 300
 tctcttgccg ggtttgacta ctgggggtcag ggaaccctgg tcaccgtctc gagg 354

<210> 743
 <211> 351
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 743
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 tcctgctcag cctccggatt caccttttcct gagtctgata tgaagtgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcaagt attagtccga atggttggga tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaccggct 300
 caggttctgt ttgactactg gggtcaggga accctgggtc ccgtctcgag c 351

<210> 744
 <211> 360
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 744
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tctgtgcag cctccggatt cacctttgag cagtatgtga tgggttgggt cgcagggt	120
ccaggaagg gtctagagtg ggtctcaacg attggtacgt cgggtaagta tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaata acagcctgcg tgccgaggac accgcggtat attactgtgc gcaacgtagg	300
tctctgactc gggttcattt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc	360

<210> 745

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 745

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tctgtgcag cctccggatt cacctttggt gtggagcata tgagttgggt cgcagggt	120
ccaggaagg gtctagagtg ggtctcagcg attacgggtg atggtgatcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaata acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaacggtt	300
tcgtggaatg gtcgttttga ctactggggt caggaaccc tggtcaccgt ctcgagc	357

<210> 746

<211> 351

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 746

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ccaggaagg gtctggagtg ggtctcaagg attgctccgt ctggtattat tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaata acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggttg	300
cgtggtaagt ttgactactg gggtcagga accctgggtc cgtctcgag c	351

<210> 747

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 747

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ccaggaagg gtctagagtg ggtctcatct atttcttcgg ctggtactga tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacagtcg	300
cttaattttg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 748

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 748

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tcctgtgtag cctccggatt cacctttgat gaggagccga tgacttgggt ccgccaggct	120
ccaggaagg gtctagagtg ggtctcaatt attgatccgg gtggtggggc gacatactac	180
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ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatctaat	300
agtatgtttg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 749

<211> 363

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 749

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tcctgtgcag cctccggatt caccttttct gcgtatccta tgcattgggt ccgccaggct	120
ccaggaagg gtctagagtg ggtctcatct attgcttctt cgggtattac gacatactac	180
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ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatttact	300
cggtgcatt ttctgcgca gtttgactac tggggtcagg gaaccctggt caccgtctcg	360

agc

363

<210> 750

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 750

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ccgtatgcgt cgaagtttga ctactggggt cagggaaacc tggtcaccgt ctcgagc 357

<210> 751

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 751

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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

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<210> 752

<211> 354

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 752

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ccaggggaagg gtttagagtg ggtctcatgg attaattcga ctggttctcg tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaaattgg 300
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<210> 753
<211> 351
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggggaagg gtctagagtg ggtctcaacg attaatcggc tgggtcagag tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagtgaag 300
aagcataagt ttgactactg gggtcaggga accctgggtca ccgtctcgag c 351

<210> 754
<211> 351
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggggaagg gtctagagtg ggtctcaacg attacgaaga ctggttttcg tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgtagaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgggg 300
cagtttgatt ttgactactg gggtcaggga accctgggtca ccgtctcgag c 351

<210> 755
<211> 354
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccagggaagg gtctgagtg ggtctcaact attgatgga gtggtatggt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagattct 300
ctgaaggctt cttttgacta ctggggtcag ggaaccctgg tcaccgtctc gagg 354

<210> 756
<211> 351
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 756
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttccg ctttatggga tgtggtgggt cgcagcaggt 120
ccagggaagg gtctagagtg ggtctcatat attgggcctt atggtcatac tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaaagcgg 300
aagaagaagt ttgactactg gggtcaggga accctgggtca ccgtctcgag c 351

<210> 757
<211> 351
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 757
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttcct aggtatcgga tgagttgggt cgcagcaggt 120
ccagggaagg gtctagagtg ggtctcaagt attactccgt atggtgctca tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatggt 300
aagtggatt ttgactactg gggtcaggga accctgggtca ccgtctcgag c 351

<210> 758
<211> 351

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 758

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gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttaat gagtatgcga tgaggtgggt cgcgcaggct      120
ccagggaagg gtctagagtg ggtctcaacg attgatcgtc tgggtcttca tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaagtggg      300
ccttttacgt ttgactactg gggtcaggga accctgggtca ccgtctcgag c              351
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<210> 759

<211> 351

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 759

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tcctgtgcag cctccggatt cacctttgag cgggtataata tgcgttgggt cgcgcaggct      120
ccagggaagg gtctagagtg ggtctcaacg attgatcggc tgggtcttgc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgggt      300
tcgtgggtctt ttgactactg gggtcaggga accctgggtca ccgtctcgag c              351
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<210> 760

<211> 354

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 760

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tcctgtgcag cctccggatt cacctttggt atttatgata tgaagtgggt cgcgcaggct      120
ccagggaagg gtctagagtg ggtctcaacg atttcgtcgt cgggtactca tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatcct      300
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cagccttatc cttttgacta ctgggggtcag ggaaccctgg tcaccgtctc gage 354

<210> 761
 <211> 354
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 761
 gaggtgcagc tattggagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt caccttttgg gtgtatgata tgcgttgggt ccgccaggct 120
 ccaggaaggt gtctagagtg ggtctcaacg atttctgcga ctggtgtgca tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatccg 300
 cctgctggtc ggtttgacta ctgggggtcag ggaaccctgg tcaccgtctc gage 354

<210> 762
 <211> 357
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 762
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt caccttttcg acttatgata tgatttgggt ccgccaggct 120
 ccaggaaggt gtctagagtg ggtctcagct atttctccta atggtactgg tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctccg 300
 caggtgaata ctgagtttga ctaccgggggt caggggaaccc tggtcaccgt ctcgagc 357

<210> 763
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 763
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgag aaggaggata tggggtgggt ccgccaggct 120

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ccagggaagg gtctagagtg ggtctcacat atttcgccga atgggttatgc gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaagttgg      300
tctagttttg actactgggg tcagggaacc ctggtcaccg tctcgagc                    348

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<210> 764
<211> 354
<212> ADN
<213> Secuencia Artificial

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<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 764
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttagt gctactccga tggagtgggc ccgccaggct      120
ccagggaagg gtctagagtg ggtctcaact atttctgaga gtgggttatag tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatggaat      300
tcgactactg gttttgacta ctggggtcag ggaaccctgg tcaccgtctc gagc            354

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<210> 765
<211> 351
<212> ADN
<213> Secuencia Artificial

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<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 765
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttaat acggtggata tggagtgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcaagt attagtccga atggttggga tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagctccg      300
catcgggcgt ttgactactg gggtcaggga accctgggtca ccgtctcgag c              351

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<210> 766
<211> 357
<212> ADN
<213> Secuencia Artificial

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<220>

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<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 766
gaggtgcagc tgttgagtc tggggggggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgag gataaggaga tgagttgggt ccgccaggct 120
ccaggaagg gtctagagtg ggtctcacgg attgatgctt tgggtgattc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaagggatg 300
gttcctcgtc tgaagtttga ctactggggc cagggaaccc tggtcaccgt ctcgagc 357

<210> 767

<211> 342

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 767
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tcctgtgcag cctccggatt cacctttagt gatcattcga tgatgtgggt ccgccaggct 120
ccaggaagg gtctagagtg ggtctcagat attgagccgc atggtgttca tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaatcctact 300
tttgactact ggggtcaggg aaccctggtc accgtctcga gc 342

<210> 768

<211> 366

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 768
gaggtgcagc tgttgagtc tggggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt caccttttcg ccgcatacta tgcattgggt ccgccaggct 120
ccaggaagg gtctagagtg ggtctcaggt attggtccgg atggtactac tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacgttcg 300
tatagttggg atcgtgggtg gacgtttgac tactgggggc agggaaccct ggtcaccgtc 360

tcgagc

366

<210> 769

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 769

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tcctgtgcag cctccggatt caccttttat gcttcggata tgaagtgggt ccgccaggct 120

ccaggaagg gtctagagtg ggtctcaagt attagtccga atggttggga tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagctgat 300

tatacttatac attcttttga ctactgggggt caggggaccc tggtcaccgt ctcgagc 357

<210> 770

<211> 351

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 770

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tcctgtgcag cctccggatt cacctttgcg cattataata tgcggtgggt ccgccaggct 120

ccaggaagg gtctagagtg ggtctcaacg attacgaaga ctggttttcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgtagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgggg 300

cagtttgatt ttgactactg gggtcaggga accctgggtca ccgtctcgag c 351

<210> 771

<211> 354

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 771

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tcctgtgcag cctccggatt caccttttcg cattatcata tgggttgggc ccgccaggct 120

ccaggaagg gtctagagtg ggtctcagtt attgggccga ggggtatttc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatcgctt 300
tcgcgtcata ggtttgacta ctgggggtcag ggaaccctgg tcaccgtctc gagg 354

<210> 772

<211> 351

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 772

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tcctgtgcag cctccggatt cacctttaat gagtatgcga tgaggtgggt ccgccaggct 120
ccaggaagg gtctagagtg ggtctcaacg attgatcgtc tgggtcttca tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaagtggg 300
ccttttacgt ttgactactg gggtcagga accctggta ccgtctcgag c 351

<210> 773

<211> 369

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 773

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctctc 60
tcctgtgcag cctccggatt cacctttggt aattatagta tgaagtgggc ccgccaggct 120
ccaggaagg gtctagagtg ggtctcaact attactcctg atggttggtta tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagtggg 300
gatgctgttt gggggtggat tgggtgggtt gactactggg gtcaggaac cctggtcacc 360
gtctcgagc 369

<210> 774

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 774

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tcctgtgcag cctccggatt cacctttggg gattatggta tgaagtgggt ccgccaggct	120
ccaggaagg gtctagagtg ggtctcagct attacgtcta atggtgattt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatctttg	300
tataagtttg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 775

<211> 369

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 775

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tcctgtgcag gctccggatt cacctttcct acttataaga tggggtgggt ccgccaggct	120
ccaggaagg gtctagagtg ggtctcattt attgattatt ggggttggcg gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaagtccg	300
tattcttggg ctcgatag tcctcatttt gactactggg gtcaggaac cctggtcacc	360
gtctcgagc	369

<210> 776

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 776

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tcctgtgcag cctccggatt cacctttagg ccttatacga tgtgttgggc ccgccaggct	120
ccaggaagg gtctagagtg ggtctcatgt attagtgtg ctggttcttt tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaaggatg	300
tcttcttttg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 777
 <211> 366
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 777
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 tcctgtgcag cctccggatt cacctttcag aattatcaga tggcttgggt cgcagggt 120
 ccaggaagg gtctagagtg ggtctcaact attagtggga ctggtaagaa tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaactcct 300
 cagaattatt ttagtgtgcg tcggtttgac tactgggggc agggaaccct ggtcaccgct 360
 tcgagc 366

<210> 778
 <211> 354
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 tcctgtgcag cctccggatt cacctttggg gcgtatacta tggggtgggt cgcagggt 120
 ccaggaagg gtctagagtg ggtctcaaag atttcgacgt ctgggtgggca gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctttg 300
 aattggtggg cgtttgacta ctggggtcag ggaaccctgg tcaccgtctc gagg 354

<210> 779
 <211> 351
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 779
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 tcctgtgcag cctccggatt cacctttaat gcgtatccta tgacttgggt cgcagggt 120

ccagggaagg gtctagagtg ggtctcacgg attgatgggt atggtcggca tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggatt 300
attcctaatt ttgactactg gggtcaggga accctgggtca cegtctcgag c 351

<210> 780
<211> 357
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 780
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tcctgtgcag cctccggatt cacctttggg gcggttgata tgacgtgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcagcg atttcgccta gtggttctgc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggcgt 300
gtgccggatc ttggttttga ctactggggt cagggaaccc tggtcaccgt ctcgagc 357

<210> 781
<211> 351
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 781
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tcctgtgcag cctccggatt cacctttgat agttatgcga tggggtgggc ccgccaggct 120
ccagggaagg gtctagagtg ggtctcagct attggggcta agggtttgtc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcggct 300
aggggtaagt ttgactactg gggtcaggga accctgggtca cegtctcgag c 351

<210> 782
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 782
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tcctgtgcag cctccggatt cacctttact cggatcaga tgggttgggt cgcagcaggt 120
ccagggaagg gtctagagtg ggtctcagtt attaatgttt ggggttcgag tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaatgtct 300
gggaagtgtt cctactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 783
<211> 351
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 783
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tcctgtgcag cctccggatt cacctttggg aattatagta tgatgtgggt cgcagcaggt 120
ccagggaagg gtctagagtg ggtctcaacg attattcctg ctggtacgtc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccgtcg 300
attaggttgt ttgactactg gggtcaggga accctgggtc ccgtctcgag c 351

<210> 784
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 784
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttggt gcgtatgata tgggttgggt cgcagcaggt 120
ccagggaagg gtctagagtg ggtctcatgg atttctccga atgggtatga tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggggg 300
gtgaagtgtt actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 785
<211> 369

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 785

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ccaggaagg gtctagagtg ggtctcaacg attcaggctg atggtgagca gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagcttcg      300
tatgctcttg tgtatcctcc tgaggagttt gactactggg gtcaggaac cctggtcacc      360
gtctcgagc                                     369
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<210> 786

<211> 366

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 786

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tcctgtgcag cctccggatt cacctttacg aattatagga tgtcttgggt cgcgcaggct      120
ccaggaagg gtctagagtg ggtctcagct attgatgac tgggtgtgtc gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatggagg      300
cttaagaata gtcagccgac ggattttgac tactgggggc aggaaccct ggtcaccgct      360
tcgagc                                     366
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<210> 787

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 787

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ccaggggaagg gtctagagtg ggtctcattt attaatcctt cgggttatta tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaccttcg 300
cttagtccgt cttcttttga ctactggggg caggggaaccc tggtcaccgt ctcgagc 357

<210> 788

<211> 354

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 788

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tcctgtgcag cctccggatt cacctttgag actggtcaga tgggttgggc ccgccaggct 120
ccaggggaagg gtctagagtg ggtctcaaatt attgatgggt ctggtacgta tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaagtacg 300
cagaattatc ggtttgacta ctgggggtcag ggaaccctgg tcaccgtctc gagc 354

<210> 789

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 789

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ccaggggaagg gtctagagtg ggtctcatct attcataagg atggtaggat tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacagggg 300
acgccgggtg atgggtttga ctactggggg caggggaaccc tggtcaccgt ctcgagc 357

<210> 790

<211> 363

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 790

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gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
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ccaggaaggt gtctagagtg ggtctcaacg attgagactg gtggtacggg gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaatggat      300
gggtctggta catggcagac gtttgactac tggggtcagg gaaccctggg caccgtctcg      360
agc                                                                           363

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<210> 791
<211> 348
<212> ADN
<213> Secuencia Artificial

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<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 791
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ccaggaaggt gtctagagtg ggtctcatat attcgggctg aggggtgctta tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaatatctt      300
gcggattctg actactgggg tcaggaacc ctggtcaccg tctcgagc                    348

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<210> 792
<211> 360
<212> ADN
<213> Secuencia Artificial

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<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 792
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ccaggaaggt gtctagagtg ggtctcaggt attgatcata ttggtggtgg gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagatgat      300
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<210> 793

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<211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 793
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 ccaggaaggt gtctagagtg ggtctcaagt attggggcta gtggtgcgta tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaaacgggg 300
 ggtaggttag actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 794
 <211> 357
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 794
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 tcctgtgcag cctccggatt cacctttgat gaggggcata tggggtgggt ccgccaggct 120
 ccaggaaggt atctagagtg ggtctcatat attgggagtc tgggtttgca tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacgggag 300
 tttagtaatg gggggtttga ctactggggc caggaaccc tggtcaccgt ctcgagc 357

<210> 795
 <211> 363
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 795
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 tcctgtgcag cctccggatt cacctttaag actagtccta tgtattgggt ccgccaggct 120
 ccaggaaggt gtctagagtg ggtctcatcg attgatcgga ctggtgggca tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacaggct 300
 ctgcttactg atgcgaagcg ttttgactac tggggtcagg gaaccctggt caccgtctcg 360
 agc 363

<210> 796
 <211> 360
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 796
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 tcctgtgcag cctccggatt cacctttgat ggtcgggata tggtttgggt ccgccaggct 120
 ccaggaaggt gtctagagtg ggtctcagct attagtccga gtggtctgga tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggaacgtcct 300
 cagatgctgg ttactaattt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc 360

<210> 797
 <211> 357
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 797
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 ccaggaaggt gtctagagtg ggtctcaggg attggtcggg aggggtgattc tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagattct 300
 atgcccgcac agccgtttga ctactggggg caggaacccc tggtcaccgt ctcgagc 357

<210> 798
 <211> 357
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 798
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tcctgtgcag cctccggatt cacctttgat gagacttata tgaagtgggt cgcgcaggt 120
ccagggaagg gtctagagtg ggtctcagcg attggggcgt cgggtgctga tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatttacg 300
catctgaatg gtcggtttga ctactggggg cagggaaccc tggtcaccgt ctcgagc 357

<210> 799
<211> 357
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 799
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tcctgtgcag cctccggatt cacctttggg ggggtggccta tgggggtgggt cgcgcaggt 120
ccagggaagg gtctagagtg ggtctcaggt attgatattg atgggtgctcc gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagaggag 300
gcgggttctt ggtcttttga ctactggggg cagggaaccc tggtcaccgt ctcgagc 357

<210> 800
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 800
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tcctgtgcag cctccggatt cacctttagt gatcaggcga tgtgggtgggc cgcgcaggt 120
ccagggaagg gtctagagtg ggtctcattt attcagggtg atgggtggtt tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacctagt 300
aagccgtttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 801
<211> 354

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 801

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ccagggaagg gtctagagtg ggtctcaaatt attgatgggt ctggtacgta tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaataa acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagcgggtg      300
cggaattttg cttttgacta ctgggggtcag ggaaccctgg tcaccgtctc gaggc          354
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<210> 802

<211> 372

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 802

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tcctgtgcag cctccggatt cacctttagt gggcatgata tgtcttgggt cgcgcaggct      120
ccagggaagg gtctagagtg ggtctcagct attagtcctc atggtacgca tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaataa acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagggatt      300
aggggttga ttggtcatga tacgcagcct tttgactact ggggtcaggg aaccctgggc      360
accgtctcga gc                                372
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<210> 803

<211> 357

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 803

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tcctgtgcag cctccggatt cacctttgag agtaaggata tgctttgggt cgcgcaggct      120
ccagggaagg gtctagagtg ggtctcatct atttcgtcgg atggtactca tacatactac      180
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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gcaagagctg 300
 ggtgggtctt ggcagtttga ctactggggt cagggaaacc tggtcaccgt ctcgagc 357

<210> 804
 <211> 366
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 804
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 ccaggaaggt gtctagagtg ggtctcaggt attggggcgt cgggtacgtc tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac gccgcggtat attactgtgc gaaaggtggg 300
 acgggtccta ctgatttgtg ggattttgac tactgggggc agggaaccct ggtcaccgtc 360
 tcgagc 366

<210> 805
 <211> 357
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 805
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 ccaggaaggt gtctagagtg ggtctcaagt attagtgtga gtggtctgca tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagaggag 300
 gcgggttctt ggtcttttga ctactggggt cagggaaacc tggtcaccgt ctcgagc 357

<210> 806
 <211> 357
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 806
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tcctgtgcag cctccggatt cacctttggg caggagagga tgatttgggt ccgccaggct 120
cctgggaagg gtctagagtg ggtctcagat atttcggctt cgggtgggac tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagaggag 300
gcgggttctt ggtcttttga ctactggggg cagggaaccc tggtcaccgt ctcgagc 357

<210> 807
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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tcctgtgcag cctccggatt cacctttgag tggtatgaga tgcagtgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcagcg atttctggtg atggttatcg tacatactac 180
gcagactccg tgaaaggccg gttcaccatc tcccgcgaca attccatgaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt 300
gggtattttg actacagggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 808
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 808
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ccagggaagg gactagagtg ggtctcagcg atttctggtg atggttatcg tacatactac 180
gcagactccg tgaaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt 300
gggtattttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 809
<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 809

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgag tggtatgaga tgcagtgggt ccgccgggt	120
ccagggaagg gtctagagtg ggtctcagcg atttctggtg atggttatcg tacatactac	180
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ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt	300
gggtattttg actaccgggt tcagggaacc ctggtcaccg tctcgagc	348

<210> 810

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 810

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ccagggaagg gtctagagtg ggtctcagcg atttctggtg atggttatcg tacatactac	180
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<210> 811

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 811

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tcctgtgcag cctccggatt cacctttgag tggtatgaga tgcagtgggt ccgccaggct	120
ccagggaagg gtctagagtg gatctcagcg atttctggtg atggttatcg tacatactac	180
gcagactccg tgaaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt 300
 gggatattttg actacagggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 812
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 812
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 ccaggggaagg gtctagagtg ggtctcagcg atttctggtg atggttatcg tacatactac 180
 gcagactccg tgaaaggccg gttcaccatc tcccgcgaca attccgagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt 300
 gggatattttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 813
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 813
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 gcagactccg tgaaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatgg acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt 300
 gggatattttg actactgggg tcggggaacc ctggtcaccg tcacgagc 348

<210> 814
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 814
 gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

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tctgtgcag cctccggatt cacctttgag tggatgaga tgcagtgggt cgcagggt 120
ccaggaagg gtctagagtg ggtctcagcg atttctggtg atggttatcg tacatactac 180
gcagactccg tgaaaggccg gttcaccatc tcacgcgaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt 300
gggtattttc actactgggg tcggggaacc ctggtcaccg tctcgagc 348

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<210> 815
<211> 348
<212> ADN
<213> Secuencia Artificial

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<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 815
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ccaggaatg gtctagagtg gatctcagcg atttctggtg atggttatcg tacatactac 180
gcagactccg tgaaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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<210> 816
<211> 348
<212> ADN
<213> Secuencia Artificial
<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 816
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ccaggaagg gtctagagtg ggtctcagcg atatctggtg atggttatcg tacatactac 180
gcagactccg tgaaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgctaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt 300
gggtattttc actactgggg tcggggaacc ctggtcaccg tctcgagc 348

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<210> 817
<211> 348
<212> ADN
<213> Secuencia Artificial

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<220>

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<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 817
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tcctgtgcag cctccggatt cacctttgag tggtatgaga tgcagtgggt ccgcaaggct 120
ccaggaagg gtctagagtg ggtctcagcg atttctggtg atggttatcg tacatactac 180
gcagactccg tgaaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaata acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt 300
gggtattttg actacagggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 818
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 818
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tcctgtgcag cctccggatt cacctttgag tggtatgaga tgcagtgggt ccgccgggct 120
ccaggaagg gtctagagtg ggtctcagcg atttctggtg atggttatcg tacatactac 180
gcagactccg tgaaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaata acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt 300
gggtattttg actacagggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 819
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 819
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tcctgtgcag cctccggatt cacctttgag tggtatgaga tgcagtgggt ccgccgggct 120
ccaggaagg gattagagtg ggtctcaatg atttccgggg atggttatcg tacatactac 180
gcagactccg tgaaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaata acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt 300
gggtattttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 820
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 820
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 ccaggaagg gactagagtg ggtctcagcg atttctggtg acggttggcg cacatactac 180
 gcagactccg tgaaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctt 300
 gggatattttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 821
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 821
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 tcctgtgcag cctccggatt cacctttggg tggtatgaga tgcagtgggt ccgccgggct 120
 ccaggaagg gactagagtg ggtctcagcg atttctggtg atggttatcg tacatactac 180
 gcagactccg tgaaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctg 300
 ctctactttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 822
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 822
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 tcctgtgcag cctccggatt cacctttgag tggtatgaga tgcagtgggt ccgccgggct 120
 ccaggaagg gactagagtg ggtctcagcg atttctggtg atggttatcg tacatactac 180

gcagactccg tgaaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctg 300
 gggttctttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 823
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 823
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgag tggtatgaga tgcagtgggt ccgccgggct 120
 ccaggaagg gactagagtg ggtctcagcg atttctggtg atggttatcg tacatactac 180
 gcagactccg tgaaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagttg 300
 gagtattttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 824
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 824
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 tcctgtgcag cctccggatt cacctttgag tggtatgaga tgcagtgggt ccgccgggct 120
 ccaggaagg gactagagtg ggtctcagcg atttctggtg atggttatcg tacatactac 180
 gcagactccg tgaaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagggttg 300
 gagtattttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 825
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 825

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 tcctgtgcag cctccggatt cacctttgag tggtatgaga tgcagtgggt ccgccgggct 120
 ccaggaagg gactagagt ggtctcagcg atttctggtg atggttatcg tacatactac 180
 gcagactccg tgaaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctg 300
 gccttctttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 826
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 826
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 tcctgtgcag cctccggatt cacctttgag tggtatgaga tgcagtgggt ccgccgggct 120
 ccaggaagg gactagagt ggtctcagcg atttctggtg atggttatcg tacatactac 180
 gcagactccg tgaaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctc 300
 ttgtactttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 827
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 827
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 tcctgtgcag cctccggatt cacctttgag tggtatgaga tgcagtgggt ccgccgggct 120
 ccaggaagg gactagagt ggtctcagcg atttctggtg atggttatcg tacatactac 180
 gcagactccg tgaaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagttg 300
 gagttctttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 828
 <211> 348
 <212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 828

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ccaggaagg gactagagtg ggtctcagcg atttctggtg atggttatcg tacatactac      180
gcagactccg tgaaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagctg      300
cagttctttg actactgggg tcggggaacc ctggtcaccg tctcgagc      348
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<210> 829

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 829

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgctctc      60
tcctgtgcag cctccggatt cacctttgag tggtatgaga tgcagtgggt cgcgggggt      120
ccaggaagg gactagagtg ggtctcagcg atttctggtg atggttatcg tacatactac      180
gcagactccg tgaaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagctg      300
ctcttctttg actactgggg tcggggaacc ctggtcaccg tctcgagc      348
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<210> 830

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 830

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tcctgtgcag cctccggatt cacctttgag tggtatgaga tgcagtgggt cgcgggggt      120
ccaggaagg gactagagtg ggtctcagcg atttctggtg atggttatcg tacatactac      180
gcagactccg tgaaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagttg      300
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gagttctttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 831
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 831
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 tcctgtgcag cctccggatt cacctttgag tggtatgaga tgcagtgggt ccgccgggct 120
 ccaggggaagg gactagagtg ggtctcagcg atttctggtg atggttatcg tacatactac 180
 gcagactccg tgaaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagttg 300
 ctcttctttg actaccgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 832
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 832
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 tcctgtgcag cctccggatt catctttgag tggtatgaga tgcagtgggt ccgccgggct 120
 ccaggggaagg gactagagtg ggtctcagcg atttctggtg atggttatcg tacatactac 180
 gcagactccg tgaaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaaaacttg 300
 gagtatcttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 833
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 833
 gaggtgcggc tgttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttgag tggtatgaga tgcagtgggt ccgccgggct 120

ccagggaagg gactagagtg ggtctcagcg atttctggtg atggttatcg tacatactac 180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagttg 300
cagttctttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 834
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 834
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tcctgtgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgttc gaaagagccg 300
tttcgttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 835
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 835
gagggtgcagc tggtggcgtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgtcaggct 120
ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300
tttcgttatg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 836
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 836
gaggtgcagc tgttggcgtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct 120
ccagggaagg gtctagagtg gatctcagct attagtggaa gtggtggtag cacatactac 180
gcagactccg tgaagggccg gtttaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300
tttcgttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 837
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 837
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tcctgtgcag cctccggatt cacctttggg aaggaggaga tgatttgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcatct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaggaa cacgctgtat 240
ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300
tttcgttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 838
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 838
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tcctgtgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300
tttcgttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 839
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 839

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tcctgtgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgctaatac acagcctgcg tgccgaggat accgcggtat attactgttc gaaagagccg	300
tttcgttttg actactgggg tcaggagacc ctggtcaccg tctcgagc	348

<210> 840

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 840

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tcctgtgcag cctccggatt cacctttggg aaggaggaga tgatttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcatct attagtggta gtggtggtag cacatactac	180
gcagactccg ttaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagccg	300
ttacgttttg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 841

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 841

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tcctgtgcag cctccggatt cacctttgag gaggaggaga tgatctgggt ccgccaggct	120
cctgggaagg gtctagagtg gatctcagct attagtggta gtggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc caccgcgaca attctaagaa cactctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgttc gaaagagccg	300
tttcgttttg actacagggg tctgggaacc ttggtcaccg tctcgagc	348

<210> 842
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 842
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 tcctgtgcag cctccggatt cacctttggg aaggaggaga tgatttgggt ccgccaggct 120
 ccaggaagg gtctagagtg ggtctcatct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaggaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagccg 300
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<210> 843
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 843
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 ccaggaagg gtctagagtg gatctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtgt attactgtgc gaaagagccg 300
 tttcgttttg actactgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 844
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 844
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 tcctgtgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct 120
 ccaggaagg gtctagagtg gatctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaataa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gagagagccg 300
 tttcgttttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 845
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 845
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 ccaggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcacgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300
 tttcgttttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 846
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 846
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 ccaggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300
 tttcgttttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 847
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 847
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ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300
ttctactacg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 848
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 848
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ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300
ttctacttcg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 849
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 849
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tcttgcgcag cctccggatt cacctttgag gagaaggaga tgatttgggt ccgtcaggct 120
ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300
ttcttctacg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 850
<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 850

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ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg      300
tttcgttatg actactgggg tcagggaacc ctggtcaccg tctcgagc      348
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<210> 851

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 851

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tcctgcgcag cctccggatt cacctttttc gccgccgaga tgatttgggt ccgccaggct      120
ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg      300
tttcgttatg actactgggg tcagggaacc ctggtcaccg tctcgagc      348
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<210> 852

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 852

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tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct      120
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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg      300
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tttcggttatg actactgggg tcaggggaacc ctgggtcaccg tctcgagc 348

<210> 853

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 853

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tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt cgcgcaggt 120

ccaggggaagg gtctagagtg ggtctcagct attagtcgga tgggtttcag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaata acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300

tttcggttatg actactgggg tcaggggaacc ctgggtcaccg tctcgagc 348

<210> 854

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 854

gaggtgcagc tgttggcgctc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60

tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt cgcgcaggt 120

ccaggggaagg gtctagagtg ggtctcagct attagtcggt ggggtcacag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

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<210> 855

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 855

gaggtgcagc tgttggcgctc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60

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tcttgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct      120
ccaggaaggt gtctagagtg ggtctcagct attagtcgcc tcggttggag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg      300
tttcgttatg actactgggg tcaggaacc ctggtcaccg tctcgagc                    348

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<210> 856

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 856

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gaggtgcagc tggtggcgtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcttgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgtcaggct      120
ccaggaaggt gtctagagtg ggtctcagct attagtcgct ggggtgccag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg      300
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<210> 857

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 857

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gaggtgcagc tggtggcgtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcttgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgtcaggct      120
ccaggaaggt gtctagagtg ggtctcagct attagtaggc aggggtgggag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgtgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg      300
tttcgttatg actactgggg tcaggaacc ctggtcaccg tctcgagc                    348

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<210> 858

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 858
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tcttgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt cgcgcaggct 120
ccaggaaggt gtctagagtg ggtctcagct attagtgtgt ccggttgag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300
tttcgttatg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 859
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 859
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tcttgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt cgcgcaggct 120
ccaggaaggt gtctagagtg ggtctcagct attagtcggt ggggttgag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300
tttcgttatg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 860
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 860
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tcttgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt cgcgcaggct 120
ccaggaaggt gtctagagtg ggtctcagct attagtcgga acggtctgag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300
tttcgttatg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 861
<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 861

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tcctgcgag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcagct attagtgggc tgggttgag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaata acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg	300
tttcgttatg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 862

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 862

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tcctgcgag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcagct attagtgcgt tgggttgag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaata acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg	300
tttcgttatg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 863

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 863

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tcctgcgag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcagct attagtgcga ggggttacag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300
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<210> 864
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 864
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 ccaggggaagg gtctagagtg ggtctcagct attagtaggc acggttggag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300
 ttctgttatg actactgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 865
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 865
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 ccaggggaagg gtctagagtg ggtctcaagc attagcagga gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300
 ttctgttatg actactgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 866
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 866
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tcttgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt cgcgcaggct	120
ccaggaaggt gtctagagtg ggtctcagct attagtcgga tcggtaacag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg	300
tttcggttatg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 867

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 867

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ccaggaaggt gtctagagtg ggtctcagct attagtggtc acggttggtg cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg	300
tttcggttatg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 868

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 868

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ccaggaaggt gtctagagtg ggtctcagct atttcgaggt ggggtggtg cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg	300
tttcggttatg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 869

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 869

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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg      300
ttcatgtatg actactgggg tcaggaacc ctggtcaccg tctcgagc      348
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<210> 870

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 870

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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg      300
ttcccgtagc actactgggg tcaggaacc ctggtcaccg tctcgagc      348
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<210> 871

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 871

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ccaggaagg gtctagagtg ggtctcagct attagtggta gtggtggtgg cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg      300
tttcgttatg actactgggg tcaggaacc ctggtcaccg tctcgagc      348
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<210> 872
 <211> 348
 <212> ADN
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<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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<210> 873
 <211> 348
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<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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<210> 874
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccagggaagg gtctagagtg ggtctcagct attagttaga acggtttcag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300
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<210> 875
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccaggggaagg gtctagagtg ggtctcagct attagtcgca cgggtgggag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300
 ttctggttatg actactgggg tcaggggaacc ctgggtcacccg tctcgagc 348

<210> 876
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
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 ccaggggaagg gtctagagtg ggtctcagct attagtcggg aggggtgggag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300
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ccaggggaagg gtctagagtg ggtctcagct attagtcggc aggggttgag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300
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<210> 878
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggggaagg gtctagagtg ggtctcagct attagtaggg gcggtgggag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300
tttcgttatg actactgggg tcaggggaacc ctgggtcacccg tctcgagc 348

<210> 879
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggggaagg gtctagagtg ggtctcagct attagtcgca cgggttacag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300
tttcgttatg actactgggg tcaggggaacc ctgggtcacccg tctcgagc 348

<210> 880
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 880
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ccagggaagg gtctagagtg ggtctcagct attagtagga acggtaggag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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tttcggttatg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 881
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccagggaagg gtctagagtg ggtctcagct attagtagga acggttacag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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tttcggttatg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 882
<211> 348
<212> ADN
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<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccagggaagg gtctagagtg ggtctcagct attagtagga agggtagcag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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tttcggttatg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 883
<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 883

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tcctgcgag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcagct attagtcggg gcggttggag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg	300
tttcgttatg actactgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 884

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 884

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tcctgcgag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcagct attagtcgct cgggttacag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg	300
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<210> 885

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccagggaagg gtctagagtg ggtctcagct attagtagga acggtatgag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300
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<210> 886
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 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccaggggaagg gtctagagtg ggtctcagct attagtagga acggttacag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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<210> 887
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 <212> ADN
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<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 tcctgtgcag cctccggatt cacctttact gagcatgaga tgatttgggt ccgccaggct 120
 ccaggggaagg gtctggagtg ggtctcatct atttcgggta atggtgctaa tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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 cttaggtttg actactgggg ccaggggaacc ctggtcaccg tctcgagc 348

<210> 888
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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tcctgtgcag cctccggatc cacctttact gagtatgaga tgatttgggt ccgccaggct	120
ccaggaagg gtctggagtg gatctcatct atttcgggta atgggtgctaa tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat atttctgtgc gaaagagccg	300
cttaggtttg actacagggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 889

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 889

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ccaggaagg gtatggagtg ggtctcatct atttcgggta atgggtgctaa tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa catgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg	300
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<210> 890

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggaagg gtctggagtg ggtctcatct atttcgggta atgggtgctaa tacatactac	180
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ctacaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg	300
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<210> 891

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg 300
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<210> 892
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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cttaggtttg actactggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 893
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggaag gtctggagt ggtctcatct atttcgggta atggtgctaa tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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<210> 894
 <211> 348
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<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<210> 895
 <211> 348
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 ccagggaagg gtatggagtg ggtctcatct atttcgggta atgggtgctaa tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccagggaagg gtctggagtg ggtctcatct atttcgggta atgggtgctaa tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagaaccg 300
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<210> 897
 <211> 348
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<220>
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 ccaggggaagg gtctggagtg ggtctcatct atttcgggta atgggtgctaa tacatactac 180
 gcagactccg tgaagggccg gttctccgtc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg 300
 cttagggtttg actactgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 898
 <211> 348
 <212> ADN
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<220>
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 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg 300
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<210> 899
 <211> 348
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<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggaagg gtctggagtg ggtctcatca atttcgggta atggtgctaa tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg 300
cttaggtttg actactgggg tcagggagcc ctggtcaccg tctcgagc 348

<210> 900
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggaagg gtctggagtg ggtctcatct atttcgggta atggtgctaa tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg 300
cttaggtttg acaactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 901
<211> 369
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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tctgtacag cctccggatt cacctttaat atgtatgaga tgctgtgggt ccgccaggct 120
ccaggaagg gtctagagtg ggtctcaggt attagtagac gtggttttac tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagccg 300
attacgtatg atttgaggta tgcgcgtttt gactactcgg gtcaggaac cctggtcacc 360
gtctcgagc 369

<210> 902
<211> 369

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 902

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tcctgtacag cctccggatt cacctttaat atgtatgaga tgtcgtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcaggt attagtagac gtgggttttac tacatactac      180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cagctgtat      240
ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagccg      300
attacgtatg ctacaggta tgcgcgtttt gactactggg gtcaggaac cctggtcacc      360
gtctcgagc                                     369
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<210> 903

<211> 369

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 903

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gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctctc      60
tcctgtacag cctccggatt cacctttaat atgtatgaga tgtcgtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcaggt attagtaggc gtgggttttac tacatactac      180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca atttcaagaa cagctgtat      240
ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagccg      300
attacgtatg atatgaggta tgcgcgtttt gactacgggg gtcaggaac cctggtcacc      360
gtctcgagc                                     369
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<210> 904

<211> 369

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 904

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tcctgtacag cctccggatt cacctttaat atgtatgaga tgtcgtgggt ccgccaggct      120
ccaggaagg gtctagagtg ggtctcaggt attagtaggc gtgggttttac tacatactac      180
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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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 attacgtatg atatgaggta tgcgcgtttt gacaactggg gtcagggaac cctggtcacc 360
 gtctcgaac 369

<210> 905
 <211> 369
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 905
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 tcctgtacag cctccggatt cacctttaat acgtatgaga tgtcgtgggt ccgccaggct 120
 ccagggaaag gtctagagtg ggtctcaggt attggtaggc gtggttttac tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagccg 300
 attacgtatg atttgaggta tgcgcgtttt gactactcgg gtcagggaac cctggtcacc 360
 gtctcgagc 369

<210> 906
 <211> 369
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 906
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 tcctgtacag cctccggatt ctcctttaat atgtatgaga tgtcgtgggt ccgccaggct 120
 ccagggaaaag gtctagagtg ggtctcaggt attagtaggc gtggttatac tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagccg 300
 attacgtatg atatgaggta tgcgcgtttt gactactggg gtcggggaac cctggtcacc 360
 gtctcgagc 369

<210> 907
 <211> 369
 <212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 907
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tcctgtacag cctccggatt cgcctttaat atgtatgaga tgcctgggt cgcagcagct 120
ccaggaagg gactagagtg ggtctcaggt attagtaggc atgggtttac tacgtactac 180
gcagactccg tgaaggccg gttcaccgtc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagccg 300
attacgtatg atatgcgga tgccgcttct gactactggg gtcaggaac cctggtcacc 360
gtctcgagc 369

<210> 908

<211> 369

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 908
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tcctgtacag cctccggatt cacctttaat atgtatgaga tgcctgggt cgcagcagct 120
ccaggaagg gtctagagtg ggtctcaggt attagtaggc gtgggtttac tacatactac 180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat atttctgtgc gaaagagccg 300
attacgtatg atatgagga tgccgcttct gactactggg gtcaggaac cctggtcacc 360
gtctcgagc 369

<210> 909

<211> 369

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 909
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tcctgtacag cctccgggtt cacctttaat atgtatgaga tgcctgggt cgcagcagct 120
ccaggaagg gtctagagtg ggtctcaggt attagtaggc gtgggtttac tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagccg 300
 attacgtatt ctatgaggtg tgcgcgtttt gactactcgg gtctgggaac catggtcacc 360
 gtctcgagc 369

<210> 910
 <211> 369
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 910
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 tcctgtacag cctccggatt cacctttaat atgtatgaga tgtcgtgggt ccgccaggct 120
 ccaggaaggt gtctagagtg ggtctcaggt attagtaggc gtggttttac tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagccg 300
 attacgtatg atatgaggtg tgcgcgtttt gactacagtg gtcaggaac cctggtcacc 360
 gtctcgagc 369

<210> 911
 <211> 369
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 911
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 ccaggaaggt gtctagagtg ggtctcaggt attagtaggc atggttttac tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagccg 300
 attacgtatg atatgaggtg tgcgcgtttt gactactggg gtcaggaac cctggtcacc 360
 gtctcgagc 369

<210> 912
 <211> 369
 <212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 912
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tcctgtacag cctccggatt cacctttaat atgtatgaga tgcgtgggt cgcagcaggt 120
ccaggaagg gtctagagtg ggtctcaggt attagtaggc gtggttttac tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaggagccg 300
attacgtatg atatgaggta tgcgcgtttt gactactggg gtcggggaac cctggtcacc 360
gtctcgagc 369

<210> 913

<211> 369

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 913
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tcctgtacag cctccggttt cacctttaat atgtatgaga tgcgtgggt cgcagcaggt 120
ccaggaagg gtctagagtg ggtctcaggt attagtaggc gtggttttac tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagccg 300
attacgtatg atatgaggta tgcgcgtttt gactactggg gtcggggaac cctggtcacc 360
gtctcgagc 369

<210> 914

<211> 369

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 914
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tcctgtacag cctccggatt ctctttaat atgtatgaga tgcgtgggt cgcagcaggt 120
ccaggaagg gtctagagtg ggtctcaggt attagtaggc gtggttttac tacatactac 180

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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagccg 300
attacgtatg atatgaggta tgcgcgtttt gactactggg gtcaggaac cctggtcacc 360
gtctcgggc 369
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<210> 915
 <211> 369
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 915
gaggtgcagc tgttgagtc tgggggaggc ttggtacaac ctggggggtc cctgcgtctc 60
tcctgtacag cctccggatt cacctttaat atgtatgaga tgtcgtgggt ccgcaaggct 120
ccaggaagg gtctagagtg ggtctcaggt attagtaggc gtggttttac tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgtgaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagccg 300
attacgtatg atatgaggta tgcgcgtttt gactactggg gtcaggaac cctggtcacc 360
gtctcagc 369
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<210> 916
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 916
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120
ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300
tttacttttg aggactggg tcaggaacc ctggtcaccg tctcagc 348
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<210> 917
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 917

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tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300
tttacttttg acgactggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 918

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 918

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tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtac gaaacttccg	300
tttatttttg aatactggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 919

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 919

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tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300
tttatgtttg acgaccggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 920
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 920
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 tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120
 ccaggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac 180
 gcagactccg tgatgggccc gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300
 ttactttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 921
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 921
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 tcctgtgcag cctccggatt ctcttttcgg gattatgaga tgtggtggta ccgccaggct 120
 ccaggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatattac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300
 ttattttttg acaaccgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 922
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 922
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 tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120
 ccaggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggat acctcggtat atcactgtgc gaaacctccg 300
 tttatTTTTg gcgactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 923
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 923
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 tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120
 ccggggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180
 gcagactccg tgaagggccg gttcacgatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300
 tttactTTTTg aggactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 924
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 924
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 tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120
 ccagggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180
 gcagactccg tgatgggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat actgcggtat attactgtgc gaaacttccg 300
 tttatgTTTTg acgaccgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 925
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 925
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60

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ccaggaagg ttctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa catgctgtat      240
ctgcaaatac acagcctgcg tgccgaggat actgcggtat attactgtgc gaaacttccg      300
tttatgtttg acgaccgggg tcaggaacc ctggtcaccg tctcgagc                  348

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<210> 926
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

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<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético
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tctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cgcagggt      120
ccaggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatac acagcctgcg agccgaggat actgcggtat attactgtgc gaaacttccg      300
tttatgtttg acgaccgggg tcaggaacc ctggtcaccg tctcgagc                  348

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<210> 927
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 927
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ccaggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgttt gaaacttccg      300
tttatgtttg actactgggg tcaggaacc ctggtcaccg tctcgagc                  348

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<210> 928
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 928
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tctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cgcagcaggt 120
ccaggaaggt gtctagagcg ggtctcagct attaacccgc aggttacgcg tacatactat 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgatgat accgcggtat atcactgtac gaaacttccg 300
tttatttttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 929
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 929
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ccagggatgg ttctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctatat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300
tttttttttg actccagggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 930
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 930
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ccaggaaggt gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180
gcagactctg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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<210> 931
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<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccagggaagg gtctagagcg ggtctcagct attaatccgc agggtagcgc tacatactac	180
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ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg	300
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<210> 932

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccagggaagg gtctagagcg ggtctcagct attaatccgc agggtagcgc tacatattac	180
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ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg	300
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<210> 933

<211> 348

<212> ADN

<213> Secuencia Artificial

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<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccagggaagg ttctagagcg ggtctcagct attaatccgc agggtagcgc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa catgctgtat	240

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 <213> Secuencia Artificial

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 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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<210> 935
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtac gaaacttccg 300
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<210> 936
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgttt gaaacttccg	300
tttacttttg aggactggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 937
 <211> 348
 <212> ADN
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<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggaagg gtctagagcg ggtctcagct attaaccgc aggtacgcg tacatactat	180
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ctgcaaatga acagcctgcg tgccgatgat accgcggtat atcactgtac gaaacttccg	300
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<210> 938
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac	180
gcagactccg tgatgggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagaacct	300
tatagttttg actcctggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 939
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 <212> ADN
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<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac	180
gcagactccg tgatgggccc gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat atcactgtgc gaaagaacct	300
tatagttatg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 940

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 940

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tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccgggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac	180
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ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300
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<210> 941

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccgggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac	180
gcagactccg tgatgggccc gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat actgcggtat attactgtgc gaaacttccg	300
tttatgtttg acgaccgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 942
 <211> 348
 <212> ADN
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<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180
 gcagactccg tgatgggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat actgcggtat attactgtgc gaaacttccg 300
 tttatgtttg acgactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 943
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 <212> ADN
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<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 tcctgtgcag cctccggatt cacctttgct gggtatgagt tgtggtgggt ccgccaggct 120
 ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180
 gcagactccg tgatgggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300
 tttacttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 944
 <211> 348
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 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 tcctgtgcag cctccggatt cacctttgct gggtatgagt tgtggtgggt ccgccaggct 120
 ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180

gcagactccg tgatgggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat actgcggtat attactgtgc gaaacttccg 300
 tttatgtttg acgaccgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 945
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 tcctgtgcag cctccggatt cacctttgct gggtatgaga tgtggtggtt ccgccaggct 120
 ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180
 gcagactccg tgatgggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300
 tttacttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 946
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 tcctgtgcag cctccggatt cacctttgct gggtatgaga tgtggtggtt ccgccaggct 120
 ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180
 gcagactccg tgatgggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat actgcggtat attactgtgc gaaacttccg 300
 tttatgtttg acgaccgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 947
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggaaggt gtctagagtg ggtctcagct attaatccgc aggttacgcg tacatactac 180
gcagactccg tgatgggccc gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300
tttacttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 948
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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tctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cgcagcaggt 120
ccaggaaggt gtctagagtg ggtctcagct attaatccgc aggttacgcg tacatactac 180
gcagactccg tgatgggccc gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat actgcggtat attactgtgc gaaacttccg 300
tttatgtttg acgaccgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 949
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 949
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tctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cgcagcaggt 120
ccaggaaggt gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180
gcagactccg tgaagggccc gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300
acctactttt ccgaccgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 950
<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 950

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ccagggaagg gtctagagcg ggtctcagct attaatccgc agggtagcgc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaataa acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg      300
tttttctttg aggagtgggg tcagggaacc ctggtcaccg tctcgagc                    348
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<210> 951

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 951

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tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccagggaagg gtctagagcg ggtctcagct attaatccgc agggtagcgc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaataa acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg      300
acgtacttta aggactgggg tcagggaacc ctggtcaccg tctcgagc                    348
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<210> 952

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccagggaagg gtctagagcg ggtctcagct attaatccgc agggtagcgc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
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ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300
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<210> 953
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 <212> ADN
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<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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<210> 954
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300
 tttccgtttt ccgagtgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 955
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaattg acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg	300
tttactttt cagagtggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 956

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 956

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tctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cgcaggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccgt acggtaacct cacatactac	180
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ctgcaaattg acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300
tttacttttg aggactggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 957

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggaagg gtctagagcg ggtctcagct attaatccgc ccgtacctt gacatactac	180
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ctgcaaattg acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300
tttacttttg aggaccggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 958

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 958

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ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggtggctt gacatactac	180
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ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300
tttacttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 959

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 959

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tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccga tgggtgggtt cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300
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<210> 960

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 960

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ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggttcgca cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300
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<210> 961
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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<210> 962
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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<210> 963
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccaggaagg gtctagagcg ggtctcagct attaatccgg ccggtcggtt gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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<210> 964
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggtagctt gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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 ttactttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 965
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcy tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat atcactgtgc gaaacttccg 300
 ttactttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 966
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggaaggt gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300
tttacttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 967
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggaaggt gtctagagcg ggtctcagct attaatccgt acggtgggt gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300
tttacttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 968
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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tcctgtgcag cctccggatt cacctttccg gattatgaga tgtggtgggt cgcgcaggt 120
ccaggaaggt gtctagagcg ggtctcagct attaatccgt ggggtaacca cacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300
tttacttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 969
<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 969

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ccagggaagg gtctagagcg ggtctcagct attaatccgc acggtggcta cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaataa acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg      300
tttacttttg aggactgggg tcagggaacc ctggtcaccg tctcgagc                    348
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<210> 970

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 970

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ccagggaagg gtctagagcg ggtctcagct attaatccgc cgggtatgct cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaataa acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg      300
tttacttttg acgactgggg tcagggaacc ctggtcaccg tctcgagc                    348
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<210> 971

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 971

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tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cgcgcaggct      120
ccagggaagg gtctagagcg ggtctcagct attaatccgt ggggtcagtt gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
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ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300
 tttacttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 972
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 972
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 tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120
 ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggtggcta cacatactac 180
 gcagactccg tgaagggccg attcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300
 tttacttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 973
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 973
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 ccaggaagg gtctagagcg ggtctcagct attaatccgt cgggtgggt gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300
 tttacttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 974
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 974
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tctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cgcaggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccgt cgggtgggtt gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300
tttacttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 975

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 975

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tctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cgcaggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccgt cgggtacgct cacatactac	180
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ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300
tttacttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 976

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 976

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ccaggaagg gtctagagcg ggtctcagct attaatccgt acggttcggt gacatactac	180
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ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300
tttacttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 977

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 977

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ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggtggcta cacatactac	180
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ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300
tttacttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 978

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 978

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ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300
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<210> 979

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300
tttacttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 980
 <211> 348
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<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ttactttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 981
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<210> 982
 <211> 348
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<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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<210> 983
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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<210> 984
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccaggaagg gtctggagcg ggtctcagct attaatccgg cgggtatggt gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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<210> 985
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggaaggt gtctagagcg ggtctcagct attaatccgc acggtacctt gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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tttacttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 986
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggaaggt gtctagagcg ggtctcagct attaatccgt ggggttcggt gacatactac 180
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tttacttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 987
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggaaggt gtctagagcg ggtctcagct attaatccgt acggtggcct gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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tttacttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 988
<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 988

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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
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tttacttttg aggactgggg tcagggaacc ctggtcaccg tctcgagc                    348
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<210> 989

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 989

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tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cgcgcaggct      120
ccagggaagg gtctggagcg ggtctcagct attaatccgt acggtggcct gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaataa acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg      300
tttacttttg aggactgggg tcagggaacc ctggtcaccg tctcgagc                    348
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<210> 990

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 990

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tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cgcgcaggct      120
ccagggaagg gtctagagcg ggtctcagct attaatccgt ggggtggggt cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
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ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300
 ttactttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 991
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 991
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 tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120
 ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggtgggtt gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300
 ttactttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 992
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 992
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 tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120
 ccaggaagg gtctagagcg ggtctcagct attaatccgt acggtgggct gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatgg acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300
 ttactttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 993
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 993
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tctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120
ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggtacgtt gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300
tttacttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 994

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 994

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tctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120
ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggtggcta cacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300
tttacttttg aggactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 995

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 995

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120
ccaggaagg gtctagagcg ggtctcagct attaatccgt acggtaacct gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300
tttacttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 996

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 996

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccgc acggtgggtt cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300
tttacttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 997

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 997

gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgctctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccgg ccggtttcta cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300
tttacttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 998

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 998

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tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccgg ccgggtggcct cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg	300
tttacttttg acgactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 999
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 999
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 tcctgtgcag cctccggatt cgcctttcgg gattatgaga tgtggtgggt ccgccaggct 120
 ccaggaagg gtctagagcg ggtctcagct attaatccgc acggttcctt cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300
 ttactttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1000
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1000
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttcgt gattatgaga tgtggtgggt ccgccaggct 120
 ccaggaagg gtctagagcg ggtctcagct attaatccgc ccggtgggta cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat atcactgtgc gaaacttccg 300
 ttactttttg aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1001
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1001
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120
 ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300
 ttttggttta cggagtgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1002
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1002
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 tcctgtgcag cctccggatt cacctttcgg gattatgaga tgttggtgggt ccgccaggct 120
 ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300
 ttcatgtttt ccgaccggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1003
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1003
 gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttcgg gattatgaga tgttggtgggt ccgccaggct 120
 ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300
 tttttgtttt aggagtgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1004
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1004
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cgcgcaggt 120
ccaggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300
acgcggtttg aggactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1005
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1005
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tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cgcgcaggt 120
ccaggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300
ttttactttc acgagtgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1006
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1006
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cgcgcaggt 120
ccaggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300
tttcgttatg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1007
<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1007

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gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cgcgcaggct      120
ccagggaagg gtctagagcg ggtctcagct attaatccgc agggtagcgc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaataa acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg      300
acgttcttta aggactgggg tcagggaacc ctggtcaccg tctcgagc                    348
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<210> 1008

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1008

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tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cgcgcaggct      120
ccagggaagg gtctagagcg ggtctcagct attaatccgc agggtagacg tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaataa acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg      300
tttttctttc aggagtgggg tcagggaacc ctggtcaccg tctcgagc                    348
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<210> 1009

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1009

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tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cgcgcaggct      120
ccagggaagg gtctagagcg ggtctcagct attaatccgc agggtagcgc tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
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ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300
 cagttgtttc acgaccgggg tcaggaacc ctggtcacgc tctcgagc 348

<210> 1010
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1010
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 tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120
 ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300
 cagctctttg aggactgggg tcaggaacc ctggtcacgc tctcgagc 348

<210> 1011
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1011
 gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120
 ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat atcactgtgc gaaacttccg 300
 tttgggtttt ccgagtgggg tcaggaacc ctggtcacgc tctcgagc 348

<210> 1012
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1012
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tctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cgcagggt      120
ccaggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg      300
cagttgtttc aggactggg tcaggaacc ctggtcaccg tctcgagc                    348

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<210> 1013

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1013

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gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cgcagggt      120
ccaggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg      300
tttttctttc acgagtggg tcaggaacc ctggtcaccg tctcgagc                    348

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<210> 1014

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1014

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gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
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ccaggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg      300
cactacttta aggactggg tcaggaacc ctggtcaccg tctcgagc                    348

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<210> 1015

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1015
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ccaggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac 180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaata acagcctgcg tgccaggat accgcggtat attactgtgc gaaacttccg 300
ttttactttg aggagtggg tcaggaacc ctggtcaccg tctcgagc 348
<210> 1016
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1016
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ccaggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac 180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaata acagcctgcg tgccaggat accgcggtat attactgtgc gaaacttccg 300
tttaggtttt ccgaccggg tcaggaacc ctggtcaccg tctcgagc 348
<210> 1017
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1017
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ccaggaagg gtctagagcg ggtctcagct attaatccgc aggtacgcg tacatactac 180
gcagactccg tgaaggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaata acagcctgcg tgccaggac accgcggtat attactgtgc gaaacttccg 300
acgctgtttc aggactggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1018

<211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1018
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120
 ccaggaaggt gtctagagcg ggtctcagct attaatccgc agggtagcgc tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300
 ttttactttt ccgagtgggg tcaggaacc ctggtcaccg tctcgaa 348

<210> 1019
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1019
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 ccaggaaggt gtctagagcg ggtctcagct attaatccgc agggtagcgc tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300
 ttttggtttc aggagtgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1020
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1020
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 ccaggaaggt gtctagagcg ggtctcagct attaatccgt ggggttcggt gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300
 ttttactttc aggagtgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1021
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1021
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 ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggttcggt gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat atcactgtgc gaaacttccg 300
 atgttctttg aggactgggg tcaggaacc ctggtcaccg tctcgaac 348

<210> 1022
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1022
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 ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggttcggt gacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300
 ttttactttc acgagtgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1023
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1023

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gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc      60
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ccaggaaggt gtctagagcg ggtctcagct attaatccgt ggggttcggt gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg      300
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<210> 1024
<211> 348
<212> ADN
<213> Secuencia Artificial

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<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 1024
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ccaggaaggt gtctagagcg ggtctcagct attaatccgt ggggttcggt gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg      300
tttttctttc acgagtgggg tcaggaacc ctggtcaccg tctcgagc                      348

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<210> 1025
<211> 348
<212> ADN
<213> Secuencia Artificial

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<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 1025
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc      60
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ccaggaaggt gtctagagcg ggtctcagct attaatccgt ggggtggggt cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg      300
ttttactttc aggagtgggg tcaggaacc ctggtcaccg tctcgagc                      348

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<210> 1026
<211> 348
<212> ADN

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<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1026

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tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cgcagggt	120
ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggtgggtt cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat atcactgtgc gaaacttccg	300
atgttctttg aggactgggg tcaggaacc ctggtcaccg tctcgaa	348

<210> 1027

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1027

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggtc cctgctctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cgcagggt	120
ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggtgggtt cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg	300
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<210> 1028

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1028

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tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cgcagggt	120
ccaggaagg gtctagagcg ggtctcagct attaatccgt ggggtgggtt cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg	300

tttttctttc aggagtgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 1029

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1029

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggggaagg gtctagagcg ggtctcagct attaatccgt ggggtggggt cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

tttttctttc acgagtgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 1030

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1030

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tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

ccaggggaagg gtctagagcg ggtctcagct attaatccgt ggggtggggt gacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300

ttttactttc aggagtgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 1031

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1031

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120

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ccaggggaagg gtctagagcg ggtctcagct attaatccgt ggggtggggtt gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat atcactgtgc gaaacttccg      300
atgttctttt aggactgggg tcaggggaacc ctggtcaccg tctcgaaac      348

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<210> 1032

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 1032
gagggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct      120
ccaggggaagg gtctagagcg ggtctcagct attaatccgt ggggtggggtt gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg      300
ttttactttc acgagtgggg tcaggggaacc ctggtcaccg tctcgagc      348

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<210> 1033

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 1033
gagggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc      60
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ccaggggaagg gtctagagcg ggtctcagct attaatccgt ggggtggggtt gacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg      300
tttttctttc aggagtgggg tcaggggaacc ctggtcaccg tctcgagc      348

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<210> 1034

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1034
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tcctgtgcag cctccggatt caccttttcg gattatgaga tgtggtgggt ccgccaggct 120
ccagggaagg gtctagagcg ggtctcagct attaatccgt ggggtgggtt gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaacttccg 300
tttttctttc acgagtgggg tcagggaacc ctggtcaccg tctcgagc 348
<210> 1035
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1035
gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
tcctgtgcag cctccggatt caccttttcg gattatgaga tgtggtgggt ccgccaggct 120
ccagggaagg gtctagagcg ggtctcagct attaatccgc aggggtacgcg tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat atcactgtgc gaaacttccg 300
atgttctttt aggactgggg tcagggaacc ctggtcaccg tctccagc 348
<210> 1036
<211> 357
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1036
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tcctgtgcag cctccggatt caccttttcg acttatcata tgcagtgggt ccgccgggct 120
ccagggaagg gcctggagtg ggtctcaatg attgatgcg atggtcttgg gacatactac 180
gcagaccccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccaaggac accgcggtat attactgtgc gagaccgggt 300
ccgcagtttg gtcagtttga ctacttgggt cagggaaccc tggtcaccgt ctcgagc 357
<210> 1037
<211> 357
<212> ADN
<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1037

gaggtgcagc tgtttgagtc tgggggaggc ttggtacaga ctgggggggc cctgcgtctc	60
tcctgtgcag cctccggatt caccttttcg acttatcata tgcagtgggt ccgccaggct	120
ccagggaagg gtctggagtg ggtctcaatg attgatgcgg atggtcttgg gaaatactac	180
gcagaccccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgt gaaaccgggt	300
ccgcagtttg gtcagtatga ctactggggg cagggaaccc tggtcaccgt ctcgagc	357

<210> 1038

<211> 363

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1038

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tcctgttcag cttccggatt caccttttcg gggtatgata tgcagtgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcaacg attagtgcgt cgggtgttta tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatcct	300
aatcggtttg cgcttaatac ttttgactac aggggtcggg gaaccctggg caccgtctcg	360
agc	363

<210> 1039

<211> 363

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1039

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tcctgtgcag cttccggatt caccttttcg gggtatgata tgcagtgggt ccgccaggct	120
ccagggaggg gtctagagtg ggtctcaacg attagtgcgt cgggtgttta tacatactac	180
acagactccg tgaagggccg gttcaccacc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtac gaaatatcca	300

aatcggttttg cgcgtaataa ttttgactac tgggggtcagg gaaccctggt caccgtctcg 360
agc 363

<210> 1040
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1040
gacatcctga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaaataag ttctattttg tgggcgtag ctgtgtacca gcagaaacca 120
ggggaagccc ctaagctcct gatcgagagt tcttcgggtt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtgttcag aatgcggttt ggcctggtac gttcagccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1041
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1041
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atcacttgcc gggcagacag ttctattttg tgggcgtag ctgtgtacca gcagaaacca 120
gggaaagccc ctaagctcct gatcgagagt tcatccggtt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtgttcag aatgcggttt ggcctggtac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1042
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1042

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gacatccaga tgaccgtgtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcagatag ttctattttg tgggcgtag cttggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatcgagagt tcttcggat tgcaaagcgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtgttcag aatgcggttt ggctggtac gttcgccaa      300
gggaccaagg tggaaatcaa acgg                                             324
<210> 1043
<211> 324
<212> ADN
<213> Secuencia Artificial

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<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 1043
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atcacttgcc gggcaaata tag ttctattttg tgggcgtag cttggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatcgagagt tcttcgggtt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtgttcag aatgcggttt ggctggtac gttcgacaa      300
gggaccaagg tggaaatcaa acgg                                             324

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<210> 1044
<211> 324
<212> ADN
<213> Secuencia Artificial

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<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 1044
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atcacttgcc gggcaaata tag ttctattttg tgggcgtag cttggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatcgagagt tctaccggtt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtgttcag aatgcggttt ggctggtac gttcgccaa      300
gggaccaagg tggaaatcaa acgg                                             324

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<210> 1045
<211> 324
<212> ADN
<213> Secuencia Artificial

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<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1045

gacatccaga tgaccgtgtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaaata tag ttctattttg tgggcgttag cttggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatcgagagt tcttcggat tgcaaagcgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtgttcag aatgcgggtt ggcttggtac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1046

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1046

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcagatag ttctattttg tgggcgttag cttggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatcgagagt tcttcgggtt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtgttcag aatgcgggtt ggcttggtac gttcgaccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1047

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1047

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atcacttgcc gggcaaata tag ttctattttg tgggcgttag cttggtacca gcagaaacca	120
gggaaagccc ctgagctcct gatcgagagt tcttcgggtc tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtgttcag aatgcgggtt ggcttggtac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1048
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1048
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 atcacttgcc gggcgaatag ttctatattg tgggcgttg cttggtacca gcagaaacca 120
 gggaaagccc ctaagctcct gatcgagagt tcttccggtt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtgttcag aatgcggtt ggcctggtac gttcggccaa 300
 gggaccaagg tggaaaacaa acgg 324

<210> 1049
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1049
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 atcacttgcc gggcaaata tag ttctattctg tgggcgttag cttggtacca gcagaaacct 120
 gggaaagccc ctaagctcct gatcgagagt tcttccggtt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtgttcag aatgcggtt ggcctggtac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1050
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1050
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 atcacttgcc gggcaaata tag ttctattttg tgggcgttag cttggtacca gcagaaacca 120
 gggaaagccc ctaagctcct gatcgagagt tcttccggtt tgcaaagtgg gatcccatca 180

cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtgttcag aatgcggttt ggctggtac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1051
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1051
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgttgaga cctgtgcacc 60
atcacttgcc gggcaaatac ttctattttg tgggcgtag cttggtacca gcagaaacca 120
gggaaagccc ctaagctcct gatcgagagt tcttcggat tgcaaagcgg ggtcccatca 180
cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtgttcag aatgcggttt ggctggtac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1052
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1052
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atcacttgcc gggcaaatac ttctattttg tgggcgtag cttggtacca gcagaaacca 120
gggaaagccc ctaagctcct gatcgagagt tcttcggat tgcaaagtgg ggtcccatca 180
cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtgttcag aatgcggttt ggctggtac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1053
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1053
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaaatag ttctattttg tgggcgtttag cttggtacca gcagaaacca 120
gggaaagccc ctaagctcct gatcgagagt tcttcggtt tgcaaagtgg ggtcccatca 180
cgtttcagtg gaagtggaac tgggacagat ttcactctca ccatcagcgg tctgcaacct 240
gaagattttg ctacgtacta ctgtgttcag aatgcggttt ggcttggtac gttcgaccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1054
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1054
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcccttgcc gggcaaatag ttctattttg tgggcgtttag cttggtacca gcagaaacca 120
gggaaagccc ctaagctcct gatcgagagt tcttcggtt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtgcac tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtgttcag aatgcggttt ggcttggtac gttcggccaa 300
gggaccaagg tggagatcaa acgg 324

<210> 1055
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1055
gacatccaga tggcccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca gacgattgag cgtcgtttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatctt gcttcccggtt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcatcag tatgcgagtc cacctttgac gttaggccaa 300
gggaccaaag tggaaatcaa acgg 324

<210> 1056
<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1056

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagtgtcacc	60
atcacttgcc gggcaagtca gacgattgag cgtcgtttaa attggtatca gcagaaacca	120
ggggaagccc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgccatcag tatgcgagtc cacctttgac gttcggccaa	300
gggaccaatg tggaaatcaa acgg	324

<210> 1057

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1057

gacatccaga tgacccagtc tccatcctcc ctatctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gacgattgag cgtcgtttaa attggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctgcgacta ctgtcatcag tacgagagtc cacctttgac gtttgccaa	300
gggaccaaag tggaaatcaa acgg	324

<210> 1058

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1058

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtcg gacgattgag cgtcgtttaa attggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatctt gcttcgcggt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa	300

gggaccaaag tggaaatcaa acgg

324

<210> 1059

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1059

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atcacttgcc gggcaagtca gacgattgag cgtcgtttta attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatca 180

cgtttcagtgc gcagtggatc tgggacagat ttactctca ccatcagcaa tctgcaacct 240

gaagattctg ctacgtacta ctgtcatcag tatgcgagtc cacctttgac gttaggccaa 300

gggaccaaag tggaaatcaa acgg 324

<210> 1060

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1060

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagcca gacgattgag cgtcgtttta attggtatca gcagaaacca 120

gggaaggccc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatca 180

cgtttcagtgc gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcatcag tatgcgagtc cacctttgac gttaggccaa 300

gggaccaaag tggaaatcaa acgg 324

<210> 1061

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1061

gacatccaga taaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gacgattgag cgtcgtttta attggtatca gcagaaacca 120

gggaaagacc ctaagctcct gatctatctt ggttcccggt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcatcag tatgagagtc ctcctttgac gttcggccaa 300
 gggaccaaag tggaaatcaa acgg 324
 <210> 1062
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1062
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca gacgattgag cgtcgtttaa attggtatca gcagaaacca 120
 ggggaagccc ctaagctcct gatctatctt ggttcccggt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300
 gggaccaaag tggaaatcaa atgg 324

<210> 1063
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1063
 gacatccagt tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc 60
 atcacttgcc gggcaagtca gacgattgag cgtcgtttaa attggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatctt ggttcccggt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagaa ttactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300
 gggaccaaag tggaaatcaa acgg 324

<210> 1064
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1064
gacatccaga tgtcccagtc tccatccacc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca gacgattgag cgtcgtttta attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatctt gcttcccgtt tgcaaagtgg ggtcccatca 180
cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagatcttg ctacgtacta ctgtcatcag tatgagagtc cacctttgat gttcggccaa 300
gggaccaaag tggaaatcaa acgg 324

<210> 1065
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1065
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
attacttgcc gggcaagtca gacgattgag cgtcgtttta attggtatca gcagaaacca 120
gggaaagacc ctaagctcct gatctatctt gcttcccgtt tgcaaagtgg ggtcccatca 180
cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacca 240
gaagatcttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300
gggaccaaag tggaaatcaa acgg 324

<210> 1066
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1066
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ccgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca gacgattgag cgtcgtttta actggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatctt gcttcccgtt tgcaaagtgg ggtcccatca 180
cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagatcttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300
gggaccaaag tggaaatcaa acgg 324

<210> 1067
<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1067

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atcacttgcc gggcaagtca gacgattgag cgtcgtttaa attggtatca gcagaaacca      120
gggaaagccc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa      300
gggaccaaag tggaaatcaa acgg                                           324
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<210> 1068

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1068

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atcacttgcc gggcaagtca gtcgattgag cgtcgtttaa attggtatca gcagaaacca      120
ggggaagccc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa      300
gggactaaag tggaaatcaa acgg                                           324
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<210> 1069

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1069

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atcacttgcc gggcaagtcg gacgattgag cgtcgtttaa attggtatca gcagaaacca      120
gggaaagccc ctaagctcct gatctatctt gcttcgcggt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct      240
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gaagattttg ctacgtacta ctgtcatccg tatgagagtc cacctttgac gttcggccaa 300
 gggaccaaag tggaaatcaa acgg 324

<210> 1070
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1070
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca ggcgattgag cgtcgtttaa attggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatct 180
 cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcagcca 240
 gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gtcggccaa 300
 gggaccaaag tggaaatcaa acgg 324

<210> 1071
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1071
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 atcacttgcc gggcaagtca ggcgattgag cgtcgtttaa attggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatctt gcttctcggt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300
 gggaccaaag tggaaatcaa acgg 324

<210> 1072
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1072
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

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atcacttgcc gggcaagtca gacgattggg cgtcgtttta attggtatca gcagaaacca    120
gggaaagccc ctaagctcct gatctatctt gtttcccggt tgcaaagtgg ggtcccatca    180
cgtttcagtg gcagtggatc tgggtcagat ttactctca ccatcagcag tctgcaacct    240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa    300
gggaccaaag tggaaatcaa acgg                                           324

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<210> 1073
<211> 324
<212> ADN
<213> Secuencia Artificial

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<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 1073
gacatccaga tgaccagtc tccatcctcc ctttctgcat ctgtaggaga ccgtgtcacc    60
atcacttgcc gagcaagtca gacgattgag cgtcgtttta attggtatca gcagaaacca    120
gggaaagccc ctaagctcct gatctatctt gtttcccggt tgcaaagtgg ggtcccatca    180
cgtttcagtg gcagtggatc tgggacagaa ttactctca ccatcagcag tctgcaacct    240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa    300
gggaccaaag tggaaatcaa acgg                                           324

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<210> 1074
<211> 324
<212> ADN
<213> Secuencia Artificial

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<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 1074
gacatccaga tgaccagac tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc    60
atcacttgcc gggcaagtca gacgattgag cgtcgtttta attggtatca gcagaaacca    120
ggggaagccc ctaagctcct gatctatctt gtttcccggt tgcaaagtgg ggtcccatca    180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct    240
gaagattttg ccacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa    300
gggaccaaag tgaaaatcaa acgg                                           324

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<210> 1075
<211> 324
<212> ADN
<213> Secuencia Artificial

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<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1075

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagtgtcacc	60
atcacttgcc gggcaagtca gacgattgag cgtcggttaa attggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaaccc	240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa	300
gggaccaaag tggaaatcaa acgg	324

<210> 1076

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1076

cacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gacgattgag cgtcggttaa attggtatca gcagaaacca	120
gggaaagccc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgccatcag tatgagagtc cacctttgac gttcggccaa	300
gggaccaaag tggaaatcaa acgg	324

<210> 1077

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1077

gaggtccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gacgattgag cgtcggttaa attggtatca gcagaaacca	120
ggggaagccc ctaagctcct gatctatctt acttcccggt tgcaaagcgg ggtcccatca	180
cgtttcagtg gtagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgccatcag tatgcgagtc cacctttgac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1078
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1078
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 atcacttgcc gggcaagtca gacgattgag cgtcgtttaa attggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcaccag tatgagagtc cacctttgac gttcggccaa 300
 gggaccaaag tggtaatcaa acgg 324

<210> 1079
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1079
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc 60
 atcacttgcc gggcaagtca gacgattgag cgtcgtttaa attggtatca gcagaaacct 120
 gggaaagccc ctaggctcct gatctatctt gctaccggt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300
 gggaccaaag tggaaatcaa acgg 324

<210> 1080
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1080
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 atcacttgcc gggcaagtca gccgattgag cgtcgtttaa attggtatca gcagaagcca 120
 gggaaagccc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatca 180

cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacatacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300

gggaccaaag tggaaatcaa acgg 324

<210> 1081

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1081

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gacgattggg cgtcgtttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatctt gtttcccggt tgcaaagtgg ggtcccatca 180

cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300

gggaccaaag tggaaatcaa acgg 324

<210> 1082

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1082

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca gtcgattgag cgccgtttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatctt gtttcccggt tgcaaagtgg ggtcccatca 180

cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtcatcag tatgagagtc ctcttttgac gttcggccaa 300

gggaccaaag tggaaatcat acgg 324

<210> 1083

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1083

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc 60

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atcacttgcc gggcaagtca gacgattgag cgtcgtttta attggtatca gcagaaacct 120
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cgcttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300
gggaccaaag tggaaatcaa acgg 324

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<210> 1084
<211> 324
<212> ADN
<213> Secuencia Artificial

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<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 1084
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
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gggaaagccc ctaagctcct gatctatctt gcttcccggt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc ctctttgac gttcggccaa 300
gggaccaaag tggaaatcaa acgg 324

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<210> 1085
<211> 324
<212> ADN
<213> Secuencia Artificial

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<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 1085
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc 60
atcacttgcc gggcaagtca gacgattgag cgtcgtttta attggtatca gcagaaacct 120
gggaaagccc ctaggctcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca 180
cgcttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcatcag ttcgagcacc cacctttgac gttcggccaa 300
gggaccaaag tggaaatcaa acgg 324

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<210> 1086
<211> 324
<212> ADN
<213> Secuencia Artificial

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<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1086

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atcacttgcc gggcaagttt cccattgac cgtcgtttta attggtatca gcagaaacct	120
gggaaagccc ctaggctcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca	180
cgcttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa	300
gggaccaaag tggaaatcaa acgg	324

<210> 1087

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1087

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc	60
atcacttgcc gggcaagttc caccattggc cgtcgtttta attggtatca gcagaaacct	120
gggaaagccc ctaggctcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca	180
cgcttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa	300
gggaccaaag tggaaatcaa acgg	324

<210> 1088

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1088

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atcacttgcc gggcaagttc ccagattggg cgtcgtttta attggtacca gcagaaacca	120
gggaaagccc ctaggctcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca	180
cgcttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa	300
gggaccaaag tggaaatcaa acgg	324

<210> 1089
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1089
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 gggaaagccc ctaggctcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca 180
 cgcttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300
 gggaccaaag tggaaatcaa acgg 324

<210> 1090
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1090
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 atcacttgcc gggcaagtca gcagattggc cgccgtttaa attggtatca gcagaaacct 120
 gggaaagccc ctaggctcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca 180
 cgcttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300
 gggaccaaag tggaaatcaa acgg 324

<210> 1091
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1091
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 atcacttgcc gggcaagtca gccgattgcc cgccgtttaa attggtacca gcagaaacca 120
 gggaaagccc ctaggctcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca 180

cgcttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300
gggaccaaag tggaaatcaa acgg 324

<210> 1092
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1092
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atcacttgcc gggcaagtgg gaacattggc cgtcgtttta attggtacca gcagaaacca 120
gggaaagccc ctaggctcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca 180
cgcttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300
gggaccaaag tggaaatcaa gcgg 324

<210> 1093
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1093
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc 60
atcacttgcc gggcaagtgg gaacattgac cgtcgtttta attggtacca gcagaaacca 120
gggaaagccc ctaggctcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca 180
cgcttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300
gggaccaaag tggaaatcaa acgg 324

<210> 1094
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1094
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc 60
atcacttgcc gggcaagtca gagcattggg cgtcgtttaa attggtacca gcagaaacct 120
gggaaagccc ctaggctcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca 180
cgcttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300
gggaccaaag tggaaatcaa acgg 324

<210> 1095
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1095
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc 60
atcacttgcc gggcaagtca gaacattggg acgcgtttaa attggtacca gcagaaacca 120
gggaaagccc ctaggctcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca 180
cgcttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300
gggaccaaag tggaaatcaa acgg 324

<210> 1096
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1096
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgagtcacc 60
atcacttgcc gggcaagtga ggtcattggg cgtcgtttaa attggtacca gcagaaacca 120
gggaaagccc ctaggctcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca 180
cgcttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300
gggaccaaag tggaaatcaa acgg 324

<210> 1097
<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1097

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atcacttgcc gggcaagtga ggcgattggc cgtcgtttaa attggtatca gcagaaacca      120
gggaaagccc ctaggctcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca      180
cgcttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa      300
gggaccaaag tggaaatcaa acgg                                           324
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<210> 1098

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1098

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atcacttgcc gggcaagtac cagcattgcg cgtcgtttaa attggtatca gcagaaacct      120
gggaaagccc ctaggctcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca      180
cgcttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa      300
gggaccaaag tggaaatcaa acgg                                           324
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<210> 1099

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1099

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atcacttgcc gggcaagttt gaacattggg cgtcgtttaa attggtacca gcagaaacca      120
gggaaagccc ctaggctcct gatctatctt gctaccggtt tgcaaagtgg ggtcccatca      180
cgcttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
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gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300

gggaccaaag tggaaatcaa acgg 324

<210> 1100

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1100

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gggaaagccc ctaggctcct gatctatctt tcgtcgaagt tgcaaagtgg ggtcccatca 180

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gaagattttg ctacgtacta ctgtcatcag tatgagagtc cacctttgac gttcggccaa 300

gggaccaaag tggaaatcaa acgg 324

<210> 1101

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1101

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tcctgtgcag cctccggatc caccattgct gggatatgaga tgtggtgggt ccgccaggct 120

ccagggaagg gtctagagcg tgtctcagct attagtggta gtggtggtag cacatactac 180

gcagactccg tgaagggccg gttcaccatc tcccagagcg attccaagaa cacgctgtat 240

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tatagttttg actactgggg tcagggaacc ctggtcacccg tctcgagc 348

<210> 1102

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1102

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tcctgtgcag cctccggatt cacctttgct gggatatgaga tgtggtgggt ccgccaggct 120

ccaggggaagg gtctagagcg gatctcagct attagcggtg gtggtggttag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gagagatcct 300
tatagtttttg actactgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 1103
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1103
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tcctgtgcag ccaccggatc cacctttgct gggtatgaga tgtggtgggt ccgccaggct 120
ccaggggaagg gtctagagcg ggtctcagct attagtggta gtggtggttag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gagagatcct 300
tacagttatg actactgggg tcaggggaacc ctggtctccg tctcgagc 348

<210> 1104
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1104
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tcctgtgcag cctccggact cacctttgct gggtatgaga tgtggtgggt ccgccaggca 120
ccaggggaagg gtctagagcg ggtctcagct attagtggta gtggtggttag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggat accgcagtat atcactgtgc gagagatcct 300
tatagtttttg actactgggg tcaggggaacc ctggtcaccg tctcgagc 348

<210> 1105
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1105
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tcctgtgcag cctccggatt cacctttgct gggtatgaga tgtggtgggt cgcgcaggt 120
ccagggaagg gtctagagcg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactctg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tgccgaggat accgcggtat atcactgtgc gaaagaacct 300
tatagttatg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 1106
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1106
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tcctgtgcag cctccggatc cacctttgct gggtatgaga tgtggtgggt cgcgcaggt 120
ccagggaagg gtctagagcg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tcccgaggat accgcggtat attactgtgt gaaagatcct 300
tatagttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 1107
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1107
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tcctgtgcag cctccggatc caccattgcc gggtatgaga tgtggtgggt cgcgcaggt 120
ccggggaagg gtctagagcg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgc gagagatcct 300
tatagttttg actactgggg tcagggaacc cgggtcaccg tctcgagc 348

<210> 1108
<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1108

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ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatcct	300
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<210> 1109

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1109

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ccagggaagg gtctagagcg ggtctcagct attagtggta gtggtggtag cacgtactac	180
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ctgcaaatac acagcctgcg tgccgaggat accgcagtat attactgtgc gaaagaacct	300
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<210> 1110

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1110

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ccagggaagg gtctagagcg ggtctcagct attagtggta gtggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat	240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatcca 300
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<210> 1111
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccaggggaagg gtctagagcg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gagagaccct 300
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<210> 1112
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccaggggaagg gtctagagcg ggtctccgct attagtggta gtggtggtag cacatactac 180
 gcggactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatcct 300
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<210> 1113
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccaggaagg gtctagagcg ggtctcagct attagtggta gtggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc acccgcgacg attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagagcct	300
tatagttttg actactgggg tcaggaacc ctggtcaccg tctcgagc	348

<210> 1114

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1114

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ccaggaagg gtctagagcg ggtctcagct attagtggta gtggtggtag cacatactac	180
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ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatcct	300
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<210> 1115

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gagagatcct	300
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<210> 1116

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1116

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ccagggaagg gtctagagcg gatctcagct attagtggta gtggtggtag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat      240
ctgaaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatcct      300
tatagttttg actactgggg tcagggaacc ctggtcaccg tctcgagc      348
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<210> 1117

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1117

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ccagggaagg gtctagagcg ggtctcagct attagtggta gtggtggtag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gagagatcct      300
tatagttttg actactgggg tcagggaacc ctggtcaccg tctcgagc      348
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<210> 1118

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1118

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ccagggaagg gtctagagcg ggtcgcagct attagtggta gtggtggtag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gagagatcct      300
tatagttttg actactgggg tcagggaacc ctggtcaccg tctcgagc      348
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<210> 1119
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccaggaagg gtctagagcg ggtctcagct attagtggaa gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240
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<210> 1120
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccaggaagg gtctagagcg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagaacct 300
 tatagttttg actactgggg tcaggaacc ctggtcaccg tctcgagc 348

<210> 1121
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1121
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gcagactccg tgaagggccg gttcaccacc tcccgcgacg attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gagagatcct 300
 tatagttttg actactgggg tcggggaacc ctggtcaccg tctcgagc 348

<210> 1122
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1122
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 ccaggaaggt gtctagagcg ggtctcagct attagtggta gcggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagaacct 300
 tatagttatg actactgggg tcatggaacc ctggttactg tctcgagc 348

<210> 1123
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccaggaaggt gtctagagcg ggtctcagct attagtggta gtggtggtaa cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accggggtat attactgtgc gagagatcct 300
 tatagttttg actactgggg tcagggtacc ctggtcaccg tctcgagc 348

<210> 1124
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1124
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ccagggaagg gtctagagcg ggtctcagct attagtggta gtggtggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagaacct 300
tatagttttg actcctgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 1125
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1125
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ccagggaagg gtctagagcg cgtctcagct attagtggta gtggcggtag cacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgc gagagatcct 300
tatagttttg actactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 1126
<211> 348
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1126
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ccagggaagg gtctagagcg ggtctcagct attagtggta gtggtggtag cacatactac 180
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tatagttttg accactgggg tcagggaacc ctggtcaccg tctcgagc 348

<210> 1127
<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1127

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ccagggaagg gtctagagcg ggtctcagct attagtggta gtggtggtag cacatactac	180
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ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gagagatcct	300
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<210> 1128

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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ccagggaagg gtctagagcg ggtctcagct attagtggta gtggtggtag cacatactac	180
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ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatcct	300
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<210> 1129

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1129

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ccagggaagg gtctagagcg ggtctcagct attagtggta gtggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat	240

ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagaacct 300
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<210> 1130
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccaggaagg gtctagagcg ggtctcagct attagtggta gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240
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<210> 1131
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<210> 1132
 <211> 348
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatcct      300
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<210> 1133

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1133

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<210> 1134

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

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<400> 1134

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ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatcct      300
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<210> 1135

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<210> 1136

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

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<400> 1136

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ccagggaagg gtctagagtg ggtctcagct attagtggta gtggtggtag cacatactac	180
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ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatcct	300
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<210> 1137

<211> 348

<212> ADN

<213> Secuencia Artificial

<220>

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<400> 1137

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ccagggaagg gtctagagcg ggtctcagct attagtggaa gtggtggtag cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat	240
ctgcaaatac acagcctgcg tgccgaggat accgcggtat attactgtgc gaaagatcct	300
tatagttttg actaccgggg tcagggaacc ctggtcaccg tctcgagc	348

<210> 1138
 <211> 348
 <212> ADN
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<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1138
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 ccagggaagg gtctagagcg ggtctcagct attagtggaa gtggtggtag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgacg attccaagaa cacgctgtat 240
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<210> 1139
 <211> 360
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccagggaagg gtctagagtg ggtctcatct atttcggcta gtggtgggtc tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg 300
 gtgagttatg tggcgacgtt tgactactgg ggtcaggga cctggtcac cgtctcgagc 360

<210> 1140
 <211> 360
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 tcctgtgcag cctccggatt cacctttccg actgctgaga tggtgtgggt cgcagggt 120
 ccagggaagg gtccagagtg ggtctcatca atttcggcta gtggtgggtc tacatactat 180

gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg 300
 gtgagttatg tggcgacggt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc 360

<210> 1141
 <211> 360
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccagggatgg gtctagagtg ggtctcatct atttcggcta gtggtggtta tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa catgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg 300
 gtgagttatg tggcgacggt tgactactgg ggtcagggag ccctgggtcac cgtcacgagc 360

<210> 1142
 <211> 360
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 ccaggaaggt gtctagagtg ggtctcatct atttcggcta gtggtggttc tacatactac 180
 gcagactccg tgaagggccg gttctccatc tcccgcgacg attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg 300
 gtgagttatg tggcgacggt tgactactgg ggtcatggag ccctgggtcac cgtctcgagc 360

<210> 1143
 <211> 360
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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tcctgtgcag cctccggatt cacatttccg actgctgaga tgttgtgggt cgcgcaggt 120
ccagggaagg gtctagagtg ggtctcatct atttcggcta gtggtggttc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgcg agccgaggac accgcggtat attactgtgc gaaagagccg 300
gtgagttatg tggcaacggt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc 360

<210> 1144
<211> 360
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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tcctgtgcag cctccggatt cacctttccg actgctgaga tgggtgtgggt cgcgcaggt 120
ccagggaagg gtctagagtg gatctcatct atttcggcta gtggtggttc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaattga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg 300
gtgagttatg tggcgacggt tgactactgg ggtcggggaa ccctgggtcac cgtctcgagc 360

<210> 1145
<211> 360
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1145
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tcctgtgcag cctccggatt cacatttccg actgctgaga tgttgtgggt cgcgcaggt 120
ccagggaagg gtctagagtg ggtctcatct atttcggcta gtggtggttc tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagag cacgctgtat 240
ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg 300
gtgagttatg tggcgacggt tgactactgg ggtccaggag ccctgggtcac cgtctcgagc 360

<210> 1146
<211> 360

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1146

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tcctgtgcag cctccggatt cacctttccg actgctgaga tgctgtgggt ccgcaaggct	120
ccagggaagg gtctagagtg ggtctcatct atttcggcta gtgggtggttc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgttt	240
ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc caaagagccg	300
gtgagttatg tggcgacggt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc	360

<210> 1147

<211> 360

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1147

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tcctgtgcag cctccggatt cacatttccg actgctgaga tgttgtgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcatct atttcggcta gtgggtggttc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatac acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg	300
gtgagttatg tggcgacggt tgactactgg ggtccaggag ccctggtcac cgtctcgagc	360

<210> 1148

<211> 360

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1148

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tcctgtgcag cctccggatt cacctttccg actgctgaga tgctgtgggt ccgccaggct	120
ccagggaagg gtctagagtg ggtctcatct atttcggcta gtgggtggttc tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240

ttgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagagccg 300
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<210> 1149
 <211> 360
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1149
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 tcctgtgcag cctccgatt cacctttccg actgctgaga tgctgtgggt ccgcaaggct 120
 ccagggaagg gtctagagtg ggtctcatct atttcggcta gtggtggttc tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac gccgcggtat attactgtgc gaaagagccg 300
 gtgagttatg tggcgacggt tgactactgg ggtcagggaa ccctgggtcac cgtctcgagc 360

<210> 1150
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1150
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 gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtgggtcag ggggtgctgt ggctgcgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1151
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1151
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atcacttgcc gggcaagtca ttttattggt actctgttat cttggtacca gcagaaacca    120
cggaagccc ctaaactcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca    180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcatcct    240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggctccgac gttcgggtcaa    300
gggaccaagg tggaaatcaa acgg                                           324

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<210> 1152
<211> 324
<212> ADN
<213> Secuencia Artificial

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<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 1152
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gggaaagccc ctaagctcct ggtcacttat ggttccttgt tgcaaagtgg ggtcccatca    180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcaa tctgcaacct    240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggctcctac gttcggccaa    300
gggaccaagg tggaaaacat acgg                                           324

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<210> 1153
<211> 324
<212> ADN
<213> Secuencia Artificial

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<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 1153
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gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca    180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct    240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggctccgac gttcggccaa    300
gggaccaagg tggaaatcaa acgg                                           324

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<210> 1154
<211> 324
<212> ADN
<213> Secuencia Artificial

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<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1154

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atcacttgcc gggcaagtca ttttattgct actctgttat cttggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggctccgac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1155

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1155

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca ttttattggt actctgttat cttggtacca gcagaaacca	120
gggaaagcca ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagactttg ctacgtacta ctgtggtcag ggggtgctgt ggccccgac gttcggccag	300
gggaccaagg tggaaatcaa acgt	324

<210> 1156

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1156

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atcacttgcc gggcaagtca ttttattggt tctctgttat cttggtacca gcataaacca	120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggctgcgac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1157
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 atcacttgcc gggcaagtca ttttattggt actctgttat cttggtacca gcataaacca 120
 gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggctgcgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1158
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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 atcacttgcc gggcaagtca ttttattggt actctgttat cttggtacca gcataaacca 120
 gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg caacgtacta ctgtggtcag ggggtgctgt ggctgcgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1159
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1159
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 atcacttgcc gggcaagtca ttttattggt actctgttat cctggtacca gcataaacca 120
 gggaaagccc ctaagctcct gatcacctat ggttccttgt tgcaaagtgg ggtcccatca 180

cgtttcagtgc gcagtggatc tgggacagaa ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtggtcag ggagtgtgtt ggctgcgcac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1160
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1160
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atcacttgcc gggcaagtca ttttatttgt actctgttat cttggtacca gcataaacca 120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180
cgtttcagtgc gcagtggatc tgggacagaa ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtggtcag ggggtgtgtt ggctgcgcac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1161
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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atcacttgcc gggcaagtca ttttatttgt actctgttat cttggtacca gcataaacca 120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180
cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtggtcag ggggtgtgtt ggctgcgcac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1162
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1162
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atcaattgcc gggcaagtca ttttattggt actctgttat cttggtacca gcataaacca 120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180
cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggctcgac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1163
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1163
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atcacttgcc gggcaagtca ttttattggt actctgttat cttggtacca gcagaaacca 120
gggaaagcca ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180
cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggctccgac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1164
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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atcacttgcc gggtaagtca ttttattggt actctgttat cttggtacca gcagaaacca 120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180
cgtttcagtgc gcagtggatc tgggacagat ttcactctca gcatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggccccgac gttcggacaa 300
gggaccaagg tggaaatcaa acag 324

<210> 1165
<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1165

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atcacttgcc gggcaagtca ttttattggt actctgttat cttggtacca gcagaaacca	120
aggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggctccgac gttcgccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1166

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1166

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atcacttgcc gggcaagtca ttttattggt actctgttat cttggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggctccgac gttcgccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1167

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1167

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atcacttgcc gggcaagtca ttttattggt actctgttat cttggtacca gctgaaacca	120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggctgcgac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> 1168

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1168

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ttttattggt actctgttat cttggtacca gctgaaacca 120

gggaaagccc caaagctcct gatcacttat ggttcctggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggctgcgac gttcggccaa 300

gggaccaagg tagaaaacaa acgg 324

<210> 1169

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1169

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ttttattggt actctgttat cttggtacca gcttaaacca 120

gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaacgtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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gggaccaagg tggaaatcaa acgg 324

<210> 1170

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1170

gacatccaga tgaccaggc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

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atcacttgcc gggcaagtca ttttattggt actctgttat cttggtacca gctgaaacca      120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcagagtgg ggtcccatca      180
cgtttcagtg gtagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggctgcgac gttcggccaa      300
gggaccaagg ttgaaaacaa acgg                                              324

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<210> 1171
<211> 324
<212> ADN
<213> Secuencia Artificial

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<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 1171
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gggaaagccc caaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcgctctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggctgcgac gttcggccaa      300
gggaccaagg tggaaatcaa acgg                                              324

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<210> 1172
<211> 324
<212> ADN
<213> Secuencia Artificial

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<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 1172
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gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggctgcgac gttcggccaa      300
gggacaacgg tggaaatcaa acgg                                              324

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<210> 1173
<211> 324
<212> ADN
<213> Secuencia Artificial
<220>

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<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1173
gacatcctga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca ttttattggt agtctgttat cttggtacca gcagaaacca 120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggctgcgac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1174
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1174
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca ttttattggt actctggtat cttggtacca gcagaaaccg 120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggctgcgac gtacggccaa 300
gggaccaagg tggaaatcaa acgg 324

<210> 1175
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1175
gacatccaga tgaccagtc tccatcctct ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca ttttattggt actctggtat cttggtacca gcagaaacca 120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggctgcgac tttcggccaa 300
gggaccaagg tggaaaacaa acgg 324
<210> 1176

<211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1176
 gacatcaaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
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 gggaaagccc caaagctcct gatcacttat ggttccatgt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggctgcgcac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1177
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1177
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc aggcaagtca ttttattggt actctggtat cctggtacca gcagaaacca 120
 gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcccgcgcac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1178
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1178
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
 atcacttgcc gggcaagtca ttttattggt actctgttat cttggtacca gcagaaacca 120
 gggaaagccc ctaagctcct gatcacttat ggttccttgg tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1179
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1179
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgttgaga ccgtgtcacc 60
 atcacttgcc gggcaagtca ttttattggt actctgttat cttggtacca gctgaaacca 120
 gggaaagccc ctaagctcct gatcacttat ggttcctggt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgg 324

<210> 1180
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1180
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
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 gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatt tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtggtcag gaggtgctgt ggcctgcgac gttcggccaa 300
 gggactaagg tggaaatcaa acgg 324

<210> 1181
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1181

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gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtctcc      60
atcacttgcc gagcaagtca ttttattggt actctgttat cttggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatt tgggacagat ttactctca ccatcagcag tctgcaacct      240
gaagatcttg ctacgtacta ctgtggtcag gaggtgctgt ggcctgcgac gttcgccaa      300
gggaccaagg tggaaatcaa acgg                                              324

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<210> 1182
<211> 324
<212> ADN
<213> Secuencia Artificial

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<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 1182
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc aggcaagtca ttttattggt actctgttat cttggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatt tgggacagat ttactctca ccatcagcag tctgcaaccc      240
gaagatcttg ctacgtacta ctgtggtcag gaggtgctgt ggcctgcgac gttcgccaa      300
gggaccaagg tggaaatcaa acgg                                              324

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<210> 1183
<211> 324
<212> ADN
<213> Secuencia Artificial

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<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 1183
gacatccaga tgacccagtc tccatcctcc ctgtctgcat cagtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtca ttttattggt actctgttat cttggtacca gcagaaacct      120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatt tgggacagaa ttactctca ccatcggcag tctgcaacct      240
gaagatcttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcgccaa      300
gggaccaagg tggaaatcaa acgg                                              324

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<210> 1184
<211> 324
<212> ADN

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<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1184

gacatccaga tgacccagtc accatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca ttttattggt actctgttat cttggtacca gcagaaacca	120
gggaaagcca ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctccgac gttcggccaa	300
gggaccaagg tggaaatcaa acgg	324

<210> 1185

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1185

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca cttcattgcc agtctgttat cttggtacca ggtgaaacca	120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgagac gttcggccaa	300
gggacaacgg tggaaatcaa acgg	324

<210> 1186

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1186

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca tttcattgcc cagctgttat cttggtacca ggtgaaacca	120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgagac gttcggccaa	300

gggacaacgg tggaaatcaa acgg

324

<210> 1187

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1187

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atcacttgcc gggcaagtca ttccattgcc cagctgttat cttggtacca ggtgaaacca 120

gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa 300

gggacaacgg tggaaatcag acgg 324

<210> 1188

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1188

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atcacttgcc gggcaagtca ttacattgcc tccctgttat cttggtacca ggtgaaacca 120

gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcagagtgg ggccccatca 180

cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa 300

gggacaacgg tggaaatcaa acgg 324

<210> 1189

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

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<400> 1189

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gggaaagccc ctaagctcct gatcacttgg gcctcctact tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggctgcgac gttcggccaa      300
gggacaacgg tggaaatcaa acgg                                             324

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<210> 1190
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 1190
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
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gggaaagccc ctaagctcct gatcacttgg acgtcctact tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggctgcgac gttcggccaa      300
gggacaacgg tggaaatcaa acgg                                             324

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<210> 1191
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 1191
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtca ttttattggg agtctgttat cttggtacca ggtgaaacca      120
gggaaagccc ctaagctcct gatcacttgg tgcctcctact tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggctgcgac gttcggccaa      300
gggacaacgg tggaaatcaa acgg                                             324

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<210> 1192
 <211> 324
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1192
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atcacttgcc gggcaagtca ttttattggt agtctgttat cttggtacca ggtgaaacca 120
gggaaagccc ctaagctcct gatcacttgg gggctcctggt tgcaaagtgg ggtcccatca 180
cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggctgcgac gttcgccaa 300
gggacaacgg tggaaatcaa acgg 324

<210> 1193
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1193
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca ttttattggt agtctgttat cttggtacca ggtgaaacca 120
gggaaagccc ctaagctcct gatcacttgg ggcctcctggt tgcaaagtgg ggtcccatca 180
cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggctgcgac gttcgccaa 300
gggacaacgg tggaaatcaa acgg 324

<210> 1194
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1194
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atcacttgcc gggcaagtca ttttattggt agtctgttat cttggtacca ggtgaaacca 120
gggaaagccc ctaagctcct gatcacttgg agctcctggt tgcaaagtgg ggtcccatca 180
cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggctgcgac gttcgccaa 300
gggacaacgg tggaaatcaa acgg 324

<210> 1195
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1195

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atcacttgcc gggcaagtca ttggattgcc cagctgttat cttggtacca ggtgaaacca	120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcaactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa	300
gggacaacgg tggaaatcaa acgg	324

<210> 1196

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1196

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca ttttatttgt tcgctcttac gctggtacca ggtgaaacca	120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcaactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa	300
gggacaacgg tggaaatcaa acgg	324

<210> 1197

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1197

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca tcggattgcc cagctgttat cttggtacca ggtgaaacca	120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcaactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa	300

gggacaacgg tggaaatcaa acgg

324

<210> 1198

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1198

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

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gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa 300

gggacaacgg tggaaatcaa acgg 324

<210> 1199

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1199

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ttttatttgt agtctgttat cttggtacca ggtgaaacca 120

gggaaagccc ctaagctcct gatccggttc ggctccttgt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa 300

gggacaacgg tggaaatcaa acgg 324

<210> 1200

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1200

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60

atcacttgcc gggcaagtca ttttatttgt agtctgttat cttggtacca ggtgaaacca 120


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gggaaagccc ctaagctcct gatcacttac aagtcctact tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcgcccaa      300
gggacaacgg tggaaatcaa acgg                                             324

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<210> 1201

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 1201
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
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gggaaagccc ctaagctcct gatcacttgg ggctcctact tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcgcccaa      300
gggacaacgg tggaaatcaa acgg                                             324

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<210> 1202

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 1202
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtca ttttatttgt gggcccttat cttggtacca ggtgaaacca      120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct      240
gaagattctg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcgcccaa      300
gggacaacgg tggaaatcaa acgg                                             324

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<210> 1203

<211> 324

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1203
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atcacttgcc gggcaagtca ttggattgcc accctgttat cttggtacca ggtgaaacca 120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180
cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagatTTTTG ctacgtacta ctgtggtcag ggggtgctgt ggctgcgac gttcgccaa 300
gggacaacgg tggaaatcaa acgg 324

<210> 1204
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1204
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca ttttatttgg gggcccttat cttggtacca ggtgaaacca 120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180
cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagatTTTTG ctacgtacta ctgtggtcag ggggtgctgt ggctgcgac gttcgccaa 300
gggacaacgg tggaaatcaa acgg 324

<210> 1205
<211> 324
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1205
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcacttgcc gggcaagtca ttttatttgg agcctcttaa actggtacca ggtgaaacca 120
gggaaagccc ctaagctcct gatcacttat ggttccttgt tgcaaagtgg ggtcccatca 180
cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagatTTTTG ctacgtacta ctgtggtcag ggggtgctgt ggctgcgac gttcgccaa 300
gggacaacgg tggaaatcaa acgg 324

<210> 1206
<211> 324
<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1206
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 gggaaagccc ctaagctcct gatcacttac gggtcctggt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtggtcag ggggtgctgt ggcctgcgac gttcggccaa 300
 gggacaacgg tggaaatcaa acgg 324

<210> 1207

<211> 5

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1207
 Gly Gly Gly Gly Ser
 1 5

<210> 1208

<211> 15

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Péptido Sintético

<400> 1208
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

<210> 1209

<211> 25

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Péptido Sintético

<400> 1209
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25

<210> 1210

<211> 227

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1210

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Tyr Phe Gln Glu Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser Ala Ser Thr Asp Ile Gln Met Thr Gln Ser Pro Ser
115 120 125

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
130 135 140

Ser Arg Pro Ile Gly Thr Thr Leu Ser Trp Tyr Gln Gln Lys Pro Gly
145 150 155 160

Lys Ala Pro Lys Leu Leu Ile Leu Trp Asn Ser Arg Leu Gln Ser Gly
165 170 175

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
180 185 190

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ala
 195 200 205

Gln Ala Gly Thr His Pro Thr Thr Phe Gly Gln Gly Thr Lys Val Glu
 210 215 220

Ile Lys Arg
 225

<210> 1211

<211> 227

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1211

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Tyr Phe Gln Glu Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser Ala Ser Thr Asp Ile Gln Met Thr Gln Ser Pro Ser
 115 120 125

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
 130 135 140

Ser Arg Pro Ile Gly Thr Met Leu Ser Trp Tyr Gln Gln Lys Pro Gly
 145 150 155 160

Lys Ala Pro Lys Leu Leu Ile Leu Ala Phe Ser Arg Leu Gln Ser Gly
 165 170 175

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 180 185 190

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ala
 195 200 205

Gln Ala Gly Thr His His Thr Thr Phe Gly Gln Gly Thr Lys Val Glu
 210 215 220

Ile Lys Arg
 225

<210> 1212

<211> 227

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1212

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser Ala Ser Thr Asp Ile Gln Met Thr Gln Ser Pro Ser
 115 120 125

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
 130 135 140

Ser Arg Pro Ile Gly Thr Thr Leu Ser Trp Tyr Gln Gln Lys Pro Gly
 145 150 155 160

Lys Ala Pro Lys Leu Leu Ile Leu Trp Asn Ser Arg Leu Gln Ser Gly
 165 170 175

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 180 185 190

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ala
 195 200 205

Gln Ala Gly Thr His Pro Thr Thr Phe Gly Gln Gly Thr Lys Val Glu
 210 215 220

Ile Lys Arg
 225

<210> 1213

<211> 227

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1213

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser Ala Ser Thr Asp Ile Gln Met Thr Gln Ser Pro Ser
 115 120 125

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
 130 135 140

Ser Arg Pro Ile Gly Thr Met Leu Ser Trp Tyr Gln Gln Lys Pro Gly
 145 150 155 160

Lys Ala Pro Lys Leu Leu Ile Leu Ala Phe Ser Arg Leu Gln Ser Gly
 165 170 175

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 180 185 190

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ala
 195 200 205

Gln Ala Gly Thr His His Thr Thr Phe Gly Gln Gly Thr Lys Val Glu
 210 215 220

Ile Lys Arg
 225

<210> 1214

<211> 230

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1214

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Thr
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Leu Trp Asn Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
115 120 125

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg
130 135 140

Asp Tyr Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
145 150 155 160

Arg Val Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp
165 170 175

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
180 185 190

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
195 200 205

Tyr Cys Ala Lys Leu Pro Phe Tyr Phe Gln Glu Trp Gly Gln Gly Thr
210 215 220

Leu Val Thr Val Ser Ser
225 230

<210> 1215

<211> 230

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1215

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Leu Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His His Thr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
 115 120 125

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg
 130 135 140

Asp Tyr Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 145 150 155 160

Arg Val Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp
 165 170 175

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 180 185 190

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 195 200 205

Tyr Cys Ala Lys Leu Pro Phe Tyr Phe Gln Glu Trp Gly Gln Gly Thr
 210 215 220

Leu Val Thr Val Ser Ser
 225 230

<210> 1216

<211> 230

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1216

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Thr
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Leu Trp Asn Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
 115 120 125

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg
 130 135 140

Asp Tyr Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 145 150 155 160

Arg Val Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp
 165 170 175

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 180 185 190

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 195 200 205

Tyr Cys Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr
 210 215 220

Leu Val Thr Val Ser Ser
 225 230

<210> 1217

<211> 230

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1217

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Leu Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His His Thr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
 115 120 125

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg
 130 135 140

Asp Tyr Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 145 150 155 160

Arg Val Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp
 165 170 175

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 180 185 190

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 195 200 205

Tyr Cys Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr
 210 215 220

Leu Val Thr Val Ser Ser
225 230

<210> 1218

<211> 230

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1218

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Leu Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
115 120 125

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg
130 135 140

Asp Tyr Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
145 150 155 160

Arg Val Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp
165 170 175

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
180 185 190

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 195 200 205

Tyr Cys Ala Lys Leu Pro Phe Tyr Phe Gln Glu Trp Gly Gln Gly Thr
 210 215 220

Leu Val Thr Val Ser Ser
 225 230

<210> 1219

<211> 230

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1219

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Leu Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Val Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
 115 120 125

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg
 130 135 140

Asp Tyr Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 145 150 155 160

Arg Val Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp
 165 170 175

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 180 185 190

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 195 200 205

Tyr Cys Ala Lys Leu Pro Phe Tyr Phe Gln Glu Trp Gly Gln Gly Thr
 210 215 220

Leu Val Thr Val Ser Ser
 225 230

<210> 1220

<211> 230

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1220

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Leu Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Val His Pro Thr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
 115 120 125

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg
 130 135 140

Asp Tyr Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 145 150 155 160

Arg Val Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp
 165 170 175

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 180 185 190

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 195 200 205

Tyr Cys Ala Lys Leu Pro Phe Tyr Phe Gln Glu Trp Gly Gln Gly Thr
 210 215 220

Leu Val Thr Val Ser Ser
 225 230

<210> 1221

<211> 230

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1221

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Thr
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Leu Trp Asn Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
 115 120 125

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu
 130 135 140

Glu Glu Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 145 150 155 160

Trp Val Ser Ala Ile Ser Arg Asn Gly Tyr Ser Thr Tyr Tyr Ala Asp
 165 170 175

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 180 185 190

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 195 200 205

Tyr Cys Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr
 210 215 220

Leu Val Thr Val Ser Ser
 225 230

<210> 1222

<211> 227

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1222

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Arg Asn Gly Tyr Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser Ala Ser Thr Asp Ile Gln Met Thr Gln Ser Pro Ser
115 120 125

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
130 135 140

Ser Arg Pro Ile Gly Thr Thr Leu Ser Trp Tyr Gln Gln Lys Pro Gly
145 150 155 160

Lys Ala Pro Lys Leu Leu Ile Leu Trp Asn Ser Arg Leu Gln Ser Gly
165 170 175

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
180 185 190

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ala
195 200 205

Gln Ala Gly Thr His Pro Thr Thr Phe Gly Gln Gly Thr Lys Val Glu
210 215 220

Ile Lys Arg
225

<210> 1223

<211> 230

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1223

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Trp Ile Gly Ser Gln
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Met Trp Arg Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Gly Leu Arg His Pro Lys
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
 115 120 125

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu
 130 135 140

Glu Glu Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 145 150 155 160

Trp Val Ser Ala Ile Ser Arg Asn Gly Tyr Ser Thr Tyr Tyr Ala Asp
 165 170 175

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 180 185 190

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 195 200 205

Tyr Cys Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr
 210 215 220

Leu Val Thr Val Ser Ser
 225 230

<210> 1224

<211> 227

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1224

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Arg Asn Gly Tyr Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser Ala Ser Thr Asp Ile Gln Met Thr Gln Ser Pro Ser
 115 120 125

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
 130 135 140

Ser Gln Trp Ile Gly Ser Gln Leu Ser Trp Tyr Gln Gln Lys Pro Gly
 145 150 155 160

Lys Ala Pro Lys Leu Leu Ile Met Trp Arg Ser Ser Leu Gln Ser Gly
 165 170 175

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 180 185 190

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ala
 195 200 205

Gln Gly Leu Arg His Pro Lys Thr Phe Gly Gln Gly Thr Lys Val Glu
 210 215 220

Ile Lys Arg
 225

<210> 1225

<211> 227

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1225

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
 20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Arg Asn Gly Tyr Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser Ala Ser Thr Asp Ile Gln Met Thr Gln Ser Pro Ser
 115 120 125

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
 130 135 140

Ser Arg Pro Ile Gly Thr Thr Leu Ser Trp Tyr Gln Gln Lys Pro Gly
 145 150 155 160

Lys Ala Pro Lys Leu Leu Ile Leu Trp Asn Ser Arg Leu Gln Ser Gly
 165 170 175

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 180 185 190

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ala
 195 200 205

Gln Ala Gly Thr His Pro Thr Thr Phe Gly Gln Gly Thr Lys Val Glu
 210 215 220

Ile Lys Arg
225

<210> 1226

<211> 227

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1226

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Glu Glu
20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Arg Asn Gly Tyr Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser Ala Ser Thr Asp Ile Gln Met Thr Gln Ser Pro Ser
115 120 125

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
130 135 140

Ser Arg Pro Ile Gly Thr Met Leu Ser Trp Tyr Gln Gln Lys Pro Gly
145 150 155 160

Lys Ala Pro Lys Leu Leu Ile Leu Ala Phe Ser Arg Leu Gln Ser Gly
165 170 175

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
180 185 190

Thr Ile Ser Asn Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ala
 195 200 205

Gln Ala Gly Thr His Pro Thr Thr Phe Gly Gln Gly Thr Lys Val Glu
 210 215 220

Ile Lys Arg
 225

<210> 1227

<211> 230

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1227

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Thr
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Leu Trp Asn Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro
 115 120 125

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu
 130 135 140

Glu Glu Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 145 150 155 160

Trp Val Ser Ala Ile Ser Arg Asn Gly Tyr Ser Thr Tyr Tyr Ala Asp
 165 170 175

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 180 185 190

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 195 200 205

Tyr Cys Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr
 210 215 220

Leu Val Thr Val Ser Ser
 225 230

<210> 1228

<211> 230

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1228

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Leu Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro
 115 120 125

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu
 130 135 140

Glu Glu Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 145 150 155 160

Trp Val Ser Ala Ile Ser Arg Asn Gly Tyr Ser Thr Tyr Tyr Ala Asp
 165 170 175

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 180 185 190

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 195 200 205

Tyr Cys Gly Lys Glu Pro Phe Arg Tyr Asp Tyr Trp Gly Gln Gly Thr
 210 215 220

Leu Val Thr Val Ser Ser
 225 230

<210> 1229

<211> 227

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1229

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Leu Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Glu
 100 105 110

Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
 115 120 125

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr Glu
 130 135 140

Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val Ser
 145 150 155 160

Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val Lys
 165 170 175

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
 180 185 190

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 195 200 205

Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr Leu Val Thr
 210 215 220

Val Ser Ser
 225

<210> 1230

<211> 231

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1230

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Leu Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ser Thr Ser
100 105 110

Gly Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
115 120 125

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
130 135 140

Arg Asp Tyr Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
145 150 155 160

Glu Arg Val Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala
165 170 175

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
180 185 190

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
195 200 205

Tyr Tyr Cys Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly
210 215 220

Thr Leu Val Thr Val Ser Ser
225 230

<210> 1231

<211> 229

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1231

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Leu Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly
 100 105 110

Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
 115 120 125

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp
 130 135 140

Tyr Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg
 145 150 155 160

Val Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser
 165 170 175

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

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
 195 200 205

Cys Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr Leu
 210 215 220

Val Thr Val Ser Ser
 225

<210> 1232

<211> 239

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1232

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Leu Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly
 100 105 110

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu
 115 120 125

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser
 130 135 140

Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr Glu Met Trp Trp Val
 145 150 155 160

Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val Ser Ala Ile Asn Pro
 165 170 175

Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr
 180 185 190

Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser
 195 200 205

Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Leu Pro Phe
 210 215 220

Tyr Phe His Glu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 225 230 235

<210> 1233

<211> 249

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1233

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10					15		

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Arg	Pro	Ile	Gly	Thr	Met
			20					25					30		

Leu	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile
		35					40					45			

Leu	Ala	Phe	Ser	Arg	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
	50					55					60				

Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Asn	Leu	Gln	Pro
65					70					75					80

Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Ala	Gln	Ala	Gly	Thr	His	Pro	Thr
				85					90					95	

Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Gly	Gly	Gly	Gly
			100					105					110		

Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser
		115					120					125			

Gly	Gly	Gly	Gly	Ser	Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu
	130						135				140				

Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe
145					150					155					160

Thr	Phe	Arg	Asp	Tyr	Glu	Met	Trp	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys
				165					170					175	

Gly	Leu	Glu	Arg	Val	Ser	Ala	Ile	Asn	Pro	Gln	Gly	Thr	Arg	Thr	Tyr
			180					185					190		

Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser
		195					200					205			

Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr
	210					215					220				

Ala Val Tyr Tyr Cys Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly
 225 230 235 240

Gln Gly Thr Leu Val Thr Val Ser Ser
 245

<210> 1234

<211> 227

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1234

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser Thr Val Ala Asp Ile Gln Met Thr Gln Ser Pro Ser
 115 120 125

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
 130 135 140

Ser Arg Pro Ile Gly Thr Met Leu Ser Trp Tyr Gln Gln Lys Pro Gly
 145 150 155 160

Lys Ala Pro Lys Leu Leu Ile Leu Ala Phe Ser Arg Leu Gln Ser Gly
 165 170 175

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 180 185 190

Thr Ile Ser Asn Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ala
 195 200 205

Gln Ala Gly Thr His Pro Thr Thr Phe Gly Gln Gly Thr Lys Val Glu
 210 215 220

Ile Lys Arg
 225

<210> 1235

<211> 231

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1235

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr Leu Val
 100 105 110

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

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
 130 135 140

Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met Leu Ser Trp Tyr Gln
145 150 155 160

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Leu Ala Phe Ser Arg
165 170 175

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
180 185 190

Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro Glu Asp Phe Ala Thr
195 200 205

Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr Thr Phe Gly Gln Gly
210 215 220

Thr Lys Val Glu Ile Lys Arg
225 230

<210> 1236

<211> 229

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1236

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
115 120 125

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
130 135 140

Arg Ala Ser Arg Pro Ile Gly Thr Met Leu Ser Trp Tyr Gln Gln Lys
145 150 155 160

Pro Gly Lys Ala Pro Lys Leu Leu Ile Leu Ala Phe Ser Arg Leu Gln
165 170 175

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
180 185 190

Thr Leu Thr Ile Ser Asn Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
195 200 205

Cys Ala Gln Ala Gly Thr His Pro Thr Thr Phe Gly Gln Gly Thr Lys
210 215 220

Val Glu Ile Lys Arg
225

<210> 1237

<211> 239

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1237

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
130 135 140

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile
145 150 155 160

Gly Thr Met Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
165 170 175

Leu Leu Ile Leu Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg
180 185 190

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn
195 200 205

Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr
210 215 220

His Pro Thr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
225 230 235

<210> 1238

<211> 249

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1238

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
 130 135 140

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
 145 150 155 160

Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met Leu Ser Trp
 165 170 175

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Leu Ala Phe
 180 185 190

Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
 195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro Glu Asp Phe
 210 215 220

Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr Thr Phe Gly
 225 230 235 240

Gln Gly Thr Lys Val Glu Ile Lys Arg
 245

<210> 1239

<211> 230

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1239

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Leu Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
 115 120 125

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg
 130 135 140

Asp Tyr Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 145 150 155 160

Arg Val Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp
 165 170 175

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 180 185 190

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 195 200 205

Tyr Cys Ala Lys Leu Pro Phe Tyr Phe His Glu Trp Gly Gln Gly Thr
 210 215 220

Leu Val Thr Val Ser Ser
 225 230

<210> 1240

<211> 681

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético
Polinucleótido

<400> 1240

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgctctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcy tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcy tgccgaggac accgcggtat attactgtgc gaaacttccg	300
ttttactttc aggagtgggg tcaggaacc ctggtcaccg tctcgagcgc tagcaccgac	360
atccagatga ccagtcctcc atcctccctg tctgcatctg taggagaccg tgtcaccatc	420
acttgccggg caagtcgtcc gattgggacg acgttaagtt ggtaccagca gaaaccaggg	480
aaagccccta agctcctgat cctttggaat tcccgtttgc aaagtggggc cccatcacgt	540
ttcagtggca gtggatctgg gacagatttc actctacca tcagcagtct gcaacctgaa	600
gattttgcta cgtactactg tgccgaggct gggacgcac ctacgacgtt cggccaaggg	660
accaaggtgg aaatcaaacg g	681

<210> 1241

<211> 681

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1241

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgctctc	60
tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcy tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcy tgccgaggac accgcggtat attactgtgc gaaacttccg	300
ttttactttc aggagtgggg tcaggaacc ctggtcaccg tctcgagcgc tagcaccgac	360
atccagatga ccagtcctcc atcctccctg tctgcatctg taggagaccg tgtcaccatc	420
acttgccggg caagtcgtcc gattgggacg atgttaagtt ggtaccagca gaaaccaggg	480
aaagccccta agctcctgat ccttgctttt tcccgtttgc aaagtggggc cccatcacgt	540
ttcagtggca gtggatctgg gacagatttc actctacca tcagcagtct gcaacctgaa	600
gattttgcta cgtactactg tgccgaggct gggacgcac atacgacgtt cggccaaggg	660
accaaggtgg aaatcaaacg g	681

<210> 1242
 <211> 681
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1242
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120
 ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300
 ttttactttc acgagtgggg tcaggaacc ctggtcaccg tctcgagcgc tagcaccgac 360
 atccagatga ccagtcctcc atcctccctg tctgcatctg taggagaccg tgtcaccatc 420
 acttgccggg caagtcgtcc gattgggacg acgttaagtt ggtaccagca gaaaccaggg 480
 aaagccccta agctcctgat cctttggaat tcccgtttgc aaagtggggc cccatcacgt 540
 ttcagtggca gtggatctgg gacagatttc actctacca tcagcagtct gcaacctgaa 600
 gattttgcta cgtactactg tgcgcaggct gggacgcac ctacgacgtt cggccaaggg 660
 accaaggtgg aaatcaaacg g 681

<210> 1243
 <211> 681
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1243
 gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc 60
 tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct 120
 ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg 300
 ttttactttc acgagtgggg tcaggaacc ctggtcaccg tctcgagcgc tagcaccgac 360
 atccagatga ccagtcctcc atcctccctg tctgcatctg taggagaccg tgtcaccatc 420
 acttgccggg caagtcgtcc gattgggacg atgttaagtt ggtaccagca gaaaccaggg 480
 aaagccccta agctcctgat ccttgctttt tcccgtttgc aaagtggggc cccatcacgt 540

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ttcagtggca gtggatctgg gacagatttc actctcacca tcagcagtct gcaacctgaa      600
gattttgcta cgtactactg tgcgcaggct gggacgcata atacgacgtt cggccaaggg      660
accaaggtgg aaatcaaacg g                                          681

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<210> 1244
<211> 690
<212> ADN
<213> Secuencia Artificial

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<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 1244
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtcg tccgattggg acgacgttaa gttggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatcctttgg aattcccgtt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtgcgcag gctgggacgc atcctacgac gttcggccaa      300
gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgaggtgca gctgttggag      360
tctgggggag gcttgggtaca gcctgggggg tccctgcgtc tctcctgtgc agcctccgga      420
ttcacctttc gggattatga gatgtggtgg gtccgccagg ctccaggga gggcttagag      480
cgggtctcag ctattaatcc gcagggtacg cgtacatact acgcagactc cgtgaagggc      540
cggttcacca tctcccgca caattccaag aacacgctgt atctgcaa at gaacagcctg      600
cgtgccgagg acaccgcggt atattactgt gcgaaacttc cgttttactt tcaggagtgg      660
ggtcagggaa ccctgggtcac cgtctccagc                                          690

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<210> 1245
<211> 690
<212> ADN
<213> Secuencia Artificial

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<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 1245
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtcg tccgattggg acgatgttaa gttggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatccttgc ttttcccgtt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtgcgcag gctgggacgc atcatacgac gttcggccaa      300
gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgaggtgca gctgttggag      360

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tctgggggag gcttgggtaca gcctggggggg tccctgcgtc tctcctgtgc agcctccgga	420
ttcacctttc gggattatga gatgtggtgg gtccgccagg ctccaggga gggctctagag	480
cgggtctcag ctattaatcc gcagggtacg cgtacatact acgcagactc cgtgaagggc	540
cgggttcacca tctcccgca caattccaag aacacgctgt atctgcaa at gaacagcctg	600
cgtgccgagg acaccgcggt atattactgt gcgaaacttc cgttttactt tcaggagtgg	660
ggtcaggga ccctgggtcac cgtctccagc	690

<210> 1246

<211> 690

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1246

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtcg tccgattggg acgacgttaa gttggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatcctttgg aattcccgtt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtgcgcag gctgggacgc atcctacgac gttcggccaa	300
gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgaggtgca gctgttggag	360
tctgggggag gcttgggtaca gcctggggggg tccctgcgtc tctcctgtgc agcctccgga	420
ttcacctttc gggattatga gatgtggtgg gtccgccagg ctccaggga gggctctagag	480
cgggtctcag ctattaatcc gcagggtacg cgtacatact acgcagactc cgtgaagggc	540
cgggttcacca tctcccgca caattccaag aacacgctgt atctgcaa at gaacagcctg	600
cgtgccgagg acaccgcggt atattactgt gcgaaacttc cgttttactt tcacgagtgg	660
ggtcaggga ccctgggtcac cgtctccagc	690

<210> 1247

<211> 690

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1247

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtcg tccgattggg acgatgttaa gttggtacca gcagaaacca	120

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gggaaagccc ctaagctcct gatccttgct ttttcccgtt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtgcgcag gctgggacgc atcatacgac gttcggccaa      300
gggaccaagg tggaatcaa acgtacggtg gctgcaccat ctgaggtgca gctgttgag      360
tctgggggag gcttggtaga gcctgggggg tccctgcgtc tctcctgtgc agcctccgga      420
ttcacctttc gggattatga gatgtggtgg gtccgccagg ctccaggga gggcttagag      480
cgggtctcag ctattaatcc gcagggtacg cgtacatact acgcagactc cgtgaagggc      540
cggttcacca tctccgcga caattccaag aacacgctgt atctgcaa atgaacagcctg      600
cgtgccgagg acaccgcggt atattactgt gcgaaacttc cgttttactt tcacgagtgg      660
ggtcaggga ccctgggtcac cgtctccagc      690

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<210> 1248

<211> 690

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 1248
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtcg tccgattggg acgatgttaa gttggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatccttgct ttttcccgtt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcaa tctgcaacct      240
gaagattttg ctacgtacta ctgtgcgcag gctgggacgc atcctacgac gttcggccaa      300
gggaccaagg tggaatcaa acgtacggtg gctgcaccat ctgaggtgca gctgttgag      360
tccgggggag gcttggtaga gcctgggggg tccctgcgtc tctcctgtgc agcctccgga      420
ttcacctttc gggattatga gatgtggtgg gtccgccagg ctccaggga gggcttagag      480
cgggtctcag ctattaatcc gcagggtacg cgtacatact acgcagactc cgtgaagggc      540
cggttcacca tctccgcga caattccaag aacacgctgt atctgcaa atgaacagcctg      600
cgtgccgagg acaccgcggt atattactgt gcgaaacttc cgttttactt tcagagtgg      660
ggtcaggga ccctgggtcac cgtctccagc      690

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<210> 1249

<211> 690

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1249

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtcg tccgattggg acgatgttaa gttggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatccttgct ttttcccggt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct	240
gaagatggtg ctacgtacta ctgtgcgag gctgggacgc atcctacgac gttcgccaa	300
gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgaggtgca gctgttgag	360
tctgggggag gcttggtaca gcctggggg tccctgcgtc tctcctgtgc agcctccgga	420
ttcacctttc gggattatga gatgtggtgg gtccgccagg ctccaggga gggctagag	480
cgggtctcag ctattaatcc gcagggtacg cgtacatact acgcagactc cgtgaagggc	540
cgggtcacca tctccgcga caattccaag aacacgctgt atctgaaat gaacagcctg	600
cgtgccgagg acaccgcggt atattactgt gcgaaacttc cgttttactt tcaggagtgg	660
ggtcaggga cctggtcac cgtctccagc	690

<210> 1250

<211> 690

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1250

gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtcg tccgattggg acgatgttaa gttggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatccttgct ttttcccggt tgcaaagtgg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttactctca ccatcagcag tctgcaacct	240
gaagatggtg ctacgtacta ctgtgcgag gctggggtgc atcctacgac gttcgccaa	300
gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgaggtgca gctgttgag	360
tctgggggag gcttggtaca gcctggggg tccctgcgtc tctcctgtgc agcctccgga	420
ttcacctttc gggattatga gatgtggtgg gtccgccagg ctccaggga gggctagag	480
cgggtctcag ctattaatcc gcagggtacg cgtacatact acgcagactc cgtgaagggc	540
cgggtcacca tctccgcga caattccaag aacacgctgt atctgaaat gaacagcctg	600
cgtgccgagg acaccgcggt atattactgt gcgaaacttc cgttttactt tcaggagtgg	660
ggtcaggga cctggtcac cgtctccagc	690

<210> 1251
 <211> 690
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1251
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 atcacttgcc gggcaagtcg tccgattggg acgacgttaa gttggtacca gcagaaacca 120
 gggaaagccc ctaagctcct gatcctttgg aattcccgtt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtgcgag gctgggacgc atcctacgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgaggtgca gctgttgag 360
 tctgggggag gcttgggtaca gcctgggggg tccctgcgtc tctcctgcgc agcctccgga 420
 ttcacctttg aggaggagga gatgatttgg gtccgccagg ctccaggga gggcttagag 480
 tgggtctcag ctattagtag gaacggttac agcacatact acgcagactc cgtgaagggc 540
 cggttcacca tctcccgca caattccaag aacacgctgt atctgcaa at gaacagcctg 600
 cgtgccgagg ataccgcggt atattactgt gggaaagagc cgtttcgtta tgactactgg 660
 ggtcagggaa ccctggtcac cgtctccagc 690

<210> 1252
 <211> 681
 <212> ADN
 <213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1252
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 tcttgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggct 120
 ccagggaagg gtctagagtg ggtctcagct attagtagga acggttacag cacatactac 180
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg 300
 tttcgttatg actactggg tccagggaacc ctggtcaccg tctcgagcgc tagcaccgac 360
 atccagatga ccagtcctcc atcctccctg tctgcatctg taggagaccg tgtcaccatc 420
 acttgccggg caagtcgtcc gattgggacg acgttaagtt ggtaccagca gaaaccaggg 480
 aaagccccta agctcctgat cctttggaat tcccgtttgc aaagtggggt cccatcacgt 540

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ttcagtggca gtggatctgg gacagatttc actctcacca tcagcagtct gcaacctgaa      600
gattttgcta cgtactactg tgcgcaggct gggacgcatc ctacgacggt cggccaaggg      660
accaaggtgg aaatcaaacg g                                              681

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<210> 1253
<211> 690
<212> ADN
<213> Secuencia Artificial

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<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 1253
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
atcacttgcc gggcaagtca gtggattggg tctcagttat cttggtacca gcagaaacca      120
gggaaagccc ctaagctcct gatcatgtgg cgttcctcgt tgcaaagtgg ggtcccatca      180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct      240
gaagattttg ctacgtacta ctgtgctcag ggtttgaggc atcctaagac gttcggccaa      300
gggaccaagg tggaaatcaa acgtacggtg gctgcaccat ctgaggtgca gctgttggag      360
tctggggggg gcttgggtaca gcctgggggg tccctgcgtc tctcctgcgc agcctccgga      420
ttcacctttg aggaggagga gatgatttgg gtccgccagg ctccaggga gggctctagag      480
tgggtctcag ctattagtag gaacggttac agcacatact acgcagactc cgtgaagggc      540
cggttcacca tctcccgca caattccaag aacacgctgt atctgcaa at gaacagcctg      600
cgtgccgagg ataccgcggt atattactgt gggaaagagc cgtttcgta tgactactgg      660
ggtcagggaa ccctgggtcac cgtctccagc                                              690

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<210> 1254
<211> 681
<212> ADN
<213> Secuencia Artificial
<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

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<400> 1254
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ccagggaagg gtctagagtg ggtctcagct attagtagga acggttacag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggat accgcggtat attactgtgg gaaagagccg      300
tttcgttatg actactgggg tcagggaacc ctggtcaccg tctcgagcgc tagcaccgac      360

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atccagatga cccagtctcc atcctccctg tctgcatctg taggagaccg tgtcaccatc      420
acttgccggg caagtcagtg gattgggtct cagttatctt ggtaccagca gaaaccaggg      480
aaagccccta agctcctgat catgtggcgt tcctcgttgc aaagtggggt cccatcacgt      540
ttcagtggca gtggatctgg gacagatttc actctacca tcagcagtct gcaacctgaa      600
gattttgcta cgtactactg tgctcagggt ttgaggcatc ctaagacgtt cggccaaggg      660
accaaggtgg aaatcaaacg g                                              681

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<210> 1255

<211> 681

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1255

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gaggtgcagc tggtggcgtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
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ccagggaagg gtctagagtg ggtctcagct attagtagga acggttacag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgtgttat      240
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tttcgttatg actactgggg tcagggaacc ctggtcaccg tctcgagcgc ttcaaccgac      360
atccagatga cccagtctcc atcctccctg tctgcatctg taggagaccg tgtcaccatc      420
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aaagccccta agctcctgat cctttggaat tcccgtttgc aaagtggggt cccatcacgt      540
ttcagtggca gtggatctgg gacagatttc actctacca tcagcagtct gcaacctgaa      600
gattttgcta cgtactactg tgccgaggct gggacgcacg ctacgacgtt cggccaaggg      660
accaaggtgg aaatcaaacg g                                              681

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<210> 1256

<211> 681

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1256

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gaggtgcagc tggtggcgtc tgggggaggc ttggtacagc ctgggggggc cctgcgtctc      60
tcctgcgcag cctccggatt cacctttgag gaggaggaga tgatttgggt ccgccaggcc      120
ccagggaagg gtctagagtg ggtctcagct attagtagga acggttacag cacatactac      180

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gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
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 ttctgttatg actactgggg tcagggaacc ctggtcaccg tctcgagcgc ttcaaccgac 360
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 acttgccggg caagtcgtcc gattgggacg atgttaagtt ggtaccagca gaaaccaggg 480
 aaagccccta agctcctgat ccttgctttt tcccgtttgc aaagtggggt cccatcacgt 540
 ttcagtggca gtggatctgg gacagatttc actctacca tcagcaatct gcaacctgaa 600
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 accaaggtgg aaatcaaacg g 681

<210> 1257

<211> 690

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1257

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 gggaaagccc ctaagctcct gatccttttg aattcccgtt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
 gaagattttg ctacgtacta ctgtgcgcag gctgggacgc atcctacgac gttcggccaa 300
 gggaccaagg tggaaatcaa acggaccgtg gcggcgccga gtgaggtgca gctgttgccg 360
 tctgggggag gcttgggtaca gcctgggggg tccctgcgtc tctcctgcgc agcctccgga 420
 ttcacctttg aggaggagga gatgatttgg gtccgccagg ctccaggga gggcttagag 480
 tgggtctcag ctattagtag gaacggttac agcacatact acgcagactc cgtgaagggc 540
 cggttcacca tctcccgca caattccaag aacacgctgt atctgcaaat gaacagcctg 600
 cgtgccgagg ataccgcggt atattactgt gggaaagagc cgtttcgtaa tgactactgg 660
 ggtcagggaa ccctgggtcac cgtctccagc 690

<210> 1258

<211> 690

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1258
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gggaaagccc ctaagctcct gatccttgct ttttcccggt tgcaaagtgg ggtcccatca 180
cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcaa tctgcaacct 240
gaagattttg ctacgtacta ctgcgcgag gctgggacgc atcctacgac gttcggccaa 300
gggaccaagg tggaaatcaa acggaccgtg gcgggcgccga gtgaggtgca actgttggcg 360
tctgggggag gcttggtaca gcctgggggg tcctgcgctc tctcctgcgc agcctccgga 420
ttcacctttg aggaggagga gatgatttgg gtccgccagg ctccagggaa ggtctagag 480
tgggtctcag ctattagtag gaacggttac agcacatact acgcagactc cgtgaagggc 540
cggttcacca tctccgcga caattccaag aacacgctgt atctgcaaat gaacagcctg 600
cgtgccgagg ataccgcggt atattactgt gggaaagagc cgtttcgtta tgactactgg 660
ggtcagggaa ccctgggtcac cgtctccagc 690

<210> 1259
<211> 681
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1259
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gggaaagccc ctaagctcct gatccttgct ttttcccggt tgcaaagtgg ggtcccatca 180
cgtttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcaa tctgcaacct 240
gaagattttg ctacgtacta ctgcgcgag gctgggacgc atcctacgac gttcggccaa 300
gggaccaagg tggaaatcaa acgtacggtg gcgaggtgc agctgttga gtctggggga 360
ggcttggtac agcctggggg gtccctgcgt ctctcctgtg cagcctccgg attcaccttt 420
cgggattatg agatgtggtg ggtccgccag gctccaggga aggtctaga gcggtctca 480
gctattaatc gcgagggtac gcgtacatac tacgcagact ccgtgaaggg ccggttcacc 540
atctcccgcg acaattcaa gaacacgctg tatctgcaa tgaacagcct gcgtgccgag 600
gacaccgcgg tatattactg tgcgaaactt ccgttttact ttcacgagtg ggtcaggga 660
accctgggtca ccgtctccag c 681

<210> 1260

<211> 693
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1260
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 gggaaagccc ctaagctcct gatccttgct ttttcccgtt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcaa tctgcaacct 240
 gaagattttg ctacgtacta ctgcgcgag gctgggacgc atcctacgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgggctagc acctcaggtc catcggaggt gcagctgttg 360
 gagtctgggg gaggcttggt acagcctggg gggtccttgc gtctctcctg tgcagcctcc 420
 ggattcacct ttcgggatta tgagatgtgg tgggtccgcc aggtccagg gaagggtcta 480
 gagcgggtct cagctattaa tccgcagggt acgcgtacat actacgcaga ctccgtgaag 540
 ggccgggttca ccatctcccg cgacaattcc aagaacacgc tgtatctgca aatgaacagc 600
 ctgcgtgccg aggacaccgc ggtatattac tgtgcgaaac ttccgtttta ctttcacgag 660
 tggggtcagg gaaccctggt caccgtctcc agc 693

<210> 1261
 <211> 687
 <212> ADN
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1261
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 atcacttgcc gggcaagtcg tccgattggg acgatgttaa gttggtacca gcagaaacca 120
 gggaaagccc ctaagctcct gatccttgct ttttcccgtt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcaa tctgcaacct 240
 gaagattttg ctacgtacta ctgcgcgag gctgggacgc atcctacgac gttcggccaa 300
 gggaccaagg tggaaatcaa acgggggtgga ggtggctctg aggtgcagct gttggagtct 360
 gggggaggct tggtagagcc tgggggggtcc ctgcgtctct cctgtgcagc ctccggattc 420
 acctttcggg attatgagat gtggtgggtc cgccaggctc cagggaaggg tctagagcgg 480
 gtctcagcta ttaatccgca gggtagcgt acatactacg cagactccgt gaagggccgg 540
 ttcaccatct cccgcgacaa ttccaagaac acgctgtatc tgcaaatgaa cagcctgcgt 600

gccgaggaca ccgcggtata ttactgtgcg aaacttccgt tttactttca cgagtgggggt 660
caggaaccc tggtcaccgt ctccagc 687

<210> 1262
<211> 717
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1262
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gggaaagccc ctaagctcct gatccttgct ttttcccggt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcaa tctgcaacct 240
gaagattttg ctacgtacta ctgcgcgcag gctgggacgc atcctacgac gttcggccaa 300
gggaccaagg tggaaatcaa acgggggtgga ggtggctctg gaggtggcgg tagcggcgga 360
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ctgcgtctct cctgtgcagc ctccgattc acctttcggg attatgagat gtggtgggtc 480
cgccaggctc caggaagggt tctagagcgg gtctcagcta ttaatccgca gggtagcgt 540
acatactacg cagactccgt gaagggccgg ttcaccatct cccgcgacaa ttccaagaac 600
acgctgtatc tgcaaatgaa cagcctgcgt gccgaggaca ccgcggtata ttactgtgcg 660
aaacttccgt tttactttca cgagtgggggt caggaaccc tggtcaccgt ctccagc 717

<210> 1263
<211> 747
<212> ADN
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1263
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gggaaagccc ctaagctcct gatccttgct ttttcccggt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcaa tctgcaacct 240
gaagattttg ctacgtacta ctgcgcgcag gctgggacgc atcctacgac gttcggccaa 300
gggaccaagg tggaaatcaa acgggggtgga ggtggctctg gaggtggcgg tagcggcggt 360

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ggcggttcag gtggcgagg ttctggaggc ggtggatctg aggtgcagct gttggagtct 420
gggggaggct tggtagacc tgggggggtcc ctgcgtctct cctgtgcagc ctccggattc 480
acctttcggg attatgagat gtggtgggtc cgccaggctc caggaagg tctagagcgg 540
gtctcagcta ttaatccgca gggtagcgt acatactacg cagactccgt gaagggccgg 600
ttcaccatct ccgcgacaa ttccaagaac acgctgtatc tgcaaatgaa cagcctgcgt 660
gccgaggaca ccgcgtata ttactgtgcg aaacttccgt ttactttca cgagtgggg 720
caggaaccc tggtcaccgt ctccagc 747

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<210> 1264

<211> 681

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1264

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ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcy tacatactac 180
gcagactccg tgaaggccg gttcaccatc tccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccaggac accgcggtat attactgtgc gaaacttccg 300
ttttactttc acgagtggg tcaggaacc ctggtcaccg tttcgagcac ggtggcggac 360
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acttgccggg caagtcgtcc gattgggacg atgttaagtt ggtaccagca gaaaccaggg 480
aaagccccta agctcctgat ccttgctttt tcccgtttgc aaagtgggt cccatcacgt 540
ttcagtggca gtggatctgg gacagatttc actctacca tcagcaatct gcaacctgaa 600
gattttgcta cgtactactg cgcgaggct gggacgcac ctacgacgtt cggccaaggg 660
accaaggtgg aatcaaacg g 681

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<210> 1265

<211> 693

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1265

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gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgcgtctc 60

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tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt cgcagggt      120
ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg      300
ttttactttc acgagtgggg tcaggaacc ctggtcaccg tctcgagcgc tagcacctca      360
ggtccatcgg acatccagat gaccagctct ccctctccc tgtctgcacg ttaggagac      420
cgtgtcacca tcacttgccg ggcaagtcgt ccgattggga cgatgttaag ttggtaccag      480
cagaaaccag ggaaagcccc taagctcctg atccttgctt tttccgttt gcaaagtggg      540
gtcccatcac gtttcagtgg cagtggatct gggacagatt tcactctcac catcagcaat      600
ctgcaacctg aagattttgc tacgtactac tgccgcgagg ctgggacgca tcctacgacg      660
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<210> 1266

<211> 687

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1266

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ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac      180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg      300
ttttactttc acgagtgggg tcaggaacc ctggtcaccg tctcgagcgc tggaggcggc      360
tctgacatcc agatgaccca gtctccatcc tccctgtctg catctgtagg agaccgtgtc      420
accatcactt gccgggcaag tcgtccgatt gggacgatgt taagttggta ccagcagaaa      480
ccagggaaag cccctaagct cctgatcctt gctttttccc gtttgcaaag tggggtccca      540
tcacgtttca gtggcagtgg atctgggaca gatttcactc tcaccatcag caatctgcaa      600
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<210> 1267

<211> 717

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1267

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ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg	300
ttttactttc acgagtgggg tcaggaacc ctggtcaccg tctcgagcgg tggaggtggc	360
tctggaggtg gcggtagcgg cgggtggcgg tcagacatcc agatgaccca gtctccatcc	420
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gggacgatgt taagttggtg ccagcagaaa ccaggaag cccctaagct cctgacctt	540
gctttttccc gtttgcaaag tggggtccca tcacgtttca gtggcagtgg atctgggaca	600
gatttcactc tcaccatcag caatctgcaa cctgaagatt ttgctacgta ctactgcgcg	660
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<210> 1268

<211> 747

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1268

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tcctgtgcag cctccggatt cacctttcgg gattatgaga tgtggtgggt ccgccaggct	120
ccaggaagg gtctagagcg ggtctcagct attaatccgc aggttacgcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacttccg	300
ttttactttc acgagtgggg tcaggaacc ctggtcaccg tctcgagcgg tggaggtggc	360
tctggaggtg gcggtagcgg cgggtggcgg tcaggtggcg gaggttcttg aggcggtgga	420
tctgacatcc agatgaccca gtctccatcc tccctgtctg catctgtagg agaccgtgtc	480
accatcactt gccgggcaag tcgtccgatt gggacgatgt taagttggtg ccagcagaaa	540
ccaggaag cccctaagct cctgacctt gctttttccc gtttgcaaag tggggtccca	600
tcacgtttca gtggcagtgg atctgggaca gatttcactc tcaccatcag caatctgcaa	660

cctgaagatt ttgctacgta ctactgcgcg caggctggga cgcacacctac gacgttcggc 720

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<210> 1269

<211> 690

<212> ADN

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1269

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gggaaagccc ctaagctcct gatccttgc ttttcccggt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcaa tctgcaacct 240

gaagattttg ctacgtacta ctgcgcgcag gctgggacgc atcctacgac gttcggccaa 300

gggaccaagg tggaatcaa acggaccgta gcggcgccga gtgaggtgca gctgttgag 360

tctgggggag gcttggtaca gcctgggggg tccctgcgtc tctcctgtgc agcctccgga 420

ttcacctttc gggattatga gatgtggtgg gtccgccagg ctccaggga ggtctagag 480

cgggtctcag ctattaatcc gcagggtacg cgtacatact acgcagactc cgtgaagggc 540

cggttcacca tctccgcga caattccaag aacacgctgt atctgcaaat gaacagcctg 600

cgtgccgagg acaccgcggt atattactgt gcgaaacttc cgttttactt tcacgagtgg 660

ggtcaggga cctggtcac cgtctccagc 690

<210> 1270

<211> 44

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polinucleótido Sintético

<400> 1270

Cys Ser Pro Gly Phe Gly Val Lys Gln Ile Ala Thr Gly Val Ser Asp
1 5 10 15

Thr Ile Cys Glu Pro Cys Pro Val Gly Phe Phe Ser Asn Val Ser Ser
20 25 30

Ala Phe Glu Lys Cys His Pro Trp Thr Ser Cys Glu
35 40

<210> 1271

<211> 44

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1271

Cys	Ser	Pro	Gly	Tyr	Arg	Val	Lys	Glu	Ala	Cys	Gly	Glu	Leu	Thr	Gly
1				5				10					15		

Thr	Val	Cys	Glu	Pro	Cys	Pro	Pro	Gly	Thr	Tyr	Ile	Ala	His	Leu	Asn
			20					25					30		

Gly	Leu	Ser	Lys	Cys	Leu	Gln	Cys	Gln	Met	Cys	Asp
		35				40					

<210> 1272

<211> 44

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1272

Cys	Gln	Pro	Gly	Gln	Lys	Leu	Val	Ser	Asp	Cys	Thr	Glu	Phe	Thr	Glu
1				5				10					15		

Thr	Glu	Cys	Leu	Pro	Cys	Gly	Glu	Ser	Glu	Phe	Leu	Asp	Thr	Trp	Asn
			20					25					30		

Arg	Glu	Thr	His	Cys	His	Gln	His	Lys	Tyr	Cys	Asp
			35			40					

<210> 1273

<211> 19

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Péptido Sintético

<400> 1273

Asp	Pro	Gly	Gly	Gly	Gly	Arg	Leu	Val	Pro	Arg	Gly	Phe	Gly	Thr
1			5				10					15		

Gly Asp Pro

<210> 1274
 <211> 5
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Péptido Sintético

<220>
 <221> MOD_RES
 <222> (1)..(1)
 <223> Asp o Gly

<220>
 <221> MOD_RES
 <222> (4)..(4)
 <223> Met o Leu

<400> 1274
 Xaa Tyr Glu Xaa Trp
 1 5

<210> 1275
 <211> 17
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Péptido Sintético

<220>
 <221> MOD_RES
 <222> (5)..(5)
 <223> Gln, Tyr, Pro, Trp o Ala

<220>
 <221> MOD_RES
 <222> (7)..(7)
 <223> Thr, Ser, Asn, Gly, Met o Gln

<220>
 <221> MOD_RES
 <222> (8)..(8)
 <223> Arg, Leu, Tyr, His o Phe

<220>
 <221> MOD_RES
 <222> (16)..(16)
 <223> Lys o Met

<400> 1275
 Ala Ile Asn Pro Xaa Gly Xaa Xaa Thr Tyr Tyr Ala Asp Ser Val Xaa
 1 5 10 15

Gly

<210> 1276
 <211> 7
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Péptido Sintético

<220>
 <221> MOD_RES
 <222> (1)..(1)
 <223> Leu o Pro

<220>
 <221> MOD_RES
 <222> (3)..(3)
 <223> Phe, Gln, Thr o Met

<220>
 <221> MOD_RES
 <222> (4)..(4)
 <223> Tyr, Pro, Leu, Thr, Ile, Phe o Met

<220>
 <221> MOD_RES
 <222> (6)..(6)
 <223> Gln, His, Asp, Ser, Lys, Glu o Gly

<220>
 <221> MOD_RES
 <222> (7)..(7)
 <223> Glu, Asp o Tyr

<400> 1276
 Xaa Pro Xaa Xaa Phe Xaa Xaa
 1 5

<210> 1277
 <211> 30
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<220>
 <221> MOD_RES
 <222> (18)..(18)
 <223> Leu o Arg

<220>
 <221> MOD_RES
 <222> (30)..(30)
 <223> Arg o Ala

<400> 1277
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Xaa Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Xaa
 20 25 30

<210> 1278

<211> 14

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Péptido Sintético

<220>

<221> MOD_RES

<222> (4)..(4)

<223> Gln o Arg

<220>

<221> MOD_RES

<222> (8)..(8)

<223> Lys o Arg

<220>

<221> MOD_RES

<222> (9)..(9)

<223> Gly o Val

<400> 1278

Trp Val Arg Xaa Ala Pro Gly Xaa Xaa Leu Glu Arg Val Ser
 1 5 10

<210> 1279

<211> 32

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<220>

<221> MOD_RES

<222> (12)..(12)

<223> Thr o Met

<220>

<221> MOD_RES

<222> (23)..(23)

<223> Glu o Asp

<220>

<221> MOD_RES

<222> (26)..(26)

<223> Ala o Ser

<220>

<221> MOD_RES

<222> (29)..(29)

<223> Tyr o His

<220>

<221> MOD_RES

<222> (31)..(31)

<223> Ala o Thr

<400> 1279

Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Xaa	Lys	Tyr	Leu	Gln
1				5					10					15	

Met	Asn	Ser	Leu	Arg	Ala	Xaa	Asp	Thr	Xaa	Val	Tyr	Xaa	Cys	Xaa	Lys
			20					25					30		

<210> 1280

<211> 11

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Péptido Sintético

<220>

<221> MOD_RES

<222> (1)..(1)

<223> Trp o Arg

<220>

<221> MOD_RES

<222> (3)..(3)

<223> Gln o Pro

<220>

<221> MOD_RES

<222> (11)..(11)

<223> Ser o Asn

<400> 1280

Xaa	Gly	Xaa	Gly	Thr	Leu	Val	Thr	Val	Ser	Xaa
1				5					10	

<210> 1281

<211> 116

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<220>

<221> MOD_RES

<222> (13)..(13)

<223> Gln o Arg

<220>

<221> MOD_RES
 <222> (99)..(99)
 <223> Glu o Gly

<220>
 <221> MOD_RES
 <222> (101)..(101)
 <223> Ala, Leu o Glu

<220>
 <221> MOD_RES
 <222> (102)..(102)
 <223> Phe o Tyr

<220>
 <221> MOD_RES
 <222> (106)..(106)
 <223> Trp o Arg

<400> 1281
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Xaa Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Glu Trp Tyr
 20 25 30

Glu Met Gln Trp Val Arg Arg Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Ser Gly Asp Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Xaa Leu Xaa Xaa Phe Asp Tyr Xaa Gly Arg Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser
 115

<210> 1282
 <211> 116
 <212> PRT
 <213> Secuencia Artificial

<220>
 <223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<220>
 <221> MOD_RES

<222> (28)..(28)

<223> Thr o Pro

<220>

<221> MOD_RES

<222> (50)..(50)

<223> Ala o Ser

<220>

<221> MOD_RES

<222> (53)..(53)

<223> Arg o Gly

<220>

<221> MOD_RES

<222> (54)..(54)

<223> Arg, Ser, Asn, Gln, Gly, His o Leu

<220>

<221> MOD_RES

<222> (56)..(56)

<223> Tyr, Phe, Trp o Gly

<220>

<221> MOD_RES

<222> (57)..(57)

<223> Ser o Gly

<220>

<221> MOD_RES

<222> (102)..(102)

<223> Arg, Met o Pro

<400> 1282

Glu Val Gln Leu Leu Ala Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Xaa Phe Glu Glu Glu
20 25 30

Glu Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Xaa Ile Ser Xaa Xaa Gly Xaa Xaa Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Gly Lys Glu Pro Phe Xaa Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 1283
<211> 118
<212> PRT
<213> Secuencia Artificial

<220>
<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<220>
<221> MOD_RES
<222> (36)..(36)
<223> Met o Leu

<220>
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<222> (39)..(39)
<223> Val o Phe

<220>
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<222> (76)..(76)
<223> Asp o Asn

<220>
<221> MOD_RES
<222> (77)..(77)
<223> Ser o Thr

<220>
<221> MOD_RES
<222> (97)..(97)
<223> Tyr o His
<220>
<221> MOD_RES
<222> (100)..(100)
<223> Lys o Arg

<220>
<221> MOD_RES
<222> (101)..(101)
<223> Asp o Glu

<220>
<221> MOD_RES
<222> (105)..(105)
<223> Tyr o Phe

<220>
<221> MOD_RES
<222> (108)..(108)
<223> Trp o Arg

<220>
<221> MOD_RES
<222> (109)..(109)
<223> Gly o Arg

<220>

<221> MOD_RES

<222> (110)..(110)

<223> Gln o His

<400> 1283

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Gly Thr
 20 25 30

Arg Tyr Glu Xaa Trp Trp Xaa Arg Gln Ala Pro Gly Lys Gly Leu Glu
 35 40 45

Arg Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp
 50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Xaa Xaa Lys Asn Thr
 65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 85 90 95

Xaa Cys Ala Xaa Xaa Pro Tyr Ser Xaa Asp Tyr Xaa Xaa Xaa Gly Thr
 100 105 110

Leu Val Thr Val Ser Ser
 115

<210> 1284

<211> 232

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1284

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala
 1 5 10 15

Pro Glu Leu Leu Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro
 20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
 50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 1285

<211> 229

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1285

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
130 135 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys
225

<210> 1286

<211> 351

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1286

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
 20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
 35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Leu Pro Phe Arg Phe Ser Asp Arg Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser Ala Ser Thr Glu Pro Lys Ser Ser Asp Lys Thr His
 115 120 125

Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
 130 135 140

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 145 150 155 160

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
 165 170 175

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 180 185 190

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
 195 200 205

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 210 215 220

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

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 245 250 255

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 260 265 270

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
275 280 285

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
290 295 300

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
305 310 315 320

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
325 330 335

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
340 345 350

<210> 1287

<211> 348

<212> PRT

<213> Secuencia Artificial

<220>

<223> Descripción de la Secuencia Artificial: Polipéptido Sintético

<400> 1287

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Asp Tyr
20 25 30

Glu Met Trp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Arg Val
35 40 45

Ser Ala Ile Asn Pro Gln Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Leu Pro Phe Arg Phe Ser Asp Arg Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser Ala Ser Thr Glu Ser Lys Tyr Gly Pro Pro Cys Pro
115 120 125

Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
 130 135 140

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 145 150 155 160

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
 165 170 175

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 180 185 190

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 195 200 205

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 210 215 220

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
 225 230 235 240

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
 245 250 255

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 260 265 270

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 275 280 285

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 290 295 300

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
 305 310 315 320

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 325 330 335

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 340 345

POD-4002

TRADUCCIÓN OFICIAL N° 0507071 al español de un documento escrito en inglés, efectuada por Jaime Armando Garavito Burgos, c.c. N° 19.130.702 de Bogotá, Traductor e Interpreté Oficial inglés-español-inglés según Resolución N° 034 de enero 11 de 1983 expedida por el Ministerio de Justicia de la República de Colombia

PODER OTORGADO POR BRISTOL-MYERS SQUIBB COMPANY

APOSTILLA

1. PAÍS: ESTADOS UNIDOS DE AMÉRICA
2. ESTE DOCUMENTO PÚBLICO HA SIDO FIRMADO POR:
SALLY B. HANSEN
3. QUIEN ACTÚA EN CALIDAD DE NOTARIO PÚBLICO DE NUEVA JERSEY
4. LLEVA EL SELLO DE:
SALLY B. HANSEN, NOTARIO

CERTIFICADO

5. EN TRENTON, NUEVA JERSEY
6. EL 28 DE JUNIO DE 2007
7. POR BRADLEY ABELOW, TESORERO DE NUEVA JERSEY
8. N° A295716
9. SELLO (APARECE ADHERIDO SELLO DORADO)
10. FIRMA (FIRMADO) BRADLEY ABELOW

Texto en inglés y en español mediante el cual **BRISTOL-MYERS SQUIBB COMPANY** domiciliada en Nueva York, Nueva York, otorga poder a **ALVARO CORREA ORDOÑEZ y/o OLGA GEORGETTE OTERO y/o RICARDO METKE y/o JUAN PABLO CONCHA**

Dado y suscrito el 30 de mayo de 2007

(Firmado) Anastasia P. Winslow, Senior Patent Counsel (Abogado de Patentes Senior)


JAIME A. GARAVITO B
TRADUCTOR E INTERPRETE OFICIAL
EN 034 DE ENERO 11 DE 1983
MINISTERIO DE JUSTICIA



TRADUCCIÓN OFICIAL N° 0507071 al español de un documento escrito en inglés, efectuada por Jaime Armando Garavito Burgos, c.c. N° 19.130.702 de Bogotá, Traductor e Intérprete Oficial inglés-español-inglés según Resolución N° 034 de enero 11 de 1983 expedida por el Ministerio de Justicia de la República de Colombia

CERTIFICACIÓN NOTARIAL

Texto en inglés y en español mediante el cual el suscrito Notario certifica el 30 de mayo de 2007 la existencia legal de la sociedad **BRISTOL-MYERS SQUIBB COMPANY** así como las funciones y firma de su representante autorizado Anastasia P. Winslow, Senior Patent Counsel (Abogado de Patentes Senior) para lo cual se basó en los documentos relacionados en inglés en el punto 6 de la certificación los cuales se traducen aquí al español, a saber:

Certificación suscrita por el Vicepresidente Senior y el Asesor Legal de Bristol-Myers Squibb Company el 7 de abril de 2007.

Certificado de Constitución Enmendado y Replanteado de Bristol-Myers Squibb Company fechado mayo 24, 2005.

[Firmado] SALLY B. HANSEN, Notario Público

[Sello en tinta que dice: "SALLY B. HANSEN, Notario Público de Nueva Jersey. Mi comisión vence el 6 de junio de 2010"]

[Aparece sello realizado]

La anterior es traducción fiel y completa de la cual se deja copia en esta oficina para su confrontación.

Jaime Armando Garavito Burgos
c.c. N° 19.130.702 de Bogotá
Traductor e Intérprete Oficial según Resolución N° 034 de enero 11 de 1983
expedida por el Ministerio de Justicia

BOGDM5 # 82106

JAIME A. GARAVITO B.
TRADUCTOR E INTERPRETE OFICIAL
SEGUN RESOLUCION N° 034 DE ENERO 11 DE 1983
MINISTERIO DE JUSTICIA

APOSTILLE

(CONVENTION DE LA HAYE DU 5 OCTOBRE 1961)

1. COUNTRY: UNITED STATES OF AMERICA
2. THIS PUBLIC DOCUMENT HAS BEEN SIGNED BY:
SALLY B HANSEN
3. ACTING IN THE CAPACITY OF:
NOTARY PUBLIC OF NEW JERSEY
4. BEARS THE SEAL/STAMP OF:
SALLY B HANSEN, NOTARY

CERTIFIED

5. AT TRENTON, NEW JERSEY
6. THE 28TH DAY OF JUNE 2007
7. BY: Bradley Abelow, NEW JERSEY TREASURER
8. NO. A295716
9. SEAL/STAMP:
10. SIGNATURE



Bradley Abelow

POWER OF ATTORNEY

The undersigned.

BRISTOL-MYERS SQUIBB COMPANY

domiciled in

Route 206 and Province Line Road, Princeton,
New Jersey 08543-4000 United States of America

declares that it hereby grants to

**ALVARO CORREA-ORDOÑEZ and/or
OLGA GEORGETTE OTERO and/or
RICARDO METKE and/or
JUAN PABLO CONCHA**

with domicile at Av. 82 No. 10 - 62, 6th floor, of Bogotá D. C., Colombia, a full and sufficient power of attorney to obtain the protection of my (our) industrial property and against the unfair competition, for which purpose I (we) authorize the said attorneys to represent me (us) before any authorities or persons, with or without jurisdiction, specially those administrative, administrative contentious and judicial, as well as before Arbitration Court, in all matters concerning the following: a) Obtainment of patents, utility models, industrial designs, integrated circuits, layout-designs and vegetal varieties; the registration of trademarks, denominations of origin, commercial names, trade emblems, slogans and domain names; its renewal, assignments, change of name or domicile, voluntary cancellation; and the registration of licenses of use of the above rights; b) Processes of protection to the consumer, unfair competition, oppositions, cancellations, nullity, precautionary injunctions, infringement, granting of licenses, writ mandamus, the protection of trade secrets, and in general the civil, penal, an administrative processes relating to those rights. And that in all the above matters they may substitute this Power of Attorney, compromise, conciliate, admit the facts of the case, desist, cancel, receive, resign, and ratify acts done by representatives without a power of attorney.

I hereby ratify all actions previously taken on behalf of this company by the aforementioned attorneys with respect to the mentioned matters.

Done and subscribed in

On the 30 day of May of 2007

Signature of the person issuing the Power



Anastasia P. Winslow
Senior Patent Counsel

PODER DE ABOGADO

La abajo firmada,

BRISTOL-MYERS SQUIBB COMPANY

domiciliada en

Route 206 and Province Line Road, Princeton,
New Jersey 08543-4000 Estados Unidos de América

declara por el presente que otorga a

**ALVARO CORREA-ORDOÑEZ y/o
OLGA GEORGETTE OTERO y/o
RICARDO METKE y/o
JUAN PABLO CONCHA**

con domicilio en la Av. 82 No. 10 - 62 Piso 6 en Bogotá D. C., Colombia, poder especial amplio y suficiente, para obtener la protección de mi (nuestra) propiedad industrial y contra la competencia desleal, a cuyo efecto autorizo (amos) a los dichos apoderados para que me (nos) representen ante cualesquiera autoridades o personas, ejerzan o no jurisdicción, especialmente ante las del orden administrativo, contencioso-administrativo y judicial, así como los tribunales de arbitramento, en todo lo concerniente a los siguientes asuntos: a) Obtención de patentes de invención, modelos de utilidad, diseños industriales, esquemas de trazado de circuitos integrados y variedades vegetales; el registro de marcas, denominaciones de origen, nombres comerciales, enseñanzas, lemas comerciales y nombres de dominio; su renovación, traspaso, cambio de nombre o domicilio, cancelación voluntaria; y el registro de licencias de uso de esos derechos; b) Los procesos para la protección del consumidor, competencia desleal, oposiciones, cancelaciones, nulidades, medidas cautelares, infracciones, concesión de licencias, la tutela, la protección de secretos industriales, y en general procesos civiles, penales, administrativos relacionados con estos derechos. Y para que en todos los asuntos arriba determinados, puedan sustituir este mandato, transigir, conciliar, admitir los hechos del caso, desistir, cancelar, recibir, renunciar, y ratificar los actos de agentes oficiales.

Igualmente, ratifico todo lo actuado hasta el momento en los mismos asuntos, por cualquiera de los mencionados apoderados en representación de esta sociedad.

Dado y firmado en

A los 30 días del mes de mayo de 2007

Firma de la persona que firma el Poder

NOTARIAL CERTIFICATION

On this 30 day of May
2007, the undersigned Notary

CERTIFIES

1. That Name of the person issuing the power
Anastasia P. Winslow
of legal age and domiciled in
Princeton, NJ USA
Address, city, state, country
set his hand on the foregoing document.
2. That the grantor is to me personally known and that he/she has legal capacity to execute the instrument.
3. That the grantor has executed the foregoing document as
Senior Patent Counsel
Position of the person issuing the Power
of the judicial person **BRISTOL-MYERS SQUIBB COMPANY**
4. That the judicial person **BRISTOL-MYERS SQUIBB COMPANY**
having its home office in
Route 206 and Province Line Road, Princeton,
New Jersey 08543-4000 United States of America
is duly organized, has present legal existence and that the purposes for which the power of attorney is granted are within the scope of its corporate purposes.
5. That the grantor has in fact the referred to authority and that his/her representation is legal.
6. That I have based certifications 3, 4 and 5 above on the following authentic documents for such purpose exhibited to me and which I mention specifically, giving their dates and their origin or source:
(Please indicate here the documents such as the articles of incorporation, by laws or resolution from the Board of Directors and their dates, on which the notary relied to grant the certification)
- Certification executed by Sr. Vice President and General Counsel of Bristol-Myers Squibb Company on April 7, 2007
- Amended and Restated Certificate of Incorporation of Bristol-Myers Squibb Company dated May 24, 2005

Notary Public

SALLY B. HANSEN
Notary Public of New Jersey
My Commission Expires June 6, 2010

CERTIFICACION NOTARIAL

A los 30 días del mes de mayo
de 2007, el suscrito Notario

DA FE

1. Que Anastasia P. Winslow
mayor y domiciliado en Princeton, NJ
Estados Unidos de América
suscrió de su puño y letra el documento que antecede.
2. Que conozco al otorgante y que éste tiene capacidad legal para el otorgamiento.
3. Que el otorgante ha suscrito el referido documento en su carácter de
Abogados de Patentes Senior
de la persona jurídica **BRISTOL-MYERS SQUIBB COMPANY**
4. Que la persona jurídica **BRISTOL-MYERS SQUIBB COMPANY**
con sede en
Route 206 and Province Line Road, Princeton,
New Jersey 08543-4000 Estados Unidos de América
está legalmente constituida, que tiene existencia legal actual y que el acto para el cual se otorga el poder está comprendido entre los que constituyen su objeto social.
5. Que el otorgante tiene efectivamente la representación que ostenta y que ésta es legítima.
6. Que he basado las certificaciones 3, 4 y 5 anteriores en los siguientes documentos auténticos que al efecto se me exhibieron y que menciono específicamente con expresión de sus fechas y de su origen o procedencia:
- Certificación suscrita por el Vicepresidente Senior y el Asesor Legal de Bristol-Myers Squibb Company el 7 de abril de 2007.
- Certificado de Constitución Enmendado y Replanteado de Bristol-Myers Squibb Company fechado el 4 de mayo de 2005.

El Notario Público

Yo, el infrascrito, Sebastian Jack Robert LABOVITCH, Notario Público de la Ciudad de Londres, Inglaterra, por la Autoridad Real debidamente admitido y juramentado,

CERTIFICO:

QUE el Poder que se adjunta ha sido firmado el día de hoy en mi presencia y en nombre y representación de la Sociedad inglesa denominada "DOMANTIS LIMITED" por el Señor Marcus Jonathan William DALTON, cuya identidad me consta, Apoderado de la citada Sociedad;

QUE la aludida "DOMANTIS LIMITED" es una sociedad privada de responsabilidad limitada debidamente constituida, organizada y existente de acuerdo con la ley inglesa, en actual funcionamiento, e inscrita en la Oficina de Registro de Sociedades de Inglaterra y Gales bajo el número 3907643, con domicilio social en 980 Great West Road, Brentford, Middlesex TW8 9GS, Inglaterra;

Y QUE el referido Marcus Jonathan William DALTON, en su citada capacidad, está debida y suficientemente autorizado para firmar documentos de esta clase, en virtud del Poder otorgado en su favor por la referida Sociedad fechado el 5 de enero de 2010, una copia del cual he tenido a la vista.

Y PARA QUE CONSTE donde y como convenga y fuere necesario, expido la presente que firmo y sello en dicha Ciudad de Londres, el día de hoy dieciocho de febrero del año dos mil once.


Sebastian Jack Robert LABOVITCH
Notario Público de Londres, Inglaterra

APOSTILLE

(Hague Convention of 5 October 1961 / Convention de La Haye du 5 octobre 1961)

UNITED KINGDOM OF GREAT BRITAIN AND NORTHERN IRELAND

1. Country: United Kingdom of Great Britain and Northern Ireland
Pays: Royaume-Uni de Grande-Bretagne et d'Irlande du Nord
This public document / Le présent acte public
2. Has been signed by Sebastian Jack Robert Labovitch
a été signé par
3. Acting in the capacity of Notary Public
agissant en qualité de
4. Bears the seal/stamp of The Said Notary Public
est revêtu du sceau/stamp de
5. at London/Londres
6. Certified/Attesté
le 21 February 2011
7. by Her Majesty's Principal Secretary of State for Foreign and Commonwealth Affairs /
par le Secrétaire d'Etat Principal de Sa Majesté aux Affaires Etrangères et du Commonwealth.
8. Number/No 1787096
9. Stamp:
sceau:
10. Signature: D.O.Sullivan
DOS



For the Secretary of State / Pour le Secrétaire d'Etat

If this document is to be used in a country which is not party to the Hague Convention of 5th October 1961, it should be presented to the consular section of the mission representing that country.

An apostille or legalisation certificate only confirms that the signature, seal or stamp on the document is genuine. It does not mean that the content of the document is correct or that the Foreign & Commonwealth Office approves of the content.

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(461654)
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Tel: +57 1 834 1500
Fax: +57 1 376 2211
www.bakerandmckenzie.com

POWER OF ATTORNEY

The undersigned,

DOMANTES LIMITED

located at

990 Great West Road, Brentford, Middlesex TW8 9GS,
United Kingdom

declares that it hereby grants to

ÁLVARO CORREA-ORDÓÑEZ and/or
RICARDO METKE MENDEZ and/or JUAN PABLO
CONCHA-DELGADO and/or
OLGA GEORGETTE OTERO

of the firm Baker & McKenzie Colombia S.A. members of Baker & McKenzie, domiciled at Av. 82 No. 10-62, 6th floor, of Bogotá D.C., Colombia, full and sufficient power of attorney to pursue before the competent authorities the following matters:

Trademark registrations and renewals; deposit and registration of commercial names and commercial ensigns; registration and renewal of domain names; Prosecution and obtaining of patents, utility models, industrial designs, integrated circuits layout-designs and vegetal varieties; records of mergers, changes of name, assignments, changes of domicile and address; security interests; liens and other acts that affect or limit the mentioned industrial property rights; filing and prosecution of oppositions; recordal of license of use agreements; filing and prosecution of cancellation actions, amendment actions, amendment and reinstatement of right action, and all judicial actions available for the prosecution of proceedings related to intellectual property matters, unfair competition, and protection of consumers.

to which end it empowers them to file requests, petitions and lawsuits, appeals and objections, pay taxes, receive, including facilities to enter into settlement agreements, conciliations and transactions, abandon applications and renounce to intellectual property rights and, in general, to take all the actions before the competent authorities in order to duly protect our intellectual property. To the said mandatories sufficient power is granted hereby to receive notifications for and on behalf of the Company, to confer powers on those who are to represent the Company judicially and extrajudicially, to answer in court in the matter of all claims and demands that may be presented in connection with the marks and other intellectual property rights, and to do everything that may be required before administrative or judicial officers of any class to comply this power, giving them likewise faculty to substitute these persons and receive their substitution in consequence.

Marcus Jonathan William HALTON
as Attorney & Authorised Official
Done and subscribed in Brentford, Middlesex, GB

PODER

La stajo firmada.

DOMANTIS LIMITED

domiciliada en

950 Great West Road, Brentford, Middlesex TW8 9GS, United Kingdom

declara por el presente que otorga, a

ÁLVARO CORREA-ORDÓÑEZ y/o RICARDO METKE
MÉNDEZ y/o JUAN PABLO CONCHA-DELGADO y/o OLGA
GEORGETTE OTERO

de la firma Baker & McKenzie Colombia S.A., miembros de Baker & McKenzie, domiciliada en la Av. 82 No. 10-63 Piso 6 en Bogotá D.C., Colombia, poder especial amplio y suficiente, para adelantar ante las autoridades competentes los siguientes asuntos:

Registro y renovación de marcas; depósito y registro de nombres comerciales y enseñanzas comerciales; registro y renovación de nombres de dominio; trámite y obtención de solicitudes de patente de invención, modelos de utilidad, diseños industriales, esquemas de trazado de circuitos integrados y variedades vegetales; inscripción de fusiones, cambios de nombre, trasposos, cambios de domicilio y de dirección; inscripción de contratos de prenda, embargos y otros actos que afecten o limiten las mencionados derechos de propiedad industrial; presentación y tramitación de oposiciones; inscripción de licencias de uso; presentación y tramitación de acciones de cancelación; acciones de nulidad, acciones de nulidad y restablecimiento del derecho y demás acciones judiciales, relacionadas con procesos de propiedad industrial, competencia desleal y protección al consumidor.

a cuyo efecto los facultó para presentar solicitudes, peticiones y demandas, imponer recargos, reclamos, pagar impuestos y tasas, recibir, transgír y desistir, incluyendo facultades para entrar en acuerdos amistosos, conciliaciones y transacciones, abandonar solicitudes y renunciar a derechos de propiedad industrial, y en general, a dar ante las autoridades competentes todos los pasos necesarios para la debida prosecución de nuestra propiedad industrial. Asimismo se concede a los expresados mandatarios poder suficiente para recibir notificaciones a nombre de la compañía, otorgar poderes a quienes vayan a representar a la compañía judicial y extrajudicialmente, responder en juicio a todas las reclamaciones o demandas que por motivo de marcas y otros derechos de propiedad industrial se presentaren y hacer cuanto fuere necesario ante las autoridades administrativas o judiciales de cualquier orden para el cumplimiento de este mandato, dándole igualmente facultad para constituir o presenciar o para otorgar transacciones, dichos constituciones.

Dado y firmado en

18th February 2011

APOSTILLA EN PODER DE DOMANTIS LIMITED.

Certificado de Notario Público- En español firmado por Sebastian Jack Robert Labovich
En ingles en el reverso:

APOSTILLA

(Convención De La Haya del 5 octubre de 1961)

1. País Reino Unido de Gran Bretaña e Irlanda del Norte
2. Este documento Público ha sido firmado por Sebastian Jack Robert Labovich
3. Quien ejerce funciones de notario público
4. Lleva el sello de tal notario público
- CERTIFICADO 5. En Londres 6. El 21 de febrero de 2011.
7. Por el secretario de estado principal de su majestad para Asuntos Extranjeros y Mancomunidad
- 8 No. 1787096
9. Sello del secretario de estado principal de su majestad para Asuntos Extranjeros y Mancomunidad
10. Firma ilegible de D. O. Sullivan- Por el secretario de Estado

Si el documento se usa en un país que no es parte de la Convención de la Haya, del 5 de octubre de 1961, debe presentarse a la sección consular de la misión que representa a ese país. La apostilla o certificado de legalización solo confirma que la firma, sello o estampilla en el documento es auténtica. No significa que el contenido del documento sea correcto o que la oficina de asuntos extranjeros o mancomunidad apruebe el contenido

PODER

Bilingüe inglés y español, de Domantis Limited compañía del Reino Unido firmado por Marcus Jonathan William Dalton, en Brentford, Middlesex, GB el 18 de febrero de 2011.
Es traducción conforme con copia para confrontar. Bogotá. Mayo 21- 2011.

Marlen Neira Castro
MARLEN NEIRA CASTRO
Traductor e Intérprete Oficial
Inglés - Español - Inglés
Resolución No. 2117 del 7 Oct 1987



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61/477,904 21 April 2011 (21.04.2011) US
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- (72) Inventors; and
- (75) Inventors/Applicants (*for US only*): **SURI, Anish** [US/US]; Bristol-Myers Squibb Company, Route 206 & Province Line Road, Princeton, New Jersey 08543 (US). **SHERIFF, Steven** [US/US]; Bristol-Myers Squibb Company, Route 206 & Province Line Road, Princeton, New

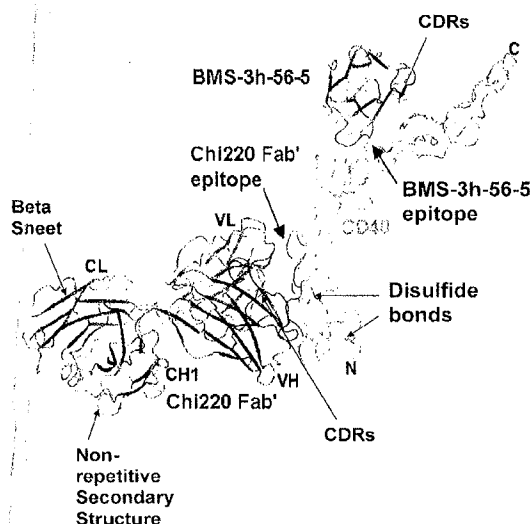
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- (74) Agents: **MEYER, Mercedes K.** et al.; Drinker Biddle & Reath LLP, 1500 K Street, N.W., Suite 1100, Washington, District of Columbia 20005-1209 (US).
- (81) Designated States (*unless otherwise indicated, for every kind of national protection available*): AF, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO,

[Continued on next page]

(54) Title: ANTIBODY POLYPEPTIDES THAT ANTAGONIZE CD40

FIG. 1



(57) Abstract: Antibody polypeptides that specifically bind a novel epitope of human CD40 are provided. The antibody polypeptides do not exhibit CD40 agonist activity. The antibody polypeptides are useful in the treatment of diseases involving CD40 activation, such as autoimmune diseases. The antibody polypeptides may be domain antibodies (dAbs) comprising a single V_L or V_H domain. The half-life of the antibody polypeptides may be increased by modifying the antibody polypeptides to be dual specific reagents that can also bind human serum albumin (HSA).

DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

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- with international search report (Art. 21(3))
- with sequence listing part of description (Rule 5.2(a))

ANTIBODY POLYPEPTIDES THAT ANTAGONIZE CD40**TECHNICAL FIELD**

Antibodies and fragments thereof that target CD40, and do not exhibit CD40 agonist activity, compositions comprising the same, and methods of using the same for treatment of diseases involving CD40 activity are provided.

CROSS-REFERENCE TO RELATED APPLICATIONS

The instant application claims the benefit of U.S. Provisional Application No. 61/477,904, filed April 21, 2011, the entire contents of which are herein incorporated by reference.

SEQUENCE LISTING

The instant application contains a Sequence Listing in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on April 20, 2012, is named 200896WO.txt and is 1,188,533 bytes in size.

BACKGROUND

CD40 is a co-stimulatory molecule belonging to the tumor necrosis factor (TNF) receptor superfamily that is present on antigen presenting cells (APC), including dendritic cells, B cells, and macrophages. APCs are activated when CD40 binds its ligand, CD154 (CD40L), on T_H cells. CD40-mediated APC activation is involved in a variety of immune responses, including cytokine production, up-regulation of co-stimulatory molecules (such as CD86), and enhanced antigen presentation and B cell proliferation. CD40 can also be expressed by endothelial cells, smooth muscle cells, fibroblasts, and epithelial cells.

CD40 activation is also involved in a variety of undesired T cell responses related to autoimmunity, transplant rejection, or allergic responses, for example. One strategy for controlling undesirable T cell responses is to target CD40 with an antagonistic antibody. For example, monoclonal antibody HCD122 (Lucatumumab), formerly known as Chiron 1212, is currently in clinical trials for the treatment of certain CD40-mediated inflammatory diseases.

See "Study of HCD122 (Lucatumumab) and Bendamustine Combination Therapy in CD40⁺ Rituximab-Refractory Follicular Lymphoma," Clinical Trials Feeds, on the Internet at [hypertext transfer protocol: clinicaltrialsfeeds.org/clinical-trials/show/NCT01275209](http://clinicaltrialsfeeds.org/clinical-trials/show/NCT01275209) (last updated January 11, 2011). Monoclonal antibodies, however, can display agonist activity. For example, the usefulness of the anti-CD40 antibody Chi220 is limited by its weak stimulatory potential. See Adams, et al., "Development of a chimeric anti-CD40 monoclonal antibody that synergizes with LEA29Y to prolong islet allograft survival," *J. Immunol.* 174: 542-50 (2005).

SUMMARY

Anti-CD40 antibody antagonists that do not possess partial agonist activity are still needed in a clinical setting. Novel antibody polypeptides that specifically bind a novel epitope of human CD40 are provided. The CD40 epitope does not overlap the Chi220 epitope, as shown by competition analysis and by the structure derived from co-crystallization of an antibody polypeptide with CD40. The antibody polypeptides advantageously do not exhibit CD40 agonist activity. The antibody polypeptides are useful in the treatment of diseases involving CD40 activation, including autoimmune diseases, transplant rejection, and allergic responses. The antibody polypeptides comprise a variable domain. In one embodiment, the antibody polypeptides are in the form of a domain antibody (dAb) that contains a single variable domain. In another embodiment, the dAbs are bi-specific reagents that comprise a second variable domain that can bind human serum albumin (HSA), for example.

Provided is an antibody polypeptide comprising a first variable domain, where said antibody polypeptide specifically binds an epitope of human CD40, where the epitope comprises the amino acid sequence of SEQ ID NO: 1, where the antibody polypeptide competes with the binding of domain antibody (dAb) BMS3h-56-269 (SEQ ID NO: 417), and where the epitope comprises at least one CD40 amino acid residue selected from the group consisting of Trp109, Leu121, His122, Ser124, Ser156, Ala157, Phe158, Glu159, and His162.

Further provided is an antibody polypeptide where the first variable domain comprises the amino acid sequence of one of the antibody polypeptides selected from the lineage group consisting of BMS3h-37, BMS3h-38, BMS3h-56, and BMS3h-198, and where the first variable domain has an apparent binding constant of 1 pM to 100 nM. Further provided is an

antibody polypeptide where the first variable domain has an apparent binding constant of 1 pM to 10 nM.

Also provided is an antibody polypeptide where the amino acid sequence of the first variable domain comprises (a) a CDR1 region which differs from the CDR1 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids, (b) a CDR2 region which differs from the CDR2 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids, (c) a CDR3 region which differs from the CDR3 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids, (d) a FR1 region which differs from the FR1 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids, (e) a FR2 region which differs from the FR2 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids, (f) a FR3 region which differs from the FR3 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids, and (g) a FR4 region which differs from the FR4 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids.

Also provided is an antibody polypeptide where the amino acid sequence of the first variable domain comprises (a) a CDR1 region which differs from the CDR1 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids, (b) a CDR2 region which differs from the CDR2 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids, (c) a CDR3 region which differs from the CDR3 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids.

Further provided is an antibody polypeptide where the amino acid sequence of the first variable domain differs from the amino acid sequence of BMS3h-56-258 (SEQ ID NO: 10) or BMS3h-56-269 (SEQ ID NO: 417) by up to 10 amino acids.

Further provided is an antibody polypeptide where the amino acid sequence of the first variable domain differs from the amino acid sequence of BMS3h-56-258 (SEQ ID NO: 10) or BMS3h-56-269 (SEQ ID NO: 417) by up to 5 amino acids.

Further provided is an antibody polypeptide where the amino acid sequence of the first variable domain differs from the amino acid sequence of BMS3h-56-258 (SEQ ID NO: 10) or BMS3h-56-269 (SEQ ID NO: 417) by two amino acids.

Further provided is an antibody polypeptide where the amino acid sequence of the first variable domain differs from the amino acid sequence of BMS3h-56-258 (SEQ ID NO: 10) or BMS3h-56-269 (SEQ ID NO: 417) by one amino acid.

Further provided is an antibody polypeptide where the antibody polypeptide is selected from the lineage group of BMS3h-56, and where the amino acid sequence of the first variable domain further comprises: (a) a CDR1 region having a sequence X_1 -Tyr-Glu- Y_1 -Trp (SEQ ID NO: 1274), where X_1 is Asp or Gly, and Y_1 is Met or Leu; (b) a CDR2 region having a sequence Ala-Ile-Asn-Pro- X_2 -Gly- Y_2 -Z₂-Thr-Tyr-Tyr-Ala-Asp-Ser-Val- A_2 -Gly (SEQ ID NO: 1275), where X_2 is Gln, Tyr, Pro, Trp, or Ala, Y_2 is Thr, Ser, Asn, Gly, Met, or Gln, Z₂ is Arg, Leu, Tyr, His, or Phe, and A_2 is Lys or Met; and (c) a CDR3 region having a sequence X_3 -Pro- Y_3 -Z₃-Phe- A_3 -B₃ (SEQ ID NO: 1276), where X_3 is Leu or Pro, Y_3 is Phe, Gln, Thr, or Met, Z₃ is Tyr, Pro, Leu, Thr, Ile, Phe, or Met, A_3 is Gln, His, Asp, Ser, Lys, Glu, or Gly, and B₃ is Glu, Asp, or Tyr.

Further provided is an antibody polypeptide where the amino acid sequence of the first variable domain comprises: (a) a FR1 region having a sequence Glu-Val-Gln-Ileu-Ileu-Glu-Ser-Gly-Gly-Gly--Leu-Val-Gln-Pro-Gly-Gly-Ser- X_1 -Arg-Leu-Ser-Cys-Ala-Ala-Ser-Gly-Phe-Thr-Phe- Y_1 (SEQ ID NO: 1277), where X_1 is Leu or Arg, and Y_1 is Arg or Ala; (b) a FR2 region having a sequence Trp-Val-Arg- X_2 -Ala-Pro-Gly- Y_2 -Z₂-Leu-Glu-Arg-Val-Ser (SEQ ID NO: 1278), where X_2 is Gln or Arg, Y_2 is Lys or Arg, and Z₂ is Gly or Val; (c) a FR3 region having a sequence Arg-Phe-Thr-Ile-Ser-Arg-Asp-Asn-Ser-Lys-Asn- X_3 -Lys-Tyr-Leu-Gln-Met-Asn-Ser-Leu-Arg-Ala- Y_3 -Asp-Thr-Z₃-Val-Tyr- A_3 -Cys-B₃-Lys (SEQ ID NO: 1279), where X_3 is Thr or Met, Y_3 is Glu or Asp, Z₃ is Ala or Ser, A_3 is Tyr or His, and B₃ is Ala or Thr; and (d)

a FR4 region having a sequence X₄-Gly-Y₄-Gly-Thr-Leu-Val-Thr-Val-Ser-Z₄ (SEQ ID NO: 1280), where X₄ is Trp or Arg, Y₄ is Gln or Pro, and Z₄ is Ser or Asn.

Further provided is an antibody polypeptide where the first variable domain comprises the amino acid sequence of BMS3h-56-258 (SEQ ID NO: 10) or BMS3h-56-269 (SEQ ID NO: 417).

Further provided is an antibody polypeptide where the antibody polypeptide is selected from the lineage group of BMS3h-37, where the first variable domain comprises the sequence Glu-Val-Gln-Leu-Leu-Glu-Ser-Gly-Gly-Gly-Leu-Val-X₁-Pro-Gly-Gly-Ser-Leu-Arg-Leu-Ser-Cys-Ala-Ala-Ser-Gly-Phe-Thr-Phe-Glu-Trp-Tyr-Glu-Met-Gln-Trp-Val-Arg-Arg-Ala-Pro-Gly-Lys-Gly-Leu-Glu-Trp-Val-Ser-Ala-Ile-Ser-Gly-Asp-Gly-Tyr-Arg-Thr-Tyr-Tyr-Ala-Asp-Ser-Val-Lys-Gly-Arg-Phe-Thr-Ile-Ser-Arg-Asp-Asn-Ser-Lys-Asn-Thr-Leu-Tyr-Leu-Gln-Met-Asn-Ser-Leu-Arg-Ala-Glu-Asp-Thr-Ala-Val-Tyr-Tyr-Cys-Ala-Lys-Y₁-Leu-Z₁-A₁-Phe-Asp-Tyr-B₁-Gly-Arg-Gly-Thr-Leu-Val-Thr-Val-Ser-Ser (SEQ ID NO: 1281); and where X₁ is Gln or Arg; Y₁ is Glu or Gly; Z₁ is Ala, Leu, or Glu; A₁ is Phe or Tyr; and B₁ is Trp or Arg.

Also provided is an antibody polypeptide where the antibody polypeptide is selected from the lineage group of BMS3h-38, where the first variable domain comprises the sequence Glu-Val-Gln-Leu-Leu-Ala-Ser-Gly-Gly-Gly-Leu-Val-Gln-Pro-Gly-Gly-Ser-Leu-Arg-Leu-Ser-Cys-Ala-Ala-Ser-Gly-Phe-X₁-Phe-Glu-Glu-Glu-Glu-Met-Ile-Trp-Val-Arg-Gln-Ala-Pro-Gly-Lys-Gly-Leu-Glu-Trp-Val-Ser-Y₁-Ile-Ser-Z₁-A₁-Gly-B₁-C₁-Thr-Tyr-Tyr-Ala-Asp-Ser-Val-Lys-Gly-Arg-Phe-Thr-Ile-Ser-Arg-Asp-Asn-Ser-Lys-Asn-Thr-Leu-Tyr-Leu-Gln-Met-Asn-Ser-Leu-Arg-Ala-Glu-Asp-Thr-Ala-Val-Tyr-Tyr-Cys-Gly-Lys-Glu-Pro-Phe-D₁-Tyr-Asp-Tyr-Trp-Gly-Gln-Gly-Thr-Leu-Val-Thr-Val-Ser-Ser (SEQ ID NO: 1282); and where X₁ is Thr or Pro; Y₁ is Ala or Ser; Z₁ is Arg or Gly; A₁ is Arg, Ser, Asn, Gln, Gly, His, or Leu; B₁ is Tyr, Phe, Trp, or Gly; C₁ is Ser or Gly; and D₁ is Arg, Met, or Pro.

Also provided is an antibody polypeptide where the antibody polypeptide is selected from the lineage group of BMS3h-198, where the first variable domain comprises the sequence Glu-Val-Gln-Leu-Leu-Glu-Ser-Gly-Gly-Gly-Leu-Val-Gln-Pro-Gly-Gly-Ser-Leu-Arg-Leu-Ser-Cys-Ala-Ala-Ser-Gly-Phe-Thr-Phe-Ala-Gly-Tyr-Glu-X₁-Trp-Trp-Y₁-Arg-Gln-Ala-Pro-Gly-Lys-Gly-Leu-Glu-Arg-Val-Ser-Ala-Ile-Ser-Gly-Ser-Gly-Gly-Ser-Thr-Tyr-Tyr-Ala-Asp-Ser-Val-Lys-Gly-Arg-Phe-Thr-Ile-Ser-Arg-Asp-Z₁-A₁-Lys-Asn-Thr-Leu-Tyr-Leu-Gln-Met-Asn-Ser-Leu-Arg-Ala-Glu-Asp-Thr-Ala-Val-Tyr-B₁-Cys-Ala-C₁-D₁-Pro-Tyr-Ser-B₁-Asp-Tyr-F₁

G₁-H₁-Gly-Thr-Lcu-Val-Thr-Val-Ser-Ser (SEQ ID NO: 1283); and where X₁ is Met or Leu; Y₁ is Val or Phe; Z₁ is Asp or Asn; A₁ is Ser or Thr; B₁ is Tyr or His; C₁ is Lys or Arg; D₁ is Asp or Glu; E₁ is Tyr or Phe; F₁ is Trp or Arg; G₁ is Gly or Arg; and H₁ is Gln or His.

Further provided is an antibody polypeptide where the antibody polypeptide is a
 5 domain antibody (dAb).

Further provided is an antibody polypeptide where the variable domain is fused to an Fc domain.

Further provided is an antibody polypeptide where the antibody polypeptide further comprises a second variable domain that specifically binds a second antigen, where the second
 10 antigen is an antigen other than human CD40.

Also provided is an antibody polypeptide where the second antigen is a cluster of differentiation (CD) molecule or a Major Histocompatibility Complex (MHC) Class II molecule.

Also provided is an antibody polypeptide where the second antigen is serum albumin
 15 (SA).

Provided is a nucleic acid encoding the antibody polypeptide disclosed herein.

Also provided is a vector comprising the nucleic acid disclosed herein.

Also provided is a host cell comprising the vector disclosed herein.

20 Provided is a pharmaceutical composition comprising a therapeutically-effective amount of the antibody polypeptide disclosed herein and a pharmaceutically acceptable carrier. Also provided is a pharmaceutical composition further comprising an immunosuppressive/immunomodulatory and/or anti-inflammatory agent.

Provided is a method of treating an immune disease in a patient in need of such
 25 treatment, comprising administering to the patient a therapeutically effective amount of the pharmaceutical composition disclosed herein. Also provided is a method where the pharmaceutical composition is administered in combination with an immunosuppressive/immunomodulatory and/or anti-inflammatory agent.

Provided is a method of treating an immune disease where the immune disease is an
 30 autoimmune disease or a graft-related disease. Further provided is a method of treating an immune disease where the immune disease is selected from the group consisting of selected

from the group consisting of Addison's disease, allergies, ankylosing spondylitis, asthma, atherosclerosis, autoimmune diseases of the ear, autoimmune diseases of the eye, autoimmune hepatitis, autoimmune parotitis, colitis, coronary heart disease, Crohn's disease, diabetes, including Type 1 and/or Type 2 diabetes, epididymitis, glomerulonephritis, Graves' disease, 5 Guillain-Barre syndrome, Hashimoto's disease, hemolytic anemia, idiopathic thrombocytopenic purpura, inflammatory bowel disease, immune response to recombinant drug products, systemic lupus erythematosus, male infertility, multiple sclerosis, myasthenia gravis, pemphigus, psoriasis, rheumatic fever, rheumatoid arthritis, sarcoidosis, scleroderma, Sjogren's syndrome, spondyloarthropathies, thyroiditis, transplant rejection, vasculitis, AIDS, 10 atopic allergy, bronchial asthma, eczema, leprosy, schizophrenia, inherited depression, transplantation of tissues and organs, chronic fatigue syndrome, Alzheimer's disease, Parkinson's disease, myocardial infarction, stroke, autism, epilepsy, Arthus's phenomenon, anaphylaxis, alcohol addiction, and drug addiction.

Also provided is a method of targeting CD40 using a first variable domain that 15 specifically binds an epitope of human CD40 comprising the amino acid sequence of SEQ ID NO: 1, where the antibody polypeptide competes with the binding of domain antibody (dAb) BMS3h-56-269 (SEQ ID NO:417).

Provided is the use in medicine of an antibody polypeptide comprising a first variable domain that specifically binds an epitope of human CD40 comprising the amino acid sequence 20 of SEQ ID NO: 1, wherein the antibody polypeptide competes with the binding of domain antibody (dAb) BMS3h-56-201 (SEQ ID NO: 9), or a pharmaceutically acceptable salt thereof.

Provided is the use of an antibody polypeptide comprising a first variable domain that specifically binds an epitope of human CD40 comprising the amino acid sequence of SEQ ID NO: 1, wherein the antibody polypeptide competes with the binding of domain antibody (dAb) 25 BMS3h-56-201 (SEQ ID NO: 9), or a pharmaceutically acceptable salt thereof, in the preparation of a medicament for treatment of an immune disease. In some embodiments, the pharmaceutical composition is administered in combination with an immunosuppressive/immunomodulatory and/or anti-inflammatory agent. In further 30 embodiments, the immune disease is an autoimmune disease or a graft-related disease. In yet further embodiments, the immune disease is selected from the group consisting of selected from the group consisting of Addison's disease, allergies, ankylosing spondylitis, asthma,

- atherosclerosis, autoimmune diseases of the ear, autoimmune diseases of the eye, autoimmune hepatitis, autoimmune parotitis, colitis, coronary heart disease, Crohn's disease, diabetes, including Type 1 and/or Type 2 diabetes, epididymitis, glomerulonephritis, Graves' disease, Guillain-Barre syndrome, Hashimoto's disease, hemolytic anemia, idiopathic
- 5 thrombocytopenic purpura, inflammatory bowel disease, immune response to recombinant drug products, systemic lupus erythematosus, male infertility, multiple sclerosis, myasthenia gravis, pemphigus, psoriasis, rheumatic fever, rheumatoid arthritis, sarcoidosis, scleroderma, Sjogren's syndrome, spondyloarthropathies, thyroiditis, transplant rejection, vasculitis, AIDS, atopic allergy, bronchial asthma, eczema, leprosy, schizophrenia, inherited depression,
- 10 transplantation of tissues and organs, chronic fatigue syndrome, Alzheimer's disease, Parkinson's disease, myocardial infarction, stroke, autism, epilepsy, Arthus's phenomenon, anaphylaxis, alcohol addiction, and drug addiction.

- Provided is an antibody polypeptide comprising a first variable domain that specifically binds an epitope of human CD40 comprising the amino acid sequence of SEQ ID NO: 1,
- 15 wherein the antibody polypeptide competes with the binding of domain antibody (dAb) BMS3h-56-201 (SEQ ID NO: 9), or a pharmaceutically acceptable salt thereof, for use in the preparation of a medicament for treatment of an immune disease. The medicament can, for example, be administered in combination with an immunosuppressive/immunomodulatory and/or anti-inflammatory agent. The immune disease can be, for example, an autoimmune
- 20 disease or a graft-related disease. The immune disease can also be selected from the group consisting of selected from the group consisting of Addison's disease, allergies, ankylosing spondylitis, asthma, atherosclerosis, autoimmune diseases of the ear, autoimmune diseases of the eye, autoimmune hepatitis, autoimmune parotitis, colitis, coronary heart disease, Crohn's disease, diabetes, including Type 1 and/or Type 2 diabetes, epididymitis, glomerulonephritis,
- 25 Graves' disease, Guillain-Barre syndrome, Hashimoto's disease, hemolytic anemia, idiopathic thrombocytopenic purpura, inflammatory bowel disease, immune response to recombinant drug products, systemic lupus erythematosus, male infertility, multiple sclerosis, myasthenia gravis, pemphigus, psoriasis, rheumatic fever, rheumatoid arthritis, sarcoidosis, scleroderma, Sjogren's syndrome, spondyloarthropathies, thyroiditis, transplant rejection, vasculitis, AIDS,
- 30 atopic allergy, bronchial asthma, eczema, leprosy, schizophrenia, inherited depression, transplantation of tissues and organs, chronic fatigue syndrome, Alzheimer's disease,

Parkinson's disease, myocardial infarction, stroke, autism, epilepsy, Arthus's phenomenon, anaphylaxis, alcohol addiction, and drug addiction.

BRIEF DESCRIPTION OF THE FIGURES

The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

FIG. 1 depicts the binding modes of two different co-crystal structures of human CD40 (SEQ ID NO: 1), one with the dAb BMS3h-56-5 (SEQ ID NO: 321) and one with the Fab' of Chi220 antibody. The BMS3h-56-5 and Chi 220 Fab' molecules are shown as cartoons with β -strands (represented as arrows in the dAb) and non-repetitive secondary structure (represented as loops in the dAb). Complementarity-determining regions (CDRs) are also shown. CD40 is also shown as a cartoon with the BMS3h-56-5 epitope residues of human CD40. The Chi220 epitope residues are also shown. Disulfide bonds are also shown. The N-terminus (N) and C-terminus (C) of CD40 are labeled.

FIG. 2 depicts a space filling model of BMS3h-56-5 (SEQ ID NO: 321) contacting human CD40 (SEQ ID NO: 1), which is shown as a cartoon. Surface residues of the dAb BMS3h-56-5 that contact CD40 are shown. The BMS3h-56-5 CDR3 region and FR-2 residues Leu45, Arg47, Arg56 and Phe99 are labeled. Kabat numbering (Kabat et al., *Sequences of Immunological Interest*, 5th ed., U.S. Dept. Health & Human Services, Washington, D.C. (1991)) is used in this diagram and differs from sequential numbering in that insertion residues are used to keep the residue numbering of the β -strands identical. Thus for BMS3h-56-5, sequential residue 53 becomes residue 52A, sequential residues 84, 85, and 86 become, respectively, 82A, 82B, 82C and Kabat residue number 100 is missing (it would be between sequential residues 103 and 104); CD40 is also represented as a cartoon with non-repetitive secondary structure and the BMS3h-56-5 epitope. CD40 residues that differ between human and *Macaca fascicularis* (cynomolgus monkey), Ala115, Phe99, Ser126, His162, Leu121, and Trp109, are shown in stick representation. CD40 residues that differ between human and cynomolgus monkey that are part of the BMS3h-56-5 epitope are Trp109, Leu121, and His162.

CD40 residues Trp109 and Leu121 lie in a cleft between the BMS3h-56-5 CDR3 and FR-2. Mutation of Trp109 either greatly reduces or ablates BMS3h-56-5 activity.

FIG. 3 depicts binding of a PEGylated anti-human CD40 dAb, BMS3h38-2C-P40Br, on blood samples from human and primate species. FIG. 3A shows BMS3h38-2C-P40Br binding to human and cynomolgus B cells; FIG. 3B shows BMS3h38-2C-P40Br binding to human, rhesus, and chimp B cells.

FIG. 4, FIG. 5, FIG. 6, and FIG. 7 show ClustalW2 alignments of representative domain antibody polypeptides from lineages BMS3h-56, BMS3h-37, BMS3h-38, and BMS3h-198, respectively.

10 DETAILED DESCRIPTION

Antibody polypeptides that specifically bind to human CD40 are provided. The antibody polypeptides do not exhibit CD40 agonist activity, and the antibody polypeptides are useful in the treatment of diseases involving CD40 activation, such as autoimmune diseases. The antibody polypeptides may be selected using a primary screen that utilizes cell binding assays, followed by one or more rounds of error-prone or degenerate oligonucleotide-directed affinity maturation. As a result, a genus of antibody polypeptides that specifically bind a single CD40 epitope are provided.

A "lineage" is a set of related antibody polypeptides that were prepared from a common precursor by error-prone or degenerate oligonucleotide-directed affinity maturation, as disclosed in the examples below, and that are expected to bind the same CD40 epitope. The nomenclature of the antibody polypeptides is used to designate the various lineages. The nomenclature "BMS3h-56," for example, refers to antibody polypeptides of lineage 56, which were raised against human CD40. "Lineage BMS3h-56" antibody polypeptides include BMS3h-56-1 through BMS3h-56-33, and BMS3h-56-202 through BMS3h-56-288.

Accordingly, in one aspect, an antibody polypeptide comprises a variable domain that specifically binds human CD40, where the antibody polypeptide competes with the binding of any one of the domain antibodies (dAbs) listed in TABLE 3. For example, the dAb may belong to a lineage selected from the group consisting of BMS3h-37, BMS3h-38, BMS3h-41, BMS3h-43, BMS3h-56, BMS3h-131, BMS3h-198, and BMS3h-202, such as the dAb BMS3h-56-5, BMS3h-56-201, or BMS3h-56-258, for instance. In another aspect, an antibody

polypeptide specifically binds the same human CD40 epitope as any one of the dAbs listed in TABLE 3. For example, the antibody polypeptide may comprise a variable domain that specifically binds the same human CD40 epitope as the dAb BMS3h-56-5, BMS3h-56-201, or BMS3h-56-258, for instance. As disclosed below, the human CD40 epitope may comprise amino acid residue Trp109 of SEQ ID NO: 1, for example.

The antibody polypeptides may be domain antibodies containing a single variable domain. The antibody polypeptides also may comprise additional domains, such as an Fc domain. For instance, the antibody polypeptide may comprise a second variable domain that specifically binds human serum albumin (HSA). Such dual specific antibody polypeptides may have an increased half-life, for example.

In the Sequence Listing, SEQ ID NO: 1 is the amino acid sequence of human CD40; SEQ ID NO: 2 is the amino acid sequence of *Macaca fascicularis* CD40. The amino acid sequence of the domain antibody BMS3h-56-5 is SEQ ID NO: 321.

As used herein, “specific binding” refers to the binding of an antigen by an antibody polypeptide with a dissociation constant (K_d) of about 1 μ M or lower as measured, for example, by surface plasmon resonance. Suitable assay systems include the BIAcore™ surface plasmon resonance system and BIAcore™ kinetic evaluation software (e.g., version 2.1). The affinity or K_d for a specific binding interaction may be about 500 nM or lower or about 300 nM or lower.

The term “about” will be understood by persons of ordinary skill in the art and will vary to some extent on the context in which it is used. Generally, about encompasses a range of values that are plus/minus 10% of a referenced value.

In accordance with this detailed description, the following abbreviations and definitions apply. It must be noted that as used herein, the singular forms “a”, “an”, and “the” include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to “an antibody” includes a plurality of such antibodies and reference to “the dosage” includes reference to one or more dosages and equivalents thereof known to those skilled in the art, and so forth.

1. CD40 and CD40 Activities

Antibody polypeptides are provided that bind human CD40. CD40 is also known as B-cell surface antigen CD40, Bp50, CD40L receptor, CDw40, CDW40, MGC9013, p50, TNFRSF5, and Tumor necrosis factor receptor superfamily member 5. Relevant structural information for human CD40 can be found, for example, at UniProt Accession Numbers P25942, Q9BYU0, and Q53GN5. "Human CD40" refers to the CD40 comprising the following amino acid sequence:

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MVRLLPLQCVL WGCLLTAVHP EPPTACREKQ YLINSQCCSL CQPGQKLVSD
CTEFTETECL PCGESEFLDT WNRETHCHQH KYCDPNLGLR VQQKGTSETD
10 TICTCEEGWH CTSEACESCV LHRSCSPGFG VKQIATGVSD TICEPCPVGF
FSNVSSAFEK CHPWTSCETK DLVVQQAGTN KTDVVCQPQD RLRALVVIPI
TFGILFAILL VLVFIKKVAK KPTNKAPHPK QEPQEINFPD DLPGSNTAAP
VQETLHGCQP VTQEDGKESR ISVQERQ (SEQ ID NO: 1).

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CD40 also has been sequenced in *Mus musculus*, *Sus scrofa*, *Bos taurus*, *Gallus gallus*, *Canis familiaris*, *Macaca fascicularis* (cynomolgus monkey), *Ovis aries*, *Equus caballus*, and *Rattus norvegicus*.

Binding of the present antibody polypeptides to CD40 antagonizes CD40 activity. "CD40 activities" include, but are not limited to, T cell activation (e.g., induction of T cell proliferation or cytokine secretion), macrophage activation (e.g., the induction of reactive oxygen species and nitric oxide in the macrophage), and B cell activation (e.g., B cell proliferation, antibody isotype switching, or differentiation to plasma cells). CD40 activities can be mediated by interaction with other molecules. "CD40 activities" include the functional interaction between CD40 and the following molecules, which are identified by their Uniprot Accession Number in parentheses:

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25
CALR      (P27797);
ERP44     (Q9BS26);
FBL       (P22087);
POLR2H    (P52434);
30 RFC5     (P40937);
SGK1      (O00141);

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5 SLC30A7 (Q8NEW0);
 SLC39A7 (Q92504);
 TRAF2 (Q5T1L5);
 TRAF3 (Q13114);
 TRAF6 (Q9Y4K3);
 TXN (Q5T937);
 UGGT1 (Q9NYU2); and
 USP15 (Q9Y4E8).

10 For example, a CD40 "activity" includes an interaction with TRAF2. CD40/TRAF2
 interaction activates NF- κ B and JNK. *See* Davies et al., *Mol. Cell Biol.* 25: 9806-19 (2005).
 This CD40 activity thus can be determined by CD40-dependent cellular NF- κ B and JNK
 activation, relative to a reference.

15 As used herein, the terms "activate," "activates," and "activated" refer to an increase in
 a given measurable CD40 activity by at least 10% relative to a reference, for example, at least
 10%, 25%, 50%, 75%, or even 100%, or more. A CD40 activity is "antagonized" if the
 activity is reduced by at least 10%, and in an exemplary embodiment, at least about 20%, 30%,
 40%, 50%, 60%, 70%, 80%, 90%, 95%, 97%, or even 100% (i.e., no detectable activity),
 relative to the absence of the antagonist. For example, an antibody polypeptide may
 antagonize some or all CD40 activity, while not activating CD40. In one embodiment, the
 antibody polypeptide does not activate B cell proliferation. In another embodiment, the
 antibody polypeptide does not activate cytokine secretion by T cells, where the cytokine is at
 least one cytokine selected from the group consisting of IL-2, IL-6, IL-10, IL-13, TNF- α ,
 IFN- γ .

25 2. The CD40 Epitope

30 X-ray crystallography of a complex between human CD40 (SEQ ID NO: 1) and the
 dAb BMS3h-56-5 (SEQ ID NO: 321) was used to reveal an epitope recognized by the antibody
 polypeptides of the disclosure. Structural models of CD40 and BMS3h-56-5 were fitted to
 electron density data to yield seven models or versions of the CD40/BMS3h-56-5 complex,
 which come from three crystallographically independent complexes in one crystal form and
 four crystallographically independent complexes in a second crystal form. The versions have
 real space correlation coefficients of about 0.92 for main-chain atoms and 0.80 for side-chain
 atoms. The CD40 molecule has a certain amount of flexibility in the seven versions, but the

overall nature of the CD40/BMS3h-56-5 interaction is retained in all versions. The versions differ in the interaction between the CD40 residue Trp109 and BMS3h-56-5 Trp103 (Kabat Numbering, *see below*). BMS3h-56-5 Trp103 forms an edge-to-face interaction with CD40 Trp109 in one version, while forming a displaced stacking (*i.e.*, face-to-face) interaction in
 5 other versions.

The shape complementarity statistic, *Sc*, for the seven versions ranges from 0.70 – 0.77, which shows a higher degree of shape complementarity than for typical antibody/antigen complexes. For example, these values compare to ranges of 0.71 – 0.76 for four protease/protein inhibitor complexes, 0.70 – 0.74 for five oligomeric interfaces, and 0.64 –
 10 0.68 for six antibody/antigen complexes. *See Lawrence et al.*, “Shape Complementarity at Protein/Protein Interfaces,” *J. Mol. Biol.* 234: 946-950 (1993).

A model of the human CD40/BMS3H-56-5 complex is shown in FIG. 1. One BMS3h-56-5 dAb binds to one CD40 molecule. The BMS3h-56-5 epitope does not overlap the Chi220 Fab' fragment epitope. All versions of the complex define a set of CD40 residues
 15 that contact BMS3h-56-5: Trp109, Leu121, His122, Ser124, Ser156, Ala157, Phe158, Glu159, and His162 (with reference to SEQ ID NO: 1). CD40 residues that contact BMS3h-56-5 in some versions of the complex are Pro85, Asn86, Leu87, Gly88, Glu106, Glu107, Gly108, His110, Thr112, Cys119, Val120, Gln133, Ile134, Ala135, Thr136, Ser155, and Lys160. Val154 is a buried CD40 residue in all versions. Other CD40 residues buried in some versions
 20 are Ser118, Arg123, Thr141, Phe151, Asp153, Cys161, and Pro163.

As used herein, the term “in contact” refers to an interatomic distance whose maximum is determined by an atom type distance dependency as defined by Sheriff *et al.*, *J. Mol. Biol.* 197: 273-296 (1987) and Sheriff, *Immunomethods* 3: 191-196 (1993).

As used herein, the term “buried” refers to a residue that has a least one atom with
 25 surface area defined by the program MS (Connolly, *J. Appl. Crystallogr.* 16: 548-558 (1983)), a probe sphere of 1.7 Å, and atom type dependent Van der Waals radii as defined by Sheriff, *Immunomethods* 3: 191-196 (1993).

FIG. 2 shows the surface of BMS3h-56-5 (SEQ ID NO: 321) including contacting residues and buried residues. CD40 (SEQ ID NO: 1) is represented as a ribbon diagram with
 30 orange representing non-repetitive secondary structure and magenta representing the epitope

residues. CD40 residues Trp109, Ala115, Leu121, Ser126, and His162, which are shown, differ in various non-human primate sequences. CD40 residues Ala115 and Ser126 are on the opposite side of the BMS3h-56-5 binding site. Trp109 and Leu121 bind in a cleft that lies between CDR3 and FR-2 (residues Leu45 and Arg47) of BMS3h-56-5. His162 interacts with residues in CDR2 of BMS3h-56-5, especially Lys 56. In summary, the CD40 epitope comprises one or more residues listed in TABLE 1, with reference to the numbering used in SEQ ID NO: 1.

TABLE 1

CD40 residues contacting BMS3h-56-5:
Trp109, Leu121, His122, Ser124, Ser156, Ala157, Phe158, Glu159, His162

BMS3h-56-5, like the other dAbs listed in TABLE 3, was prepared by a screening and affinity maturation method described in more detail below, using human CD40 as the antigen. It is expected that dAbs created by affinity maturation from a common precursor dAb will bind the same human CD40 epitope. Competition studies described below, for example, indicate that dAbs generated from a common precursor dAb by affinity maturation compete for binding with each other to human CD40. The same competition studies, however, show that the dAbs do not compete with at least the Chi220 or G28-5 antibodies.

3. Antibody Polypeptides

The antibody polypeptides comprise a variable domain. In one embodiment, the antibody polypeptides are in the form of a dAb that contains a single variable domain. Antibody polypeptides may be full-length anti-CD40 immunoglobulin molecules comprising two heavy (H) chains and two light (L) chains interconnected by disulfide bonds. In this embodiment, the amino terminal portion of each chain includes a variable domain (V_L or V_H) of about 100-110 amino acids primarily responsible for antigen recognition via the complementarity determining regions (CDRs) contained therein. The carboxy-terminal "half" of each heavy chain defines a constant region (Fc) primarily responsible for effector function.

Antibody polypeptides also may be “fragments” comprising a portion of the full-length anti-CD40 immunoglobulin molecule that comprises a variable domain that specifically binds CD40. Thus, the term “antibody polypeptides” includes an antigen-binding heavy chain, light chain, heavy chain-light chain dimer, Fab fragment, F(ab')₂ fragment, Fv fragment, single chain Fv (scFv), and dAb, for example. The term “antibody polypeptides” thus includes polypeptides made by recombinant engineering and expression, as well as monoclonal antibodies produced by natural recombination and secretion by hybridoma cell clones.

Light chains are classified as kappa (κ) or lambda (λ), and are characterized by a particular constant region, C_L, as known in the art. Heavy chains are classified as γ, μ, α, δ, or ε, and define the isotype of an antibody as IgG, IgM, IgA, IgD, or IgE, respectively. The heavy chain constant region is comprised of three domains (CH1, CH2, and CH3) for IgG, IgD, and IgA; and four domains (CH1, CH2, CH3, and CH4) for IgM and IgE. Anti-CD40 antibodies may have a heavy chain constant region selected from any of the immunoglobulin classes (IgA, IgD, IgG, IgM, and IgE).

Each light chain variable domain (V_L) and heavy chain variable domain (V_H) is composed of three CDRs and four framework regions (FRs), arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. The three CDRs of the light chain are referred to as “LCDR1, LCDR2, and LCDR3” and the three CDRs of the heavy chain are referred to as “HCDR1, HCDR2, and HCDR3.”

As used herein, the term “Fc domain” refers to the constant region antibody sequences comprising CH2 and CH3 constant domains as delimited according to Kabat et al., *Sequences of Immunological Interest*, 5th ed., U.S. Dept. Health & Human Services, Washington, D.C. (1991). The Fc region may be derived from an IgG1 or an IgG4 Fc region, for example. A variable domain may be fused to an Fc domain. In this case, the carboxyl terminus of the variable domain (either a V_L or V_H domain, including dAbs) may be linked or fused to the amino terminus of the Fc CH2 domain. Alternatively, the carboxyl terminus of the variable domain may be linked or fused to the amino terminus of a CH1 domain, which itself is fused to the Fc CH2 domain. The protein may comprise the hinge region between the CH1 and CH2 domains in whole or in part.

The CDRs contain most of the residues that form specific interactions with the antigen. As shown in FIG. 2, for example, CDR2 and CDR3, plus FR4 residue Trp103, form most of the contacts between CD40 and the dAb BMS3h-56-5. For example, the variable domain of an antibody polypeptide comprises CDR1, CDR2, and CDR3 regions that have the same amino acid sequence as the CDR1, CDR2, and CDR3 regions of one of the dAbs listed in TABLE 3 or that each differ from the CDR1, CDR2, and CDR3 regions by one or two amino acids. For example, the antibody polypeptide may comprise CDR1, CDR2, and CDR3 regions that have the same amino acid sequence as the CDR1, CDR2, and CDR3 regions of BMS3h-56-5, BMS3h-56-258, or BMS3h-56-201, for example.

A “domain antibody” (dAb) comprises a single variable (V_L or V_H) domain that is capable of specifically and monovalently binding an antigen, such as CD40. For example, a dAb may have a V_{HH} structure, characteristic of a camelid dAb. A “ V_H domain” as used herein is meant to include a V_{HH} structure. In another embodiment, the V_H domains of the present invention (including all features and combination of features presented as embodiments herein) are other than V_{HH} domains. dAbs may form homo- or heterodimers in solution. Bivalent anti-CD40 antibodies are believed to exhibit agonist activity because of the ability to cross-link bound CD40 molecules on the cell surface. While not limited by any particular theory, it is believed that monovalent dAbs do not activate CD40, because the dAbs do not cross-link CD40.

As used herein, the term “variable domain” refers to immunoglobulin variable domains defined by Kabat et al., *Sequences of Immunological Interest*, 5th ed., U.S. Dept. Health & Human Services, Washington, D.C. (1991). The numbering and positioning of CDR amino acid residues within the variable domains is in accordance with the well-known Kabat numbering convention. For example, the Kabat numbering for BMS3h-56-5 (SEQ ID NO: 321) is compared in TABLE 2 to the same sequence numbered sequentially. In the Kabat numbering, BMS3h-56-5 has insertion residues 52A, 82A, 82B, 82C, and is missing residue 100. In both numbering systems, the Ser and Thr at the N-terminus that are part of the expression construct are given negative numbers.

TABLE 2

		-2-1							
BMS3h-56-5		ST							
				CDR1					
Kabat		10		20		30		40	50
Sequential		10		20		30		40	50
BMS3h-56-5		EVQLLESGGGLVQP		GGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSA					
		CDR2							
Kabat	A	60		70		80		90	
Sequential		60		70		80		90	100
BMS3h-56-5		INPQGTRITYADSV		MGRFTISRDN		SKNTLYLQMNSLRAEDTAVYYCAKLP			
		CDR3							
Kabat		101		110		116			
Sequential		110		119					
BMS3h-56-5		FTFDDWGQGLTV		TVSSAAA					
						(SEQ ID NO: 3)			

- The term "human," when applied to antibody polypeptides, means that the antibody polypeptide has a sequence, e.g., FR and/or CH domains, derived from a human immunoglobulin. A sequence is "derived from" a human immunoglobulin coding sequence
- 5 when the sequence is either: (a) isolated from a human individual or from a cell or cell line from a human individual; (b) isolated from a library of cloned human antibody gene sequences or of human antibody variable domain sequences; or (c) diversified by mutation and selection from one or more of the polypeptides above. An "isolated" compound as used herein means that the compound is removed from at least one component with which the compound is
- 10 naturally associated with in nature.

Antibody polypeptides can be administered to human patients while largely avoiding the anti-antibody immune response often provoked by the administration of antibodies from other species, e.g., mouse. For example, murine antibodies can be "humanized" by grafting murine CDRs onto a human variable domain FR, according to procedures well known in the

art. Human antibodies as disclosed herein, however, can be produced without the need for genetic manipulation of a murine antibody sequence.

Variable domains may comprise one or more framework regions (FR) with the same amino acid sequence as a corresponding framework region encoded by a human germline antibody gene segment. For example, a domain antibody may comprise the V_H germline gene segments DP47, DP45, or DP38, the V_K germline gene segment DPK9, the J_H segment JH4b, or the J_K segment JK1.

Changes may be made to antibody polypeptide sequences while retaining the ability to bind CD40 specifically. Specifically, the antibody polypeptides (e.g., a dAb) may comprise a variant variable domain that retains the function of specifically binding the same CD40 epitope as the dAb BMS3h-56-5. See TABLE 1. That is, the variant variable domain may bind a human CD40 epitope comprising at least one of Trp109, Leu121, His122, Ser124, Ser156, Ala157, Phe158, Glu159, and His162 of SEQ ID NO: 1. In one embodiment, the variant variable domain epitope may comprise Trp109, Leu121, His122, Ser124, Ser156, Ala157, Phe158, Glu159, and His162. Alternatively, the variant variable domain may specifically bind a CD40 epitope comprising CD40 residue Trp109. In yet another embodiment, the variant variable domain may compete with BMS3h-56-5 for specific binding to CD40. Error-prone affinity maturation, as disclosed in the examples below, provides one exemplary method for making and identifying antibody polypeptides with variant sequences that specifically bind the same CD40 epitope.

For example, a variant variable domain may differ from one of the variable domains listed in TABLE 3 by up to 10 amino acids or any integral value between, where the variant variable domain specifically binds CD40. Alternatively, the variant variable domain may have at least 90% sequence identity (e.g., at least 92%, 95%, or 98% sequence identity) relative to a sequence listed in the present Sequence Listing. Non-identical amino acid residues or amino acids that differ between two sequences may represent amino acid substitutions, additions, or deletions. Residues that differ between two sequences appear as non-identical positions, when the two sequences are aligned by any appropriate amino acid sequence alignment algorithm, such as BLAST.

It is provided that amino acid substitutions may be made to individual FR regions, such that one or more FR comprises up to two amino acid differences relative to the amino acid sequence of the corresponding FR encoded by a human germline antibody gene segment. It is further provided that the variant variable domain may contain one or two amino acid substitutions in one or more CDR. Representative variable domains that specifically bind CD40 are listed in TABLE 3.

ClustalW2 alignments between representative variable domains of antibody polypeptides from lineages BMS3h-56, BMS3h-37, BMS3h-38, and BMS3h-198 are shown in FIG. 4, FIG. 5, FIG. 6, and FIG. 7, respectively. As a general rule, the degree to which an amino acid is conserved in an alignment of related protein sequences is proportional to the relative importance of the amino acid position to the function of the protein. That is, amino acids that are common in all related sequences likely play an important role and cannot be easily substituted. On the other hand, positions that vary between the sequences likely can be substituted with other amino acids or otherwise modified, while maintaining the activity of the protein. The alignments shown in FIG. 4, FIG. 5, FIG. 6, and FIG. 7 and the structural relationships ascertained from FIG. 1 and FIG. 2, for example, can guide the construction of variant antibody polypeptides that specifically bind an epitope of human CD40 comprising the amino acid sequence of SEQ ID NO: 1, wherein the antibody polypeptide competes with the binding of dAb BMS3h-56-201 (SEQ ID NO: 9). Such variant antibody polypeptides include, but are not limited to, those with an amino acid modification corresponding to a substitution, insertion, or deletion with reference to any of the variable domains listed in TABLE 3. Variant antibody polypeptides also include those with an amino acid modification corresponding to an amino acid modification conserved between the sequences listed in TABLE 3.

The information regarding the boundaries of the V_L or V_H domains of heavy and light chain genes may be used to design PCR primers to amplify the variable domain from a cloned heavy or light chain coding sequence encoding an antibody polypeptide known to bind CD40. The amplified variable domain may be inserted into a suitable expression vector, e.g., pHEN-1 (Hoogenboom et al. (1991) *Nucleic Acids Res.* 19:4133-4137) and expressed, either alone or as a fusion with another polypeptide sequence, using techniques well known in the art. Based on the disclosed amino acid and polynucleotide sequences, the fusion protein can be produced and purified using only ordinary skill in any suitable mammalian host cell line, such as CHO, 293,

COS, NSO, and the like, followed by purification using one or a combination of methods, including protein A affinity chromatography, ion exchange, reverse phase techniques, or the like.

In one aspect, the antibody polypeptide is a "dual specific" antibody polypeptide comprising a first variable domain that specifically binds human CD40 comprising the amino acid sequence of SEQ ID NO: 1. Dual specific antibody polypeptides comprise a second variable domain that specifically binds a second antigen that is other than human CD40.

In another embodiment, the second antigen may be a cell surface molecule of an immune effector cell or a soluble molecule such as a cytokine, for example. Binding of the dual specificity antibody polypeptide could be used to antagonize CD40 and antagonize a biological activity of the second antigen. Cell surface molecules of immune effector cells include the cluster of differentiation (CD) molecules. Representative CD markers are listed on the Internet at [hypertext transfer protocol en.wikipedia.org/wiki/List_of_human_clusters_of_differentiation](http://hypertexttransferprotocol.en.wikipedia.org/wiki/List_of_human_clusters_of_differentiation) (last modified on February 22, 2012). Cell surface molecules of immune effector cells also include Major Histocompatibility Complex (MHC) Class II molecules. Antibodies against these cell surface molecules are known in the art and can be used as a source of a variable domain to construct a dual specific antibody polypeptide.

In one embodiment, antibody polypeptides of a dual specific ligand may be linked by an "amino acid linker" or "linker." For example, a dAb may be fused to the N-terminus of an amino acid linker, and another dAb may be fused to the C-terminus of the linker. Although amino acid linkers can be any length and consist of any combination of amino acids, the linker length may be relatively short (e.g., five or fewer amino acids) to reduce interactions between the linked domains. The amino acid composition of the linker also may be adjusted to reduce the number of amino acids with bulky side chains or amino acids likely to introduce secondary structure. Suitable amino acid linkers include, but are not limited to, those up to 3, 4, 5, 6, 7, 10, 15, 20, or 25 amino acids in length. Representative amino acid linker sequences include (GGGGS)_n (SEQ ID NO: 4), where n may be any integer between 1 and 5. Other suitable linker sequences may be selected from the group consisting of AST (SEQ ID NO: 5), TVAAAPS (SEQ ID NO: 6), TVA (SEQ ID NO: 7), and ASTSGPS (SEQ ID NO: 8).

The binding of the second antigen can increase the *in vivo* half-life of the antibody polypeptide. For example, the second variable domain of the dual specific antibody polypeptide may specifically bind serum albumin (SA), e.g., human serum albumin (HSA). The antibody polypeptide formatted to bind HSA can have an increased *in vivo* t- α ("alpha half-life") or t- β ("beta half-life") half-life relative to the same unformatted antibody polypeptide. The t- α and t- β half-lives measure how quickly a substance is distributed in and eliminated from the body. The linkage to HSA may be accomplished by fusion of the antibody polypeptide with a second variable domain capable of specifically binding HSA, for example. Anti-human serum albumin antibodies are well-known in the art. *See, e.g.*, Abcam®, Human Serum Albumin antibodies ab10241, ab2406, and ab8940, available on the Internet at
5 half-life") or t- β ("beta half-life") half-life relative to the same unformatted antibody polypeptide. The t- α and t- β half-lives measure how quickly a substance is distributed in and eliminated from the body. The linkage to HSA may be accomplished by fusion of the antibody polypeptide with a second variable domain capable of specifically binding HSA, for example. Anti-human serum albumin antibodies are well-known in the art. *See, e.g.*, Abcam®, Human
10 Serum Albumin antibodies ab10241, ab2406, and ab8940, available on the Internet at
hypertext transfer protocol www.abcam.com/index.html, or GenWay, ALB antibody, available
on the Internet at hypertext transfer protocol www.genwaybio.com. Variable domains that
specifically bind HSA can be obtained from any of these antibodies, and then fused to an
antibody polypeptide of the disclosure using recombinant techniques that are well known in the
15 art.

Alternatively, the linking of the antibody polypeptide to HSA can be accomplished by directly fusing the antibody polypeptide sequence to an HSA coding sequence using techniques well known to the skilled artisan. The HSA coding sequences can be obtained by PCR using primers derived from the cDNA sequence available at GenBank Accession No. NM000477, for
20 example.

In one embodiment, the t α -half-life of the HSA-linked domain antibody composition is increased by 10% or more. In another embodiment, the t α -half-life of the HSA-linked domain antibody composition is in the range of 0.25 hours to 6 hours. In another embodiment, the t β -half-life of the HSA-linked domain antibody composition is increased by 10% or more. In
25 another embodiment, the t β -half-life of the HSA-linked domain antibody composition is in the range of 12 to 48 hours.

In another embodiment, an antibody polypeptide may be formatted to increase its *in vivo* half-life by PEGylation. In one embodiment, the PEG is covalently linked. In another embodiment, the PEG is linked to the antibody polypeptide at a cysteine or lysine residue. In
30 yet another embodiment, the PEG-linked antibody polypeptide has a hydrodynamic size of at

least 24 kD. In yet another embodiment, the total PEG size is from 20 to 60 kD, inclusive. In yet another embodiment, the PEG-linked domain antibody has a hydrodynamic size of at least 200 kD.

PEGylation can be achieved using several PEG attachment moieties including, but not limited to N-hydroxysuccinimide active ester, succinimidyl propionate, maleimide, vinyl sulfone, or thiol. A PEG polymer can be linked to an antibody polypeptide at either a predetermined position, or can be randomly linked to the domain antibody molecule. PEGylation can also be mediated through a peptide linker attached to a domain antibody. That is, the PEG moiety can be attached to a peptide linker fused to an antibody polypeptide, where the linker provides the site (e.g., a free cysteine or lysine) for PEG attachment. Methods of PEGylating antibodies are well known in the art, as disclosed in Chapman, et al., "PEGylated antibodies and antibody fragments for improved therapy: a review," *Adv. Drug Deliv. Rev.* 54(4):531-45 (2002), for example.

Antibody polypeptides also may be designed to form a dimer, trimer, tetramer, or other multimer. Antibody polypeptides, e.g., dAbs, can be linked to form a multimer by several methods known in the art, including, but not limited to, expression of monomers as a fusion protein, linkage of two or more monomers via a peptide linker between monomers, or by chemically joining monomers after translation, either to each other directly, or through a linker by disulfide bonds, or by linkage to a di-, tri- or multivalent linking moiety (e.g., a multi-arm PEG). In one embodiment, the multimer can bind a single molecule of CD40.

4. Pharmaceutical Compositions and Methods of Treatment

A pharmaceutical composition comprises a therapeutically-effective amount of one or more antibody polypeptides and optionally a pharmaceutically acceptable carrier. Pharmaceutically acceptable carriers include, for example, water, saline, phosphate buffered saline, dextrose, glycerol, ethanol and the like, as well as combinations thereof. Pharmaceutically acceptable carriers can further comprise minor amounts of auxiliary substances, such as wetting or emulsifying agents, preservatives, or buffers that enhance the shelf-life or effectiveness of the fusion protein. The compositions can be formulated to provide quick, sustained, or delayed release of the active ingredient(s) after administration.

Suitable pharmaceutical compositions and processes for preparing them are well known in the art. *See, e.g.*, Remington, THE SCIENCE AND PRACTICE OF PHARMACY, A. Gennaro, et al., eds., 21st ed., Mack Publishing Co. (2005).

The pharmaceutical composition further may comprise an immuno-
5 suppressive/immunomodulatory and/or anti-inflammatory agent. A method of treating an immune disease in a patient in need of such treatment may comprise administering to the patient a therapeutically effective amount of the pharmaceutical composition. Antagonizing CD40-mediated T cell activation could inhibit undesired T cell responses occurring during autoimmunity, transplant rejection, or allergic responses, for example. Inhibiting CD40-
10 mediated T cell activation could moderate the progression and/or severity of these diseases.

As used herein, a "patient" means an animal, e.g. mammal, including humans. The patient may be diagnosed with an immune disease. "Treatment" or "treat" or "treating" refers to the process involving alleviating the progression or severity of a symptom, disorder, condition, or disease. An "immune disease" refers to any disease associated with the
15 development of an immune reaction in an individual, including a cellular and/or a humoral immune reaction. Examples of immune diseases include, but are not limited to, inflammation, allergy, autoimmune disease, or graft-related disease. The autoimmune disease may be selected from the group consisting of systemic lupus erythematosus, multiple sclerosis, rheumatoid arthritis, diabetes, psoriasis, scleroderma, atherosclerosis, inflammatory bowel
20 disease, and ulcerative colitis.

Diseases that can be treated by administering the pharmaceutical composition may be selected from the group consisting of Addison's disease, allergies, ankylosing spondylitis, asthma, atherosclerosis, autoimmune diseases of the ear, autoimmune diseases of the eye, autoimmune hepatitis, autoimmune parotitis, colitis, coronary heart disease, Crohn's disease,
25 diabetes, including Type 1 and/or Type 2 diabetes, epididymitis, glomerulonephritis, Graves' disease, Guillain-Barre syndrome, Hashimoto's disease, hemolytic anemia, idiopathic thrombocytopenic purpura, inflammatory bowel disease, immune response to recombinant drug products (e.g., Factor VII in hemophiliacs), systemic lupus erythematosus, male infertility, multiple sclerosis, myasthenia gravis, pemphigus, psoriasis, rheumatic fever,
30 rheumatoid arthritis, sarcoidosis, scleroderma, Sjogren's syndrome, spondyloarthropathies,

thyroiditis, transplant rejection, and vasculitis. Autoimmune-mediated conditions include, but are not limited to, conditions in which the tissue affected is the primary target, and in some cases, the secondary target. Such conditions include, but are not limited to, AIDS, atopic allergy, bronchial asthma, eczema, leprosy, schizophrenia, inherited depression, transplantation
5 of tissues and organs, chronic fatigue syndrome, Alzheimer's disease, Parkinson's disease, myocardial infarction, stroke, autism, epilepsy, Arthus' phenomenon, anaphylaxis, alcohol addiction, and drug addiction.

The pharmaceutical composition may be administered alone or in combination therapy, (i.e., simultaneously or sequentially) with an immunosuppressive/immunomodulatory and/or
10 anti-inflammatory agent. Different immune diseases can require use of specific auxiliary compounds useful for treating immune diseases, which can be determined on a patient-to-patient basis. For example, the pharmaceutical composition may be administered in combination with one or more suitable adjuvants, e.g., cytokines (IL-10 and IL-13, for example) or other immune stimulators, e.g., chemokines, tumor-associated antigens, and
15 peptides. Suitable adjuvants are known in the art.

Any suitable method or route can be used to administer the antibody polypeptide or the pharmaceutical composition. Routes of administration include, for example, oral, intravenous, intraperitoneal, subcutaneous, or intramuscular administration. A therapeutically effective dose of administered antibody polypeptide(s) depends on numerous factors, including, for
20 example, the type and severity of the immune disease being treated, the use of combination therapy, the route of administration of the antibody polypeptide(s) or pharmaceutical composition, and the weight of the patient. A non-limiting range for a therapeutically effective amount of a domain antibody is 0.1-20 mg/kg, and in an aspect, 1-10 mg/kg, relative to the body weight of the patient. The dose of antibody polypeptide(s) can be further guided by the
25 amount of antibody polypeptide(s) required for CD40 antagonism in *in vitro* and/or *in vivo* models of disease states. Representative models are described below and in the examples.

5. *In Vitro* and *In Vivo* Models

The ability of antibody polypeptides of the disclosure to antagonize CD40 can be tested in one of several available *in vitro* or *in vivo* model systems. Appropriate animal and cell model systems are described below. Further cell assay systems are described in the examples.

5.1. Inflammatory Bowel Disease (IBD) Models:

IBD is a multifactorial immune disorder of uncertain etiology. Several mouse models of mucosal inflammation that resemble IBD have provided insight into the mechanisms governing both normal and pathological mucosal immune function. IBD models include using the mucosal immunity and inflammation system of De Winter et al., *Am. J. Physiol.* 276: G1317-1321 (1999). In one aspect, the injection into immunodeficient mice of a subset of CD4(+) T lymphocytes, the CD4(+)CD45RB^{high} cells, leads to inflammation of the intestine. Pathogenesis is due in part to the secretion of proinflammatory cytokines. The induction of colitis can be prevented by co-transfer of another CD4(+) subpopulation, the CD4(+)CD45RB^{low} T cells. This population behaves analogously to the CD4(+)CD45RB^{high} population in terms of the acquisition of activation markers and homing to the host intestine. However, their lymphokine profile when activated is different, and anti-inflammatory cytokines secreted and/or induced by CD4(+)CD45RB^{low} T cells prevent colitis. De Winter et al. provide a description of the adoptive transfer model and the factors that promote and prevent colitis pathogenesis.

5.2. Spontaneous Arthritis Models:

A model of organ-specific disease provoked by systemic autoimmunity is provided by Kouskoff et al., *Cell* 87: 811-822 (1996). Rheumatoid arthritis (RA) is a chronic joint disease characterized by leukocyte invasion and synovioocyte activation followed by cartilage and bone destruction. Kouskoff et al. disclose a spontaneous mouse model of RA, generated by crossing a T cell receptor (TCR) transgenic line with the NOD strain. All offspring develop a joint disease highly reminiscent of RA in man. The trigger for the murine disorder is chance recognition of a NOD-derived major histocompatibility complex (MHC) class II molecule by the transgenic TCR; progression to arthritis involves CD4⁺ T, B, and probably myeloid cells.

5.3. Collagen Induced Arthritis (CIA) Model:

A mouse model of collagen-induced arthritis is provided by Brand et al., *Methods Mol. Med.* 102: 295-312 (2004). Collagen-induced arthritis (CIA) is an autoimmune disease that can be elicited in susceptible strains of rodents (rat and mouse) and non-human primates by immunization with type II collagen (CII), the major constituent protein of articular cartilage. After immunization, the animals develop an autoimmune polyarthritis that shares several clinical and histological features with RA. Susceptibility to CIA in rodents is linked to the class II molecules of the major histocompatibility complex (MHC), and the immune response to CII is characterized by both the stimulation of collagen-specific T cells and the production of high titers of antibody specific for both the immunogen (heterologous CII) and the autoantigen (mouse CII). Histologically, murine CIA is characterized by an intense synovitis that corresponds with the clinical onset of arthritis. This experimental data is useful evaluating CIA because of the pathological similarities between CIA and RA.

5.4. Antigen Induced T Cell Proliferation *In Vivo* Model:

The use of adoptive transfer of T cell receptor (TCR)-transgenic T cells provides an *in vivo* model for antigen-induced T-cell proliferation. Pape et al., *Immunol. Rev.* 156: 67-78 (1997) discloses adoptive transfer of TCR-transgenic T cells uniformly expressing an identifiable TCR of a known peptide/MHC specificity. The model can be used to monitor the *in vivo* behavior of antigen-specific T cells. Naive T cells are initially activated within T-cell zones of secondary lymphoid tissue to proliferate in a B7-dependent manner. If adjuvants or inflammatory cytokines are present during this period, enhanced numbers of T cells accumulate, migrate into B-cell-rich follicles, and acquire the capacity to produce IFN- γ and help B cells produce IgG2a. If inflammation is effectively antagonized, most of the initially activated antigen-specific T cells disappear without entering the follicles, and the survivors are poor producers of IL-2 and IFN- γ .

EXAMPLES

TABLE 3 lists representative anti-human CD40 variable domain amino acid sequences useful for the antibody polypeptides of the disclosure. TABLE 4 discloses representative nucleic acids that encode the variable domain sequences listed in TABLE 3. As is well known

in the art, multiple codons can encode the same amino acid. Nucleic acids encoding a protein sequence thus include nucleic acids having codon degeneracy. The antibody polypeptides disclosed in TABLE 3 specifically bind CD40 and were made using the reiterative initial/primary screening and affinity maturation methodologies described in the examples that follow.

TABLE 3

Anti-Human CD40 Variable Domain Amino Acid Sequences

10	BMS3h-56-201
	EVQLLES GGG LVQPGGSLRLSCAASGFTFRDYEMWVRQAPGKGLERVSAINPQGTRITYYADSVKGRFTISRDN SKNTL YLQMNSLR AEDTAVYYCAKLPFYFQEWGQGLTVTVSS (SEQ ID NO: 9)
15	BMS3h-56-258
	EVQLLES GGG LVQPGGSLRLSCAASGFTFRDYEMWVRQAPGKGLERVSAINPQGTRITYYADSVKGRFTISRDN SKNTL YLQMNSLR AEDTAVYYCAKLPFYFHEWGQGLTVTVSS (SEQ ID NO: 10)
20	BMS3h-37
	EVQLLES GGG LVQPGGSLRLSCAASGFTFEWYEMWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL YLQMNSLR AEDTAVYYCAKELGYFDYWGGQGLTVTVSS (SEQ ID NO: 11)
25	BMS3h-38
	EVQLLES GGG LVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWVSAISGGGSTYYADSVKGRFTISRDN SKNTL YLQMNSLR AEDTAVYYCAKEPFRFDYWGGQGLTVTVSS (SEQ ID NO: 12)
30	BMS3h-41
	EVQLLES GGG LVQPGGSLRLSCAASGFTFTEYEMIWVRQAPGKGLEWVSSISGNGANTYYADSVKGRFTISRDN SKNTL YLQMNSLR AEDTAVYYCAKEPLRFDYWGQGLTVTVSS (SEQ ID NO: 13)
35	BMS3h-43
	EVQLLES GGG LVQPGGSLRLSCTASGFTFNMYEMSWVRQAPGKGLEWVSGISRRGFTTYADSVKGRFTISRDN SKNTL YLQMNSLR AEDTAVYYCAKEPITYAMRYARFDYWGGQGLTVTVSS (SEQ ID NO: 14)
40	BMS3h-56
	EVQLLES GGG LVQPGGSLRLSCAASGFTFRDYEMWVRQAPGKGLERVSAINPQGTRITYYADSVKGRFTISRDN SKNTL YLQMNSLR AEDTAVYYCAKLPFI FDYWGGQGLTVTVSS (SEQ ID NO: 15)
	BMS3h-106
	EVQLLES GGG LVQPGGSLRLSCAASGFTFSTYHMQWVRQAPGKGLEWVSMIDADGLTYYADSVKGRFTISRDN SKNTL YLQMNSLR AEDTAVYYCAKPGPQFGQFDYWGGQGLTVTVSS (SEQ ID NO: 16)
	BMS3h-107
	EVQLLES GGG LVQPGGSLRLSCAASGFTFSGYDMQWVRQAPGKGLEWVSTISASGVFTYYADSVKGRFTISRDN SKNTL YLQMNSLR AEDTAVYYCAKYPNRFALNNFDYWGGQGLTVTVSS (SEQ ID NO: 17)

- BMS3h-131
DIQMTQSPSSLSASVGDRTITCRANSSILWALAWYQQKPKAPKLLIESSSGLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCVQAGWPGLTFGGQTKVEIKR (SEQ ID NO: 18)
- 5 BMS3h-193
DIQMTQSPSSLSASVGDRTITCRASQTIERRLNWYQQKPKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYASPLTFGGQTKVEIKR (SEQ ID NO: 19)
- 10 BMS3h-198
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMWVRQAPGKGLERVSATISGSGSTYYADSVKGRFTISRDNKNTL
YLQMNSLRRAEDTAVYYCAKDPYSFDYWGQGLTVTVSS (SEQ ID NO: 20)
- 15 BMS3h-202
EVQLLESGGGLVQPGGSLRLSCAASGFTFPTAEMWVRQAPGKGLEWVSSISASGSGSTYYADSVKGRFTISRDNKNTL
YLQMNSLRRAEDTAVYYCAKEPVSYVATFDYWGQGLTVTVSS (SEQ ID NO: 21)
- 20 BMS3h-217
DIQMTQSPSSLSASVGDRTITCRASHFIGTLLSWYQQKPKAPKLLITYGSLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCGQVLWPATFGGQTKVEIKR (SEQ ID NO: 22)
- 25 BMS3h-1
EVQLLESGGGLVQPGGSLRLSCAASGFTFPKNEMTWVRQAPGKGLEWVSAIESDGGATYYADSVKGRFTISRDNKNTL
YLQMNSLRRAEDTAVYYCAKNRIPDLVFDYWGQGLTVTVSS (SEQ ID NO: 23)
- 30 BMS3h-2
EVQLLESGGGLVQPGGSLRLSCAASGFTFDAGAMTWVRQAPGKGLEWVSSIDKEGLSTYYADSVKGRFTISRDNKNTL
YLQMNSLRRAEDTAVYYCAKGRIPGLVFDYWGQGLTVTVSS (SEQ ID NO: 24)
- 35 BMS3h-3
EVQLLESGGGLVQPGGSLRLSCAASGFTFGDAAMTWVRQAPGKGLEWVSAIQPMGDGTYADSVKGRFTVSRDNKNTL
YLQMNSLRRAEDTAVYYCAKGRIPTLQFDYWGQGLTVTVSS (SEQ ID NO: 25)
- 40 BMS3h-4
EVQLLESGGGLVQPGGSLRLSCAASGFTFEDSPMTWVRQAPGKGLEWVSAITSNGYETYYADSVKGRFTISRDNKNTL
YLQMNSLRRAEDTAVYYCAKGRIPTLHFDYWGQGLTVTVSS (SEQ ID NO: 26)
- 45 BMS3h-5
EVQLLESGGGLVQPGGSLRLSCAASGFTFDEHMSWVRQAPGKGLEWVSRIGPDGFHTYYADSVKGRFTISRDNKNTL
YLQMNSLRRAEDTAVYYCAKGRIPTLHFDYWGQGLTVTVSS (SEQ ID NO: 27)
- 50 BMS3h-6
EVQLLESGGGLVQPGGSLRLSCAASGFTFGEYHMSWVRQAPGKGLEWVSRITPLGTLTYADSVKGRFTISRDNKNTL
YLQMNSLRRAEDTAVYYCAKGRIPLTFDYWGQGLTVTVSS (SEQ ID NO: 28)
- 55 BMS3h-7
EVQLLESGGGLVQPGGSLRLSCAASGFTFGTNAMSWVRQAPGKGLEWVSRISPGGDYTYADSVKGRFTISRDNKNTL
YLQMNSLRRAEDTAVYYCAKGRVPDLLFDYWGQGLTVTVSS (SEQ ID NO: 29)
- 60 BMS3h-8
EVQLLESGGGLVQPGGSLRLSCAASGFTFPSEMSWVRQAPGKGLEWVSRISADGANTYYADSVKGRFTISRDNKNTL
YLQMNSLRRAEDAAVYYCAKGRVPDLLFDYWGQGLTVTVSS (SEQ ID NO: 30)

- 5 BMS3h-9
EVQLLESGGGLVQPGGSLRLSCAASGFTFAEDDMTWVRQAPGKGLEWVSRIAVDGDRTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGVPSLHFDYWGQGT LVTVSS (SEQ ID NO: 31)
- 10 BMS3h-10
EVQLLESGGGLVQPGGSLRLSCAASGFTFR TMDMSWVRQAPGKGLEWVSRI TGDGMNTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGVTPDLTFDYWGQGT LVTVSS (SEQ ID NO: 32)
- 15 BMS3h-11
EVQLLESGGGLVQPGGSLRLSCAASGFTFERDDMTWVRQAPGKGLEWVSRI NAGGVHTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGVTPDLTFDYWGQGT LVTVSS (SEQ ID NO: 33)
- 20 BMS3h-12
EVQLLESGGGLVQPGGSLRLSCAASGFTFDDDSMTWVRQAPGKGLEWVSRISSDGASTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGVTPDLTFDYWGQGT LVTVSS (SEQ ID NO: 34)
- 25 BMS3h-13
EVQLLESGGGLVQPGGSLRLSCAASGFTFTEEDMTWVRQAPGKGLEWVSRI DSVGEGTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGVTPDLTFDYWGQGT LVTVSS (SEQ ID NO: 35)
- 30 BMS3h-14
EVQLLESGGGLVQPGGSLRLSCAASGFTFSDSAMS WVRQAPGKGLEWVSRI DNPQGHTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGVPTLEFDYWGQGT LVTVSS (SEQ ID NO: 36)
- 35 BMS3h-15
EVQLLESGGGLVQPGGSLRLSCAASGFTFGQHSMTWVRQAPGKGLEWVSRI DGGGNTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGEVPR LHFYWGQGT LVTVSS (SEQ ID NO: 37)
- 40 BMS3h-16
EVQLLESGGGLVQPGGSLRLSCAASGFTFGQEPMTWVRQAPGKGLEWVSRI AYNGGDTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGITPNLTFDYWGQGT LVTVSS (SEQ ID NO: 38)
- 45 BMS3h-17
EVQLLESGGGLVQPGGSLRLSCAASGFTFENYPM S WVRQAPGKGLEWVSRI NATGSI TYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGVIPHL MFDYWGQGT LVTVSS (SEQ ID NO: 39)
- BMS3h-18
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYDMS WVRQAPGKGLEWVSRI TGTGNSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAQGVVPYLA FDYWGQGT LVTVSS (SEQ ID NO: 40)
- BMS3h-19
EVQLLESGGGLVQPGGSLRLSCAASGFTFEADAMTWVRQAPGKGLEWVSRI NV DGDRTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGVPTLEFDYWGQGT LVTVSS (SEQ ID NO: 41)
- BMS3h-21
EVQLLESGGGLVQPGGSLRLSCAASGFTFDRADMTWVRQAPGKGLEWVSRI SGE GKCTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGMV PNLVFDYWGQGT LVTVSS (SEQ ID NO: 42)

- BMS3h-22
EVQLLES GGG LVQP GGS LRLSCAASGFTFHWEPMSWVRQAPGKGLEWVSRINSSGWDYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGMV PNLVFDYWGQGT LVT VSS (SEQ ID NO: 43)
- 5 BMS3h-24
EVQLLES GGG LVQP GGS LRLSCAASGFTFADEPMTWVRQAPGKGLEWVSRIPPEGAPTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGITPNLTFDYWGQGT LVT VSS (SEQ ID NO: 44)
- 10 BMS3h-26
EVQLLES GGG LVQP GGS LRLSCAASGFTFHNHDMSWVRQAPGKGLEWVSRISRGGLQTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGIVPD LHF DYWGQGT LVT VSS (SEQ ID NO: 45)
- 15 BMS3h-27
EVQLLES GGG LVQP GGS LRLSCAASGFTFNEYPMSWVRQAPGKGLEWVSRINGDGANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGIIPAMQFDYWGQGT LVT VSS (SEQ ID NO: 46)
- 20 BMS3h-28
EVQLLES GGG LVQP GGS LRLSCAASGFTFGDVPMSWVRQAPGKGLEWVSRIDPYGSNTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGIMPSLTFDYWGQGT LVT VSS (SEQ ID NO: 47)
- BMS3h-29
EVQLLES GGG LVQP GGS LRLSCAASGFTFADYDMSWVRQAPGKGLEWVSRISALGATYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGQLPALEFDYWGQGT LVT VSS (SEQ ID NO: 48)
- 25 BMS3h-30
EVQLLES GGG LVQP GGS LRLSCAASGFTFKRYMTWVRQAPGK DLEWVSGIVPSGNRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGRI PDLHFDYWGQGT LVT VSS (SEQ ID NO: 49)
- 30 BMS3h-31
EVQLLES GGG LVQP GGS LRLSCAASGFTFADYDMTWVRQAPGKGLEWVSRISPTGGQTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGVIPYLSFSPFDYWGQGT LVT VSS (SEQ ID NO: 50)
- 35 BMS3h-32
EVQLLES GGG LVQP GGS LRLSCAASGFTFSKYMMGWARQAPGKGLEWVSSIDSHGAGTYADSVKGRFTISRDN SKNTL
YLQMNSLRVEDTAVYYCAKGAPKFM TTYTFDYWGQGT LVT VSS (SEQ ID NO: 51)
- 40 BMS3h-33
EVQLLES GGG LVQP GGS LRLSCAASGFTFLSYPMHVRQAPGKGLEWVSSIDSRG SVTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAK GHSWTFDYWGQGT LVT VSS (SEQ ID NO: 52)
- BMS3h-34
EVQLLES GGG LVQP GGS LRLSCAASGFTFANSNMTWVRQAPGKGLEWVSRINPDGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAEGRIPTLHFDYWGQGT LVT VSS (SEQ ID NO: 53)
- 45 BMS3h-35
EVQLLES GGG LVQP GGS LRLSCAASGFTFGPRRMGWVRQAPGKGLEWVSSIDDIGRRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAEGAQGVLLFDYWGQGT LVT VSS (SEQ ID NO: 54)
- 50 BMS3h-36
EVQLLES GGG LVQP GGS LRLSCAASGFTFEDYRMVVRQAPGKGLEWVSSISTSGELTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAETAGQFFDYWGQGT LVT VSS (SEQ ID NO: 55)

- 5 BMS3h-39
EVQLLESGGGLVQPGGSLRLSCAASGFTFPEYEMVWRQAPGKGLEWVSAISREGATYYADSVKGRFTISRDN SKNTL
YLQMNNLR AEDTAVYYCAKEPVRFDYWGQGLTVTVSS (SEQ ID NO: 56)
- BMS3h-40
EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYEMLWVRQAPGKGLEWVSSIS5SGNYTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKEPLMFDYWGQGLTVTVSS (SEQ ID NO: 57)
- 10 BMS3h-42
EVQLLESGGGLVQPGGSLRLSCAASGFTFDTEEMSWVRQAPGKGLEWVSAISPNGAFTFYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKEPILFDYWGQGLTVTVSS (SEQ ID NO: 58)
- 15 BMS3h-44
EVQLLESGGGLVQPGGSLRLSCAASGFTFGHYDMVWRQAPGRGLEWVSTINGAGLNTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAQSASRIFDYWGQGLTVTVSS (SEQ ID NO: 59)
- 20 BMS3h-45
EVQLLESGGGLVQPGGSLRLSCAASGFTFRSYEMAWVRQAPGKGLEWVSSISTLGKTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAQSSTHIFDYWGQGLTVTVSS (SEQ ID NO: 60)
- 25 BMS3h-46
EVQLLESGGGLVQPGGSLRLSCAASGFTFIRYEMAWVRQAPGKGLEWVSSISSGWTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKSDAHIFDYWGQGLTVTVSS (SEQ ID NO: 61)
- BMS3h-47
EVQLLESGGGLVQPGGSLRLSCAASGFTFYAYEMAWVRQAPGKGLEWVSSISDDGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKDLGQGFYWGQGLTVTVSS (SEQ ID NO: 62)
- 30 BMS3h-48
EVQLLESGGGLVQPGGSLRLSCAASGFTFADHGMTWVRQAPGKGLEWVSGIGPSGEATYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKDRIPLNLFYWGQGLTVTVSS (SEQ ID NO: 63)
- 35 BMS3h-49
EVQLLESGGGLVQPGGSLRLSCAASGFTFESQDMSWVRQAPGKGLEWVSGISPNGWDTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKDRSDFDYWGQGLTVTVSS (SEQ ID NO: 64)
- 40 BMS3h-50
EVQLLESGGGLVQPGGSLRLSCAASGFTFGDYDMWVRQAPGKGLEWVSRIRHPGGVTTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKAVPKGFDYWGQGLTVTVSS (SEQ ID NO: 65)
- 45 BMS3h-51
EVQLLESGGGLVQPGGSLRLSCAASGFTFRVYWMTWVRQAPGKGLEWVSSIDPQGGMTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKARIPNLEFDYWGQGLTVTVSS (SEQ ID NO: 66)
- BMS3h-52
EVQLLESGGGLVQPGESLRSLCAASGFTFSAYDMTWVRQAPGKGLEWVSRINPTGSYTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKAKIPNLFYWGQGLTVTVSS (SEQ ID NO: 67)

- BMS3h-53
EVQLLES GGG LVQP GGS LRLSCAASGFTFADSEMMWVRQAPGKGLEWVSGIAHNGGHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKAGHPQQTEAFDYWGQGLTVTVSS (SEQ ID NO: 68)
- 5 BMS3h-54
EMQLLES GGG LVQP GGS LRLSCAASGFTFATYDMYWRQAPGKGLEWVSKISPNGWSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKYQTHFDYWGQGLTVTVSS (SEQ ID NO: 69)
- 10 BMS3h-55
EVQLLES GGG LVQP GGS LRLSCAASGFTFSVYDMRWRQAPGKGLEWVSTISSSGTYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKYPKNFDYWGQGLTVTVSS (SEQ ID NO: 70)
- 15 BMS3h-57
EVQLLES GGG LVQP GGS LRLSCAASGFTFSHEDMTWVRQAPGKGLEWVSSISPNGWDTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKRTSKFDYWGQGLTVTVSS (SEQ ID NO: 71)
- 20 BMS3h-58
EVQLLES GGG LVQP GGS LRLSCAASGFTFEKYIMGWARQAPGKGLEWVSTIDYWGQHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKRSHLIPLQFDYWGQGLTVTVSS (SEQ ID NO: 72)
- BMS3h-59
EVQLLES GGG LVQP GGS LRLSCAASGFTFSYAMGWVRQAPGKGLEWVSTISVVGYYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKKALRGEAFTERFDYWGQGLTVTVSS (SEQ ID NO: 73)
- 25 BMS3h-60
EVQLLES GGG LVQP GGS LRLSCAASGFTFGPYMMHWVRQAPGKGLEWVSTIEVNGNRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKVVGSKTSSDKSFDYWGQGLTVTVSS (SEQ ID NO: 74)
- 30 BMS3h-61
EVQLLES GGG LVQP GGS LRLSCAASGFTFGTTEMAWVRQAPGKGLEWVSSIGSAGAWTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKIGGHPQGQFDYWGQGLTVTVSS (SEQ ID NO: 75)
- 35 BMS3h-62
EVQLLES GGG LVQP GGS LRLSCAASGFTFPREWMWVRQAPGKGLEWVSSIQPMGQTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKYSRNKGFFDYWGQGLTVTVSS (SEQ ID NO: 76)
- 40 BMS3h-63
EVQLLES GGG LVQP GGS LRLSCAASGFTFTSEYMGWVRQAPGKGLEWVSSIQRYSSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKHESNWETFDYWGQGLTVTVSS (SEQ ID NO: 77)
- BMS3h-70
EVQLLES GGG LVQP GGS LRLSCAASGFTFSVYSMQWVRQAPGKGLEWVSAITPNGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKTLGRGSYPGVDFDYWGQGLTVTVSS (SEQ ID NO: 78)
- 45 BMS3h-71
EVQLLES GGG LVQP GGS LRLSCAASGFTFPSYAMTWVRQAPGKGLEWVSRITADGTVTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGSIPMLTFDYWGQGLTVTVSS (SEQ ID NO: 79)
- 50 BMS3h-72
EVQLLES GGG LVQP GGS LRLSCAASGFTFTYDMIWVRQAPGKGLEWVSAISPNGTGIYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKNQSVHHAVFDYWGQGLTVTVSS (SEQ ID NO: 80)

- 5 BMS3h-73
EVQLLESGGGLVQPGGSLRLSCAASGFTTFENYEMTWVRQAPGKGLEWVSRIAPHGRLTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGQIPMLDFDYWGQGLTVTVSS (SEQ ID NO: 81)
- 10 BMS3h-74
EVQLLESGGGLVQPGGSLRLSCAASGFTTFSHYMMWVRQAPGKGLEWVSTISHFGDITYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKNDMMVMKNGGFDYWGQGLTVTVSS (SEQ ID NO: 82)
- 15 BMS3h-75
EVQLLESGGGLVQPGGSLRLSCAASGFTTFERYDMSWVRQAPGKGLEWVSRIIDSRGWSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGLVPHLRFDYWGQGLTVTVSS (SEQ ID NO: 83)
- 20 BMS3h-76
EVQLLESGGGLVQPGGSLRLSCAASGFTFANAQMTWVRQAPGKGLEWVSRIIDAMGDATYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGVPSIDYWGQGLTVTVSS (SEQ ID NO: 84)
- 25 BMS3h-77
EVQLLESGGGLVQPGGSLRLSCAASGFTFANAQMTWVRQAPGKGLEWVSRIIDAMGDATYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGVIPAFDYWGQGLTVTVSS (SEQ ID NO: 85)
- 30 BMS3h-78
EVQLLESGGGLVQPGGSLRLSCAASGFTFQNDRMHWVRQAPGKGLEWVSSISATGGDTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKQGTGTNRFDYWGQGLTVTVSS (SEQ ID NO: 86)
- 35 BMS3h-79
EVQLLESGGGLVQPGGSLRLSCAASGFTFNQPYMSWVRQAPGKGLEWVSSIDASGGTTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKDRIPNLVFDYWGQGLTVTVSS (SEQ ID NO: 87)
- 40 BMS3h-80
EVQLLESGGGLVQPGGSLRLSCAASGFTFDNENMTWVRQAPGKGLEWVSRIIDGGGYNTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGQVPELLFDYWGQGLTVTVSS (SEQ ID NO: 88)
- 45 BMS3h-81
EVQLLESGGGLVQPGGSLRLSCAASGFTFVSSNMTWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGRIPILVFDYWGQGLTVTVSS (SEQ ID NO: 89)
- BMS3h-82
EVQLLESGGGLVQPGGSLRLSCAASGFTFVSSNMTWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKDRIPNLVFDYWGQGLTVTVSS (SEQ ID NO: 90)
- BMS3h-83
EVQLLESGGGLVQPGGSLRLSCAASGFTFSDDSMSWVRQAPGKGLEWVSRIIDAGSSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGTIPLLEFDYWGQGLTVTVSS (SEQ ID NO: 91)
- BMS3h-84
EVQLLESGGGLVQPGGSLRLSCAASGFTFVSDTMSWVRQAPGKGLEWVSRIIDGTGGDTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGLIPDLQFDYWGQGLTVTVSS (SEQ ID NO: 92)

- BMS3h-85
EVQLLES GGGGLVQP GGS LRLSCAASGFTFDEEEMTWVRQAPGKGLEWVSRIIGGGHETYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGTIPLLEFDYWGQGLTVTVSS (SEQ ID NO: 93)
- 5 BMS3h-86
EVQLLES GGGGLVQP GGS LRLSCAASGFTFDNENMTWVRQAPGKGLEWVSRI TERGDVYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGTVP TLEFDYWGQGLTVTVSS (SEQ ID NO: 94)
- 10 BMS3h-87
EVQLLES GGGGLVQP GGS LRLSCAASGFTFDEEEMTWVRQAPGKGLEWVSRIIGGGHETYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGTVP TLEFDYWGQGLTVTVSS (SEQ ID NO: 95)
- 15 BMS3h-88
EVQLLES GGGGLVQP GGS LRLSCAASGFTFHETEMTWVRQAPGKGLEWVSAINRLGQDYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGRIPGLVFDYWGQGLTVTVSS (SEQ ID NO: 96)
- 20 BMS3h-89
EVQLLES GGGGLVQP GGS LRLSCAASGFTFSDDSMSWVRQAPGKGLEWVSRI NDAGSSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGTVP TLEFDYWGQGLTVTVSS (SEQ ID NO: 97)
- 25 BMS3h-90
EVQLLES GGGGLVQP GGS LRLSCAASGFTFDNENMTWVRQAPGKGLEWVSRI TERGDVYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGRIP TLFVFDYWGQGLTVTVSS (SEQ ID NO: 98)
- 30 BMS3h-91
EVQLLES GGGGLVQP GGS LRLSCAASGFTFSDDSMSWVRQAPGKGLEWVSRI NDAGSSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGTIPNLTFDYWGQGLTVTVSS (SEQ ID NO: 99)
- 35 BMS3h-92
EVQLLES GGGGLVQP GGS LRLSCAASGFTFADEPMTWVRQAPGKGLEWVSRI PPEGAPTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGLIPDLQFDYWGQGLTVTVSS (SEQ ID NO: 100)
- 40 BMS3h-93
EVQLLES GGGGLVQP GGS LRLSCAASGFTFQDSDMTWVRQAPGKGLEWVSIAIAPGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKDRI PNLRFDYWGQGLTVTVSS (SEQ ID NO: 101)
- 45 BMS3h-94
EVQLLES GGGGLVQP GGS LRLSCAASGFTFVSDTMSWVRQAPGKGLEWVSRI DGTGGDYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGQVPELLFDYWGQGLTVTVSS (SEQ ID NO: 102)
- 50 BMS3h-95
EVQLLES GGGGLVQP GGS LRLSCAASGFTFQDSDMTWVRQAPGKGLEWVSIAIAPGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKDRI PNLVFDYWGQGLTVTVSS (SEQ ID NO: 103)
- 55 BMS3h-96
EVQLLES GGGGLVQP GGS LRLSCAAGFTFDLAEMTWVRQAPGKGLEWVSRI DEGASTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDAAVYYCAEGVIPS LTFDYWGQGLTVTVSS (SEQ ID NO: 104)
- 60 BMS3h-97
EVQLLES GGGGLVQP GGS LRLSCAASGFTFDKHSWVRQAPGKGLEWVSRI SPDGTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDAAVYYCAEGVIPS LTFDYWGQGLTVTVSS (SEQ ID NO: 105)

- 5 BMS3h-98
EVQLLES GGG LVQPGGSLRLSCAASGFTFAEDDMTWVRQAPGKGLEWVSRIAVDGDRTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGKTPHLVFDYWGQGT LVT VSS (SEQ ID NO: 106)
- 10 BMS3h-99
EVQLLES GGG LVQPGGSLRLSCAAGFTFDLAEMTWVRQAPGKGLEWVSRIEDGASTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGQVPALVFDYWGQGT LVT VSS (SEQ ID NO: 107)
- 15 BMS3h-100
EVQLLES GGG LVQPGGSLRLSCAASGFTFEDSMMSWVRQAPGKGLEWVSRIIDPGGAQTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGVTPDLTFDYWGQGT LVT VSS (SEQ ID NO: 108)
- 20 BMS3h-101
EVQLLES GGG LVQPGGSLRLSCAASGFTFEHADMSWVRQASGKGLEWVSRIIDSGQSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGVTPDLTFDYWGQGT LVT VSS (SEQ ID NO: 109)
- 25 BMS3h-102
EVQLLES GGG LVQPGGSLRLSCAASGFTFSEAEMNWVRQAPGKGLEWVSRIITDGDSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGRIPTLHFDYWGQGT LVT VSS (SEQ ID NO: 110)
- 30 BMS3h-103
EVQLLES GGG LVQPGGSLRLSCAASGFTFDDSDMTWVRQAPGKSLWVSRIIGDDETYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKNRIPDLVFDYWGQGT LVT VSS (SEQ ID NO: 111)
- 35 BMS3h-108
EVQLLES GGG LVQPGGSLRLSCAASGFTFNVADMWVRQAPGKGLEWVSISPNGWDTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKHASTE GPTAFDYWGQGT LVT VSS (SEQ ID NO: 112)
- 40 BMS3h-109
EVQLLES GGG LVQPGGSLRLSCAASGFTFGPYDMGWVRQAPGKGLEWVSWISAHGSFTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKWPKFDYWGQGT LVT VSS (SEQ ID NO: 113)
- 45 BMS3h-110
EVQLLES GGG LVQPGGSLRLSCAASGFTFGSGMSWVRQAPGKGLEWVSRI GSN GADTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGMV PNLVFDYWGQGT LVT VSS (SEQ ID NO: 114)
- BMS3h-111
EVQLLES GGG LVQPGGSLRLSCAASGFTFNRFDMTWVRQAPGKGLEWVSAISGGSGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKDRI PNLVFDYWGQGT LVT VSS (SEQ ID NO: 115)
- BMS3h-112
EVQLLES GGG LVQPGGSLRLSCAASGFTFGESDMKWVRQAPGKGLEWVSISPNGWDTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKSPSSRLKFDYWGQGT LVT VSS (SEQ ID NO: 116)
- BMS3h-139
EVQLLES GGG LVQPGGSLRLSCAASGFTFDSSEMSWVRQAPGKGLEWVSSIENQGGATYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKDRI PNLVFDYWGQGT LVT VSS (SEQ ID NO: 117)

- BMS3h-140
EVQLLESGGGLVQPGGSLRLSCAASGFTLDAYPMYWRQAPGKLEWVSWIASGGGATYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKRTKNFDYWGQGLTVTVSS (SEQ ID NO: 118)
- 5 BMS3h-141
EVQLLESGGGLVQPGGSLRLSCAASGFTFMSYSMAWVRQAPGKLEWVSGITSNGNRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKSTGANSRNFYWGQGLTVTVSS (SEQ ID NO: 119)
- BMS3h-142
10 EVQLLESGGGLVQPGGSLRLSCAASGFTFEGYLSWVRQAPGKLEWVSSIAANGMQTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKPRGIWDGDFDYWGQGLTVTVSS (SEQ ID NO: 120)
- BMS3h-143
15 EVQLLESGGGLVQPGGSLRLSCAASGFTFHESMTWVRQAPGKLEWVSTIRHPGEFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGLIPDLQFDYWGQGLTVTVSS (SEQ ID NO: 121)
- BMS3h-144
EVQLLESGGGLVQPGGSLRLSCAASGFTFAMYSMSWVRQAPGKLEWVSSIAPPGGRYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKQSLTGYSRSFDYWGQGLTVTVSS (SEQ ID NO: 122)
- 20 BMS3h-145
EVQLLESGGGLVQPGGSLRLSCAASGFTFSQNPMWVRHAPGKLEWVSTIPANGRPTSYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKYSQQPGRRFYWGQGLTVTVSS (SEQ ID NO: 123)
- 25 BMS3h-146
EVQLLESGGGLVQPGGSLRLSCAASGFTFANYHMTWVRQAPGKLEWVSSIPDSGKQTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGRIPSLFDYWGQGLTVTVSS (SEQ ID NO: 124)
- BMS3h-147
30 EVQLLESGGGLVQPGGSLRLSCAASGFTFAQYHMRWVRQAPGKLEWVSTINDIGSNTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKVGGGRGSFSDYWGQGLTVTVSS (SEQ ID NO: 125)
- BMS3h-148
EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYDMKWVRQAPGKLEWVSTISASGVFTYYADSVKGRFTISRDN SKNTL
35 YLQMNSLRAEDTAVYYCAKREHAGQPPFDYWGQGLTVTVSS (SEQ ID NO: 126)
- BMS3h-149
EVQLLESGGGLVQPGGSLRLSCAASGFTFNGYAMSWVRQAPGKLEWVSTINANGKYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKKLTLASNYFDYWGQGLTVTVSS (SEQ ID NO: 127)
- 40 BMS3h-150
EVQLLESGGGLVQPGGSLRLSCAASGFTFMDYDMKWVRQAPGKLEWVSSITAGKKTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKDSVKYPLNLFYWGQGLTVTVSS (SEQ ID NO: 128)
- 45 BMS3h-151
EVQLLESGGGLVQPGGSLRLSCAASGFTFPHYTMAWVRQAPGKLEWVSSIQSPGWRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKYGDGLPLTFDYWGQGLTVTVSS (SEQ ID NO: 129)
- BMS3h-167
50 EVQLLESGGGLVQPGGSLRLSCAASGFTFSGTPMSWVRQAPGKLEWVSRIGDEGQETYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGVTPDLTFDYWGQGLTVTVSS (SEQ ID NO: 130)

- 5 BMS3h-168
EVQLLES GGGGLVQPGGSLRLSCAASGFTSSSSMSWVRQAPGKGLEWVSAIGSDGPSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGRIPTLHFDYWGQGT LVTVSS (SEQ ID NO: 131)
- BMS3h-169
EVQLLES GGGGLVQPGGSLRLSCAASGFTFNP GEMTWVRQAPGKGLEWVSSIDSGSSYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGRIPTLHFDYWGQGT LVTVSS (SEQ ID NO: 132)
- 10 BMS3h-170
EVQLLES GGGGLVQPGGSLRLSCAASGFTFPE SMHWVRQAPGKGLEWVSSIGYPGATTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGGSRDDNFDYWGQGT LVTVSS (SEQ ID NO: 133)
- 15 BMS3h-171
EVQLLES GGGGLVQPGGSLRLSCAASGFTFGQHS MHVVRQAPGKGLEWVSSISVPGPKTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKSLRDLRPGDSK SFDYWGQGT LVTVSS (SEQ ID NO: 134)
- 20 BMS3h-197
EVQLLES GGGGLVQPGGSLRLSCAASGFTFGSAAMD WVRQAPGKGLEWVSSINDMGSNTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKQGRFDYWGQGT LVTVSS (SEQ ID NO: 135)
- 25 BMS3h-199
EVQLLES GGGGLVQPGGSLRLSCAASGFTFGYDRMA WVRQAPGKGLEWVSSIDGPGGATYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAEGRRVPDFDYWGQGT LVTVSS (SEQ ID NO: 136)
- BMS3h-200
EVQLLES GGGGLVQPGGSLRLSCAASGFTFGEYEMTW VRQAPGKGLEWVSRIDPFGSETYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAEGVVPDLNFDYWGQGT LVTVSS (SEQ ID NO: 137)
- 30 BMS3h-201
EVQLLES GGGGLVQPGGSLRLSCAASGFTFDKYVMGW VRQAPGKGLEWVSTIGSYGGATYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKRLTLSATKFDYWGQGT LVTVSS (SEQ ID NO: 138)
- 35 BMS3h-203
EVQLLES GGGGLVQPGGSLRLSCAASGFTFEDYVMGW VRQAPGKGLEWVSTIAHRGDITYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKRRRLSDYRFDYWGQGT LVTVSS (SEQ ID NO: 139)
- 40 BMS3h-204
EVQLLES GGGGLVQPGGSLRLSCAASGFTFGQFDMY WVRQAPGKGLEWVSAISPAGTGTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKAGDRSSLFDYRGQGT LVTVSS (SEQ ID NO: 140)
- 45 BMS3h-205
EVQLLES GGGGLVQPGGSLRLSCAASGFTFKDTGMT WVRQAPGKGLEWVSSISSYGRDITYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLNALGFYWGQGT LVTVSS (SEQ ID NO: 141)
- BMS3h-206
EVQLLES GGGGLVQPGGSLRLSCAASGFTFGPYPM SWVRQAPGKGLEWVSGINAPGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAQMQMSGVFDYWGQGT LVTVSS (SEQ ID NO: 142)

- BMS3h-207
EVQLLES GGG LVQP GGS LRLSCAASGFTFSNQDMTWVRQAPGKGLEWVSSIDSSGQLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKVKSLARFDYWGQGLTVTVSS (SEQ ID NO: 143)
- 5 BMS3h-208
EVQLLES GGG LVQP GGS LRLSCAASGFTFPESDMKWVRQAPGKGLEWVSSISPNGWDTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKPAQVLFYWGQGLTVTVSS (SEQ ID NO: 144)
- 10 BMS3h-209
EVQLLES GGG LVQP GGS LRLSCAASGFTFEQVVMGWVRQAPGKGLEWVSTIGTSGKYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAQRRLTRVHFDYWGQGLTVTVSS (SEQ ID NO: 145)
- 15 BMS3h-210
EVQLLES GGG LVQP GGS LRLSCAASGFTFGVEHMSWVRQAPGKGLEWVSAITGDGDRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKTVSWNGRFDYWGQGLTVTVSS (SEQ ID NO: 146)
- 20 BMS3h-211
EVQLLES GGG LVQP GGS LRLSCAASGFTFAWYNMGWVRQAPGKGLEWVSRIAPSGIITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGLRGKFDYWGQGLTVTVSS (SEQ ID NO: 147)
- 25 BMS3h-212
EVQLLES GGG LVQP GGS LRLSCAASGFTFSNYEMRWVRQAPGKGLEWVSSISSAGTDYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKQSLNFDYWGQGLTVTVSS (SEQ ID NO: 148)
- 30 BMS3h-213
EVQLLES GGG LVQP GGS LRLSCVASGFTFDFEPMTWVRQAPGKGLEWVSIIDPGGGATYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKSNMFDYWGQGLTVTVSS (SEQ ID NO: 149)
- 35 BMS3h-214
EVQLLES GGG LVQP GGS LRLSCAASGFTFSAYPMHWVRQAPGKGLEWVSSIASSGITTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKFTRLHFPAQFDYWGQGLTVTVSS (SEQ ID NO: 150)
- 40 BMS3h-215
EVQLLES GGG LVQP GGS LRLSCAASGFTFADYAMGWVRQAPGKGLEWVSRISPEGSRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLRPYASKFDYWGQGLTVTVSS (SEQ ID NO: 151)
- 45 BMS3h-230
EVQLLES GGG LVQP GGS LRLSCAASGFTFRPYDMGWVRQAPGKGLEWVSTISHQGNRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKVS SHFDYWGQGLTVTVSS (SEQ ID NO: 152)
- 50 BMS3h-231
EVQLLES GGG LVQP GGS LRLSCAASGFTFSAYNMWVRQAPGKGLEWVSWINSTGSRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKNWHRGRFDYWGQGLTVTVSS (SEQ ID NO: 153)
- 55 BMS3h-232
EVQLLES GGG LVQP GGS LRLSCAASGFTFDRYRMGWVRQAPGKGLEWVSTINRLGQSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKVKKKHFDYWGQGLTVTVSS (SEQ ID NO: 154)
- 60 BMS3h-233
EVQLLES GGG LVQP GGS LRLSCAASGFTFAHYNMWVRQAPGKGLEWVSTITKTGFRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKAGQDFDYWGQGLTVTVSS (SEQ ID NO: 155)

- 5 BMS3h-234
EVQLLESGGGLVQPGGSLRLSCAASGFTFPYPSMHWVRQAPGKGLEWVSTIDGSGMFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAEDSLKASFDYWGQGLTVTVSS (SEQ ID NO: 156)
- 10 BMS3h-235
EVQLLESGGGLVQPGGSLRLSCAASGFTFPLYGMWVRQAPGKGLEWVSYIGPYGHTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKKRKKKFDYWGQGLTVTVSS (SEQ ID NO: 157)
- 15 BMS3h-236
EVQLLESGGGLVQPGGSLRLSCAASGFTFPRYMSWVRQAPGKGLEWVSSITPYGAHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKYGKWFYDYGQGLTVTVSS (SEQ ID NO: 158)
- 20 BMS3h-237
EVQLLESGGGLVQPGGSLRLSCAASGFTFNEYAMRWRQAPGKGLEWVSTIDRLGLHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKSGPFTFDYWGQGLTVTVSS (SEQ ID NO: 159)
- 25 BMS3h-238
EVQLLESGGGLVQPGGSLRLSCAASGFTFERYNMRWRQAPGKGLEWVSTIDRLGLATYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKAGSWSFYDYGQGLTVTVSS (SEQ ID NO: 160)
- 30 BMS3h-239
EVQLLESGGGLVQPGGSLRLSCAASGFTFGIYDMKWRQAPGKGLEWVSTISSGHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKYPQYPFDYWGQGLTVTVSS (SEQ ID NO: 161)
- 35 BMS3h-240
EVQLLESGGGLVQPGGSLRLSCAASGFTFWYDMRWRQAPGKGLEWVSTISATGVHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKYPAGRFDYWGQGLTVTVSS (SEQ ID NO: 162)
- 40 BMS3h-241
EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYDNIWVRQAPGKGLEWVSAISPNGTGTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKPPQVNTFDYRQGLTVTVSS (SEQ ID NO: 163)
- 45 BMS3h-243
EVQLLESGGGLVQPGGSLRLSCAASGFTFEKEDMGWRQAPGKGLEWVSHISPNGYATYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKSWSFYDYGQGLTVTVSS (SEQ ID NO: 164)
- BMS3h-244
EVQLLESGGGLVQPGGSLRLSCAASGFTFSATPMEWARQAPGKGLEWVSTISESGYSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKWNSTGFDYWGQGLTVTVSS (SEQ ID NO: 165)
- BMS3h-245
EVQLLESGGGLVQPGGSLRLSCAASGFTFNTVDMWRQAPGKGLEWVSSISPNGWDTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAEAPHRAFDFYWGQGLTVTVSS (SEQ ID NO: 166)
- BMS3h-246
EVQLLESGGGLVQPGGSLRLSCAASGFTFEDKEMSWVRQAPGKGLEWVSRIDALGDSYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAEGMVPRLKFDYWGQGLTVTVSS (SEQ ID NO: 167)

- BMS3h-247
EVQLLESGGGLVQPGGSLRLSCAASGFTFSDHSMWVRQAPGKGLEWVSDIEPHGVHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCANPTFDYWGQGT LVTVSS (SEQ ID NO: 168)
- 5 BMS3h-248
EVQLLESGGGLVQPGGSLRLSCAASGFTFSPHTMHVVRQAPGKGLEWVSGIGPDGTTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKRSYSWDRGWTFDYWGQGT LVTVSS (SEQ ID NO: 169)
- 10 BMS3h-249
EVQLLESGGGLVQPGGSLRLSCAASGFTFYASDMKWVRQAPGKGLEWVSSISPNGWDYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKADYTHSFDYWGQGT LVTVSS (SEQ ID NO: 170)
- 15 BMS3h-250
EVQLLESGGGLVQPGGSLRLSCAASGFTFAHYNMRWVRQAPGKGLEWVSTITKTGFRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKAGQDFDYWGQGT LVTVSS (SEQ ID NO: 171)
- 20 BMS3h-251
EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYHMGWARQAPGKGLEWVSVIGPRGISTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKSPSRHRFDYWGQGT LVTVSS (SEQ ID NO: 172)
- BMS3h-252
EVQLLESGGGLVQPGGSLRLSCAASGFTFNFYAMRWVRQAPGKGLEWVSTIDRLGLHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKSGPFTFDYWGQGT LVTVSS (SEQ ID NO: 173)
- 25 BMS3h-253
EVQLLESGGGLVQPGGSLRLSCAASGFTFGNYSMKWARQAPGKGLEWVSTITPDGWYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKVGDVWGWIGGFDYWGQGT LVTVSS (SEQ ID NO: 174)
- 30 BMS3h-254
EVQLLESGGGLVQPGGSLRLSCAASGFTFGDYGMKWVRQAPGKGLEWVSAITSN GDFYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKSLYKFDYWGQGT LVTVSS (SEQ ID NO: 175)
- 35 BMS3h-255
EVQLLESGGGLVQPGGSLRLSCAGSGFTFPTYKMGWVRQAPGKGLEWVSFIDYWGWRYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKSPYSWTHDSPHFDYWGQGT LVTVSS (SEQ ID NO: 176)
- 40 BMS3h-256
EVQLLESGGGLVQPGGSLRLSCAASGFTFRPYTMCWARQAPGKGLEWVSCISDAGSFYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKRMSSF DYWGQGT LVTVSS (SEQ ID NO: 177)
- BMS3h-257
EVQLLESGGGLVQPGGSLRLSCAASGFTFQNYQMAWVRQAPGKGLEWVSTISGTGKNTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKTPQNYFSVRRFDYWGQGT LVTVSS (SEQ ID NO: 178)
- 45 BMS3h-258
EVQLLESGGGLVQPGGSLRLSCAASGFTFGAYTMGWVRQAPGKGLEWVSKISTSGGQTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKPLNWWAFDYWGQGT LVTVSS (SEQ ID NO: 179)
- 50 BMS3h-272
EVQLLESGGGLVQPGGSLRLSCAASGFTFNAYPMTWVRQAPGKGLEWVSRIDGYGRHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKGIIPNFDYWGQGT LVTVSS (SEQ ID NO: 180)

- 5 BMS3h-273
EVQLLESGGGLVQPGGSLRLSCAASGFTFGAVDMTWVRQAPGKGLEWVSAISPSGSATYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGRVPDLGFDYWGQGLTVTVSS (SEQ ID NO: 181)
- 10 BMS3h-274
EVQLLESGGGLVQPGGSLRLSCAASGFTFDYAMGWARQAPGKGLEWVSAIGAKGLSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKAARGKFDYWGQGLTVTVSS (SEQ ID NO: 182)
- 15 BMS3h-275
EVQLLESGGGLVQPGGSLRLSCAASGFTFTRYQMGMWVRQAPGKGLEWVSVINWGSSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKMSGKFAYWGQGLTVTVSS (SEQ ID NO: 183)
- 20 BMS3h-276
EVQLLESGGGLVQPGGSLRLSCAASGFTFGNYSMMWVRQAPGKGLEWVSTIIPAGTSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKPSIRLFDYWGQGLTVTVSS (SEQ ID NO: 184)
- 25 BMS3h-279
EVQLLESGGGLVQPGGSLRLSCAASGFTFGAYDMGMWVRQAPGKGLEWVSWISPNGYDTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGGVKFDYWGQGLTVTVSS (SEQ ID NO: 185)
- 30 BMS3h-282
EVQLLESGGGLVQPGGSLRLSCAASGFTFVWYEMAWVRQAPGKGLEWVSTIQADGEQTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKASYALVYPPEEFDYWGQGLTVTVSS (SEQ ID NO: 186)
- 35 BMS3h-287
EVQLLESGGGLVQPGGSLRLSCAASGFTFTNYRMSWVRQAPGKGLEWVSAIDDLGVSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKWRLKNSQPTDFDYWGQGLTVTVSS (SEQ ID NO: 187)
- 40 BMS3h-292
EVQLLESGGGLVQPGGSLRLSCAASGFTFDQAHMWWVRQAPGKGLEWVSFINPSGYTYTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKPSLSPSSFDYWGQGLTVTVSS (SEQ ID NO: 188)
- 45 BMS3h-293
EVQLLESGGGLVQPGGSLRLSCAASGFTFETGMGMWARQAPGKGLEWVSNIDGSGTYTYTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKSTQNYRFDYWGQGLTVTVSS (SEQ ID NO: 189)
- BMS3h-296
EVQLLESGGGLVQPGGSLRLSCAASGFTFGAYPMYWRQAPGKGLEWVSSIHKDGRITYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKQGPVDGFDYWGQGLTVTVSS (SEQ ID NO: 190)
- BMS3h-297
EVQLLESGGGLVQPGGSLRLSCAASGFTFPDEGMTWVRQAPGKGLEWVSTIETGGTVTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKMDGSGTWQTFDYWGQGLTVTVSS (SEQ ID NO: 191)
- BMS3h-298
EVQLLESGGGLVQPGGSLRLSCAASGFTFDSLGMGMWARQAPGKGLEWVSYIRAEGAYTYTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKYLADSDYWGQGLTVTVSS (SEQ ID NO: 192)

- BMS3h-299
EVQLLES GGGGLVQP GGSRLRLSCAASGFTFSESYMEWVRQAPGKGLEWVSGIDHIGGGTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKDDGRGGS MFDYWGQGT LVTVSS (SEQ ID NO: 193)
- 5 BMS3h-300
EVQLLES GGGGLVQP GGSRLRLSCAASGFTFSGGYMMWVRQAPGKGLEWVSSIGASGAYTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKTGGRLDYWGQGT LVTVSS (SEQ ID NO: 194)
- 10 BMS3h-301
EVQLLES GGGGLVQP GGSRLRLSCAASGFTFDEGHMGWVRQAPGKLEWVSYIGSLGLHTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKREFSNGGFDYWGQGT LVTVSS (SEQ ID NO: 195)
- 15 BMS3h-302
EVQLLES GGGGLVQP GGSRLRLSCAASGFTFKTSPMYWVRQAPGKGLEWVSSIDRTGGHTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKQALLTDAKRFDYWGQGT LVTVSS (SEQ ID NO: 196)
- 20 BMS3h-303
EVQLLES GGGGLVQP GGSRLRLSCAASGFTFDGRDMWVRQAPGKGLEWVSAISPGLDYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAERPQMLVTNFDYWGQGT LVTVSS (SEQ ID NO: 197)
- BMS3h-304
EVQLLES GGGGLVQP GGSRLRLSCAASGFTFGNDPMSWVRQAPGKGLEWVSGIGREGDSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKDSMRHQPFYWGQGT LVTVSS (SEQ ID NO: 198)
- 25 BMS3h-305
EVQLLES GGGGLVQP GGSRLRLSCAASGFTFDETYMKWVRQAPGKGLEWVSAIGASGADTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKFTHLNGRFDYWGQGT LVTVSS (SEQ ID NO: 199)
- 30 BMS3h-306
EVQLLES GGGGLVQP GGSRLRLSCAASGFTFGGWPMGWVRQAPGKGLEWVSGIDIDGAPTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKEEAGSWSFYWGQGT LVTVSS (SEQ ID NO: 200)
- 35 BMS3h-307
EVQLLES GGGGLVQP GGSRLRLSCAASGFTFSDQAMWVRQAPGKGLEWVSIQGGGGFTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKPSKPFYWGQGT LVTVSS (SEQ ID NO: 201)
- 40 BMS3h-308
EVQLLES GGGGLVQP GGSRLRLSCAASGFTFETGQMGWARQAPGKGLEWVSNIDGSGTYTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKAVRNFAFDYWGQGT LVTVSS (SEQ ID NO: 202)
- BMS3h-309
EVQLLES GGGGLVQP GGSRLRLSCAASGFTFSGHMSWVRQAPGKGLEWVSAISPHGHTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKGIRGWIGHDTQPFYWGQGT LVTVSS (SEQ ID NO: 203)
- 45 BMS3h-310
EVQLLES GGGGLVQP GGSRLRLSCAASGFTFESKDMLWVRQAPGKGLEWVSSISSDGTHTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAQELGGSWQFDYWGQGT LVTVSS (SEQ ID NO: 204)
- 50 BMS3h-311
EVQLLES GGGGLVQP GGSRLRLSCAASGFTFADRDMMWVRQAPGKGLEWVSGIGASGTSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDAAYYYCAKGGTGPTDLWDFDYWGQGT LVTVSS (SEQ ID NO: 205)

- 5 BMS3h-312
EVQLLESGGGLVQPGGSLRLSCAASGFTFDDEKMLWVRQAPGKGLEWVSSISVSGLHTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKEEAGSWSF DYWGQGLTVTVSS (SEQ ID NO: 206)
- 10 BMS3h-313
EVQLLESGGGLVQPGGSLRLSCAASGFTFGQERMIWVRQAPGKGLEWVSDISAGGTTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKEEAGSWSF DYWGQGLTVTVSS (SEQ ID NO: 207)
- 15 BMS3h-37-1
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKMNTL
YLQMNSLR AEDTAVYYCAKELGYFDYRGRGLTVTVSS (SEQ ID NO: 208)
- 20 BMS3h-37-2
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKELGYFDYRGRGLTVTVSS (SEQ ID NO: 209)
- 25 BMS3h-37-3
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKELGYFDYRVQGLTVTVSS (SEQ ID NO: 210)
- 30 BMS3h-37-4
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKELGYFDYRGRGLTVTVSS (SEQ ID NO: 211)
- 35 BMS3h-37-5
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWISAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKELGYFDYRVQGLTVTVSS (SEQ ID NO: 212)
- 40 BMS3h-37-6
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKELGYFDYRGRGLTVTVSS (SEQ ID NO: 213)
- 45 BMS3h-37-7
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKELGYFDYRGRGLTVTVSS (SEQ ID NO: 214)
- BMS3h-37-8
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKELGYFHYWGRGLTVTVSS (SEQ ID NO: 215)
- BMS3h-37-9
EVQLLESGGGLVQPGGSLRLSCV ASGFTFEWYEMQWVRQAPNGLEWISAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKELGYFDYRGRGLTVTVSS (SEQ ID NO: 216)
- BMS3h-37-10
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKELGYFDYRGRGLTVTVSS (SEQ ID NO: 217)

- BMS3h-37-11
EVQLLES GGG L V Q P G G S L R L S C A A S G F T F E W Y E M Q W R K A P G K G L E W V S A I S G D G Y R T Y Y A D S V K G R F T I S R D N S K N T L
Y L Q M N S L R A E D T A V Y Y C A K E L G Y F D Y R G R G T L V T V S S (SEQ ID NO: 218)
- 5 BMS3h-37-12
EVQLLES GGG L V Q P G G S L R L S C A A S G F T F E W Y E M Q W R R A P G K G L E W V S A I S G D G Y R T Y Y A D S V K G R F T I S R D N S K N T L
Y L Q M N S L R A E D T A V Y Y C A K E L G Y F D Y R G R G T L V T V S S (SEQ ID NO: 219)
- 10 BMS3h-37-201
EVQLLES GGG L V Q P G G S L R L S C A A S G F T F E W Y E M Q W R R A P G K G L E W V S A I S G D G Y R T Y Y A D S V K G R F T I S R D N S K N T L
Y L Q M N S L R A E D T A V Y Y C A K E L G Y F D Y W G R G T L V T V S S (SEQ ID NO: 220)
- 15 BMS3h-37-202
EVQLLES GGG L V Q P G G S L R L S C A A S G F T F E W Y E M Q W R R A P G K G L E W V S A I S G D G Y R T Y Y A D S V K G R F T I S R D N S K N T L
Y L Q M N S L R A E D T A V Y Y C A K E L G Y F D Y W G R G T L V T V S S (SEQ ID NO: 221)
- 20 BMS3h-37-203
EVQLLES GGG L V Q P G G S L R L S C A A S G F T F E W Y E M Q W R R A P G K G L E W V S A I S G D G Y R T Y Y A D S V K G R F T I S R D N S K N T L
Y L Q M N S L R A E D T A V Y Y C A K E L L Y F D Y W G R G T L V T V S S (SEQ ID NO: 222)
- BMS3h-37-204
EVQLLES GGG L V Q P G G S L R L S C A A S G F T F E W Y E M Q W R R A P G K G L E W V S A I S G D G Y R T Y Y A D S V K G R F T I S R D N S K N T L
Y L Q M N S L R A E D T A V Y Y C A K E L G F F D Y W G R G T L V T V S S (SEQ ID NO: 223)
- 25 BMS3h-37-205
EVQLLES GGG L V Q P G G S L R L S C A A S G F T F E W Y E M Q W R R A P G K G L E W V S A I S G D G Y R T Y Y A D S V K G R F T I S R D N S K N T L
Y L Q M N S L R A E D T A V Y Y C A K E L E Y F D Y W G R G T L V T V S S (SEQ ID NO: 224)
- 30 BMS3h-37-206
EVQLLES GGG L V Q P G G S L R L S C A A S G F T F E W Y E M Q W R R A P G K G L E W V S A I S G D G Y R T Y Y A D S V K G R F T I S R D N S K N T L
Y L Q M N S L R A E D T A V Y Y C A K G L E Y F D Y W G R G T L V T V S S (SEQ ID NO: 225)
- 35 BMS3h-37-207
EVQLLES GGG L V Q P G G S L R L S C A A S G F T F E W Y E M Q W R R A P G K G L E W V S A I S G D G Y R T Y Y A D S V K G R F T I S R D N S K N T L
Y L Q M N S L R A E D T A V Y Y C A K E L A F F D Y W G R G T L V T V S S (SEQ ID NO: 226)
- 40 BMS3h-37-208
EVQLLES GGG L V Q P G G S L R L S C A A S G F T F E W Y E M Q W R R A P G K G L E W V S A I S G D G Y R T Y Y A D S V K G R F T I S R D N S K N T L
Y L Q M N S L R A E D T A V Y Y C A K E L L Y F D Y W G R G T L V T V S S (SEQ ID NO: 227)
- BMS3h-37-209
EVQLLES GGG L V Q P G G S L R L S C A A S G F T F E W Y E M Q W R R A P G K G L E W V S A I S G D G Y R T Y Y A D S V K G R F T I S R D N S K N T L
Y L Q M N S L R A E D T A V Y Y C A K E L E F F D Y W G R G T L V T V S S (SEQ ID NO: 228)
- 45 BMS3h-37-210
EVQLLES GGG L V Q P G G S L R L S C A A S G F T F E W Y E M Q W R R A P G K G L E W V S A I S G D G Y R T Y Y A D S V K G R F T I S R D N S K N T L
Y L Q M N S L R A E D T A V Y Y C A K E L Q F F D Y W G R G T L V T V S S (SEQ ID NO: 229)
- 50 BMS3h-37-211
EVQLLES GGG L V Q P G G S L R L S C A A S G F T F E W Y E M Q W R R A P G K G L E W V S A I S G D G Y R T Y Y A D S V K G R F T I S R D N S K N T L
Y L Q M N S L R A E D T A V Y Y C A K E L L F F D Y W G R G T L V T V S S (SEQ ID NO: 230)

- 5 BMS3h-37-212
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRRAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELEFFDYWGRGTLVTSS (SEQ ID NO: 231)
- BMS3h-37-213
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRRAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELEFFDYWGRGTLVTSS (SEQ ID NO: 232)
- 10 BMS3h-37-214
EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRRAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLEFFDYWGRGTLVTSS (SEQ ID NO: 233)
- 15 BMS3h-37-215
EVRLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRRAPGKGLEWVSAISGDGYRTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKELEFFDYWGRGTLVTSS (SEQ ID NO: 234)
- 20 BMS3h-38-1
EVQLLESGGGLVQPGGSLRLSCAASGFTFEEMIIWVRQAPGKGLEWVSAISGGGTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCSKEPFRFDYWGGTLVTSS (SEQ ID NO: 235)
- BMS3h-38-2
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEMIIWVRQAPGKGLEWVSAISGGGTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRFDYWGGTLVTSS (SEQ ID NO: 236)
- 25 BMS3h-38-3
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEMIIWVRQAPGKLEWISAISGGGTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRFDYWGGTLVTSS (SEQ ID NO: 237)
- 30 BMS3h-38-4
EVQLLDPPGGGLVQPGGSLRLSCAASGFTFGKEEMIIWVRQAPGKLEWVSAISGGGTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRFDYWGGTLVTSS (SEQ ID NO: 238)
- BMS3h-38-5
35 EVQLLESGGGLVQPGGSLRLSCAASGFTFEEMIIWVRQAPGKLEWVSAISGGGTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRFDYWGGTLVTSS (SEQ ID NO: 239)
- BMS3h-38-6
40 EVQLLEPGGGLVQPGGSLRLSCAASGFTFEEMIIWVRQAPGKLEWVSAISGGGTYADSVKGRFTISRDN SKNTL
YLLMNSLRAEDTAVYYCSKEPFRFDYWGGALVTSS (SEQ ID NO: 240)
- BMS3h-38-7
45 EVQLLDPPGGGLVQPGGSLRLSCAASGFTFGKEEMIIWVRQAPGKLEWVSAISGGGTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDYWGGTLVTSS (SEQ ID NO: 241)
- BMS3h-38-8
EVQLLESGGGLVQPGGSLRLSCAASGFTFEEMIIWVRQAPGKLEWISAISGGGTYADSVKGRFTIHRDN SKNTL
YLQMNSLRAEDTAVYYCSKEPFRFDYRGLTLVTSS (SEQ ID NO: 242)

- BMS3h-38-9
EVQLLDPGGGLVQPGGSLRLSCAASGFTFGKEEMIWVRQAPGKGLEWVSSISGSGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDYWGQGLTVTVSS (SEQ ID NO: 243)
- 5 BMS3h-38-10
EVQLLDPGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWISGISGSGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPFRFDYWGQGLTVTVSS (SEQ ID NO: 244)
- 10 BMS3h-38-11
EVQLLDPGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWISGISGSGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGREPFRFDYWGQGLTVTVSS (SEQ ID NO: 245)
- 15 BMS3h-38-12
EVRLLSGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRFDYWGQGLTVTVSS (SEQ ID NO: 246)
- 20 BMS3h-38-13
EVQQLESGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRFDYWGQGLTVTVSS (SEQ ID NO: 247)
- 25 BMS3h-38-201
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFYDYWGQGLTVTVSS (SEQ ID NO: 248)
- 30 BMS3h-38-202
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFYDYWGQGLTVTVSS (SEQ ID NO: 249)
- 35 BMS3h-38-203
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEKEMIWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFYDYWGQGLTVTVSS (SEQ ID NO: 250)
- 40 BMS3h-38-204
EVQLLASGGGLVQPGGSLRLSCAASGFTFPQEEMIWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 251)
- 45 BMS3h-38-205
EVQLLASGGGLVQPGGSLRLSCAASGFTFFAAEMIWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 252)
- 50 BMS3h-38-206
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRPGTSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 253)
- 45 BMS3h-38-207
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRMGFSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 254)
- 50 BMS3h-38-208
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRWHGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYWGQGLTVTVSS (SEQ ID NO: 255)

- 5 BMS3h-38-209
EVQLLASGGGLVQPGGSLRLSCAASGFTFEFEEEMIWVRQAPGKGLEWVSAISRLLGWSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYWGQGT LTVSS (SEQ ID NO: 256)
- 10 BMS3h-38-210
EVQLLASGGGLVQPGGSLRLSCAASGFTFEFEEEMIWVRQAPGKGLEWVSAISRWGASTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYWGQGT LTVSS (SEQ ID NO: 257)
- 15 BMS3h-38-211
EVQLLASGGGLVQPGGSLRLSCAASGFTFEFEEEMIWVRQAPGKGLEWVSAISRQGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYWGQGT LTVSS (SEQ ID NO: 258)
- 20 BMS3h-38-212
EVQLLASGGGLVQPGGSLRLSCAASGFTFEFEEEMIWVRQAPGKGLEWVSAISVSGWSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYWGQGT LTVSS (SEQ ID NO: 259)
- 25 BMS3h-38-213
EVQLLASGGGLVQPGGSLRLSCAASGFTFEFEEEMIWVRQAPGKGLEWVSAISRWGASTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYWGQGT LTVSS (SEQ ID NO: 260)
- 30 BMS3h-38-214
EVQLLASGGGLVQPGGSLRLSCAASGFTFEFEEEMIWVRQAPGKGLEWVSAISRNLSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYWGQGT LTVSS (SEQ ID NO: 261)
- 35 BMS3h-38-215
EVQLLASGGGLVQPGGSLRLSCAASGFTFEFEEEMIWVRQAPGKGLEWVSAISGLGWSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYWGQGT LTVSS (SEQ ID NO: 262)
- 40 BMS3h-38-216
EVQLLASGGGLVQPGGSLRLSCAASGFTFEFEEEMIWVRQAPGKGLEWVSAISALGWSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYWGQGT LTVSS (SEQ ID NO: 263)
- 45 BMS3h-38-217
EVQLLASGGGLVQPGGSLRLSCAASGFTFEFEEEMIWVRQAPGKGLEWVSAISRGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYWGQGT LTVSS (SEQ ID NO: 264)
- BMS3h-38-218
EVQLLASGGGLVQPGGSLRLSCAASGFTFEFEEEMIWVRQAPGKGLEWVSAISRHWSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYWGQGT LTVSS (SEQ ID NO: 265)
- BMS3h-38-219
EVQLLASGGGLVQPGGSLRLSCAASGFTFEFEEEMIWVRQAPGKGLEWVSSISRGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYWGQGT LTVSS (SEQ ID NO: 266)
- BMS3h-38-220
EVQLLASGGGLVQPGGSLRLSCAASGFTFEFEEEMIWVRQAPGKGLEWVSAISRIGNSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYWGQGT LTVSS (SEQ ID NO: 267)

- BMS3h-38-221
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEMIWVRQAPGKGLEWVSAISGHGWSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYGQGT LVTVSS (SEQ ID NO: 268)
- 5 BMS3h-38-222
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEMIWVRQAPGKGLEWVSAISRGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYGQGT LVTVSS (SEQ ID NO: 269)
- 10 BMS3h-38-223
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEMIWVRQAPGKGLEWVSAISGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYGQGT LVTVSS (SEQ ID NO: 270)
- 15 BMS3h-38-224
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEMIWVRQAPGKGLEWVSAISGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYGQGT LVTVSS (SEQ ID NO: 271)
- 20 BMS3h-38-225
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEMIWVRQAPGKGLEWVSAISGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYGQGT LVTVSS (SEQ ID NO: 272)
- 25 BMS3h-38-226
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEMIWVRQAPGKGLEWVSAISGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPLYDYGQGT LVTVSS (SEQ ID NO: 273)
- 30 BMS3h-38-227
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEMIWVRQAPGKGLEWVSAISGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYGQGT LVTVSS (SEQ ID NO: 274)
- 35 BMS3h-38-228
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEMIWVRQAPGKGLEWVSAISRNGFSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYGQGT LVTVSS (SEQ ID NO: 275)
- 40 BMS3h-38-229
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEMIWVRQAPGKGLEWVSAISRTGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYGQGT LVTVSS (SEQ ID NO: 276)
- 45 BMS3h-38-230
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEMIWVRQAPGKGLEWVSAISREGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYGQGT LVTVSS (SEQ ID NO: 277)
- 50 BMS3h-38-231
EVQLLASGGGLVQPGGSLRLSCAASGFPFEEMIWVRQAPGKGLEWVSAISRQGWSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYGQGT LVTVSS (SEQ ID NO: 278)
- 55 BMS3h-38-232
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEMIWVRQAPGKGLEWVSAISRGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYGQGT LVTVSS (SEQ ID NO: 279)
- 60 BMS3h-38-233
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEMIWVRQAPGKGLEWVSAISRTGYSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRYDYGQGT LVTVSS (SEQ ID NO: 280)

- 5 BMS3h-38-234
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEMIIWVRQAPGKGLEWVSAISRNGRSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (SEQ ID NO: 281)
- BMS3h-38-235
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEMIIWVRQAPGKGLEWVSAISRNGYSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (SEQ ID NO: 282)
- 10 BMS3h-38-236
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEMIIWVRQAPGKGLEWVSAISRNGSSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (SEQ ID NO: 283)
- 15 BMS3h-38-237
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEMIIWVRQAPGKGLEWVSAISRNGWSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (SEQ ID NO: 284)
- 20 BMS3h-38-238
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEMIIWVRQAPGKGLEWVSAISRNGYSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (SEQ ID NO: 285)
- 25 BMS3h-38-239
EVQLLASGGGLVQPGGSLRLSCAASGFTFEEMIIWVRQAPGKGLEWVSAISRNGMSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (SEQ ID NO: 286)
- BMS3h-38-240
EVQLLES GGGLVQPGGSLRLSCAASGFTFEEMIIWVRQAPGKGLEWVSAISRNGYSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCGKEPFRYDYGQGT LVTVSS (SEQ ID NO: 287)
- 30 BMS3h-41-1
EVQLLES GGLVQPGGSLRLSCAASGFTFEHEMIIWVRQAPGKGLEWVSSISGNGANTYYADSVKGRFTISRDN SKNTL
YLQMNSLR PEDTAVYYCAKEPLRFDYWGQGT LVTVSS (SEQ ID NO: 288)
- 35 BMS3h-41-2
EVQLLES GGLVQPGGSLRLSCAASGSTFTEYEMIIWVRQAPGKGLEWISSISGNGANTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYFCAKEPLRFDYWGQGT LVTVSS (SEQ ID NO: 289)
- 40 BMS3h-41-3
EVQLLEPGGGLVQPGGSLRLSCAASGFTFTEYEMIIWVRKAPGKGMWVSSISGNGANTYYADSVKGRFTISRDN SKNML
YLQMNSLR AEDTAVYYCAKEPLRFYWGQGT LVTVSS (SEQ ID NO: 290)
- 45 BMS3h-41-4
EVQLLD SGGLVQPGGSLRLSCAASGFTFTEYEMIIWVRQAPGKGLEWVSSISGNGANTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKEPLRFDYWGRT LVTVSS (SEQ ID NO: 291)
- BMS3h-41-5
EVQLLG SGGLVQPGGSLRLSCAASGFTFTEYEMIIWVRQAPGKSLWVSSISGNGANTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKEPLRYDDWGQGT LVTVSS (SEQ ID NO: 292)

- BMS3h-41-6
EVQPLESGGGLVQPGGSLRLSCASGFTFNEYEMIWVRQAPGKGLEWVSSISGNGANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDYWGQGLTVTVSS (SEQ ID NO: 293)
- 5 BMS3h-41-7
EVQPLESGGGLVQPGGSLRLSCASGFTFAEYEMIWVRQAPGKGLEWVSSISGNGANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDYWGQGLTVTVSS (SEQ ID NO: 294)
- BMS3h-41-8
10 EVQLDPPGGGLVQPGGSLRLSCASGFTFTESEMIWVRQAPGKGLEWVSSISGNGANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDYWGQGLTVTVSS (SEQ ID NO: 295)
- BMS3h-41-9
15 EVQLLEPGGGLVQPGGSLRLSCASGFTFTEYEMIWRKAPGKGMWVSSISGNGANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRPEDTAVYYCAKEPLRFDDWGQGLTVTVSS (SEQ ID NO: 296)
- BMS3h-41-10
20 EVQLLESGVGLVQPGGSLRLSCASGFTFTEYEMIWRKAPGKGLEWVSSISGNGANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDNWGQGLTVTVSS (SEQ ID NO: 297)
- BMS3h-41-11
25 EVQLLESRGGLVQPGGSLRLSCASGFTFTEHEMIWVRQAPGKGLEWVSSISGNGANTYYADSVKGRFSVSRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDYWGQGLTVTVSS (SEQ ID NO: 298)
- BMS3h-41-12
30 EVQPLESGGGLVQPGGSLRLSCASGFTFTEYEMIWVRQAPGKGLEWVSSISGNGANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDYWGQGLTVTVSS (SEQ ID NO: 299)
- BMS3h-41-13
35 EVQLLESAGGLVQPGGSLRLSCASGFTFAEYEMIWVRQAPGKGLEWVSSISGNGANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDYWGQGLTVTVSS (SEQ ID NO: 300)
- BMS3h-41-14
40 EVQLLEPGGGLVQPGGSLRLSCASGFTFTEYEMIWVRQAPGKGLEWVSSISGNGANTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPLRFDNWGQGLTVTVSS (SEQ ID NO: 301)
- BMS3h-43-1
45 EVQLLESGGGLVQPGGSLRLSCTASGFTFNMYEMSWVRQAPGKGLEWVSGISRRGFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDLRYARFDYSGQGLTVTVSS (SEQ ID NO: 302)
- BMS3h-43-2
50 EEQLLESGGGLVQPGGSLRLSCTASGFTFNMYEMSWVRQAPGKGLEWVSGISRRGFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYATRYARFDYWGQGLTVTVSS (SEQ ID NO: 303)
- BMS3h-43-3
55 EVQLLESGGGLVQPGGSLRLSCTASGFTFNMYEMSWVRQAPGKGLEWVSGISRRGFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYWGQGLTVTVSS (SEQ ID NO: 304)
- BMS3h-43-4
60 EVQLLESGGGLVQPGGSLRLSCTASGFTFNMYEMSWVRQAPGKGLEWVSGISRRGFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYWGQGLTVTVSS (SEQ ID NO: 305)

- 5 BMS3h-43-5
EVQLLESGGGLVQPGGSLRLSCTASGFTFNTYEMSWVRQAPGKGLEWVSGIGRRGFTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDLRYARFDYSGQGLTVTVSS (SEQ ID NO: 306)
- 10 BMS3h-43-6
EVQLLESGGGLVQPGGSLRLSCTASGFSFNMYEMSWVRQAPGKGLEWVSGISRRGYIYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYWGRGTLTVTVSS (SEQ ID NO: 307)
- 15 BMS3h-43-7
EVQLLESGGGLVQPGGSLRLSCTASGFAFNMYEMSWVRQAPGKGLEWVSGISRHGFTTYADSVKGRFTVSRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDMRYARSDYWGGQGLTVTVSS (SEQ ID NO: 308)
- 20 BMS3h-43-8
EVQLLESGGGLVQPGGSLRLSCTASGFTFNMYSWVRQAPGKGLEWVSGISRRGFTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYFCAKEPITYDMRYARSDYWGGQGLTVTVSS (SEQ ID NO: 309)
- 25 BMS3h-43-9
EVQLLESGGGLVQPGGSLRLSCTASGFTFNMYSWVRQAPGKGLEWVSGISRRGFTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYSGGLTMVTVSS (SEQ ID NO: 310)
- 30 BMS3h-43-10
EVQLLESGGGLVQPGGSLRLSCTASGFTFNMYSWVRQAPGKGLEWVSGISRRGFTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYSGQGLTVTVSS (SEQ ID NO: 311)
- 35 BMS3h-43-11
EVQLLESGGGLVQPGGSLRLSCTASGFTFNMYSWVRKAPGKGLEWVSGISRHGFTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYWGGQGLTVTVSS (SEQ ID NO: 312)
- 40 BMS3h-43-12
EVQLFESGGGLVQPGGSLRLSCTASGFTFNMYSWVRQAPGKGLEWVSGISRRGFTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYWGRGTLTVTVSS (SEQ ID NO: 313)
- 45 BMS3h-43-13
EVQLLESGGGLVQPGGSLRLSCTASGFTFNMYSWVRQAPGKGLEWVSGISRRGFTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYWGRGTLTVTVSS (SEQ ID NO: 314)
- BMS3h-43-14
EVQLLESGGGSVQPGGSLRLSCTASGFSFNMYEMSWVRQAPGKGLEWVSGISRRGFTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYWGGQGLTVTVSG (SEQ ID NO: 315)
- BMS3h-43-15
EVQLLESGGGLVQPGGSLRLSCTASGFTFNMYSWVRKAPGKGLEWVSGISRRGFTTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYWGGQGLTVTVSS (SEQ ID NO: 316)
- BMS3h-56-1
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPTFEDWGQGLTVTVSS (SEQ ID NO: 317)

- BMS3h-56-2
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDWGQGT LVTVSS (SEQ ID NO: 318)
- 5 BMS3h-56-3
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCTKLPFI FEYWGQGT LVTVSS (SEQ ID NO: 319)
- 10 BMS3h-56-4
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFMFDRGQGT LVTVSS (SEQ ID NO: 320)
- 15 BMS3h-56-5
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDWGQGT LVTVSS (SEQ ID NO: 321)
- 20 BMS3h-56-6
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFI FDNRGQGT LVTVSS (SEQ ID NO: 322)
- 25 BMS3h-56-7
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTSVYHCAKPPFI FDWGP GT LVTVSS (SEQ ID NO: 323)
- 30 BMS3h-56-8
EVQLLESGGGLVQPGGSRRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFI FDWGQGT LVTVSS (SEQ ID NO: 324)
- 35 BMS3h-56-9
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFMFDRGQGT LVTVSS (SEQ ID NO: 325)
- 40 BMS3h-56-10
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNML
YLQMNSLRAEDTAVYYCAKLPFMFDRGQGT LVTVSS (SEQ ID NO: 326)
- 45 BMS3h-56-11
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFMFDRGQGT LVTVSS (SEQ ID NO: 327)
- 50 BMS3h-56-12
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCLKLPFI FDYWGQGT LVTVSS (SEQ ID NO: 328)
- 55 BMS3h-56-13
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRADDTAVYHCTKLPFI FDYWGQGT LVTVSS (SEQ ID NO: 329)
- 60 BMS3h-56-14
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGMVLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFFD SRGQGT LVTVSS (SEQ ID NO: 330)

- 5 BMS3h-56-15
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWVRRAPGKGLERVSAINPQGTRITYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPFTFEDWGQGLTVTVSS (SEQ ID NO: 331)
- 10 BMS3h-56-16
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWVRRAPGKGLERVSAINPQGTRITYYADSV MGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPFTFEDWGQGLTVTVSS (SEQ ID NO: 332)
- 15 BMS3h-56-17
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWVRRAPGKGLERVSAINPQGTRITYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPFTFEDWGQGLTVTVSS (SEQ ID NO: 333)
- 20 BMS3h-56-18
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWVRRAPGKGLERVSAINPQGTRITYYADSVKGRFTISRDN SKNML
YLQMNSLR AEDTAVYYCAKLPFTFEDWGQGLTVTVSS (SEQ ID NO: 334)
- 25 BMS3h-56-19
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWVRRAPGKGLERVSAINPQGTRITYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYHCAKLPFTFEDWGQGLTVTVSS (SEQ ID NO: 335)
- 30 BMS3h-56-20
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWVRRAPGKGLERVSAINPQGTRITYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCTKLPFTFEDWGQGLTVTVSS (SEQ ID NO: 336)
- 35 BMS3h-56-21
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWVRRAPGKGLERVSAINPQGTRITYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCLKLPFTFEDWGQGLTVTVSS (SEQ ID NO: 337)
- 40 BMS3h-56-22
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWVRRAPGKGLERVSAINPQGTRITYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYHCTKLPFTFEYWGQGLTVTVSS (SEQ ID NO: 338)
- 45 BMS3h-56-23
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWVRRAPGKGLERVSAINPQGTRITYYADSV MGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKEPYSFDSWGQGLTVTVSS (SEQ ID NO: 339)
- BMS3h-56-24
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWVRRAPGKGLERVSAINPQGTRITYYADSV MGRFTISRDN SKNTL
YLQMNSLR AEDTAVYHCAKEPYSYDWGQGLTVTVSS (SEQ ID NO: 340)
- BMS3h-56-25
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWVRRAPGKGLERVSAINPQGTRITYYADSV MGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPFTFDDWGQGLTVTVSS (SEQ ID NO: 341)
- BMS3h-56-26
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWVRRAPGKGLERVSAINPQGTRITYYADSV MGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPFMFDDRQGLTVTVSS (SEQ ID NO: 342)

- BMS3h-56-27
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGRTRYADSV MGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPFMFDDWGQGT LVT VSS (SEQ ID NO: 343)
- 5 BMS3h-56-28
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYELMWVRQAPGKGLERVSAINPQGRTRYADSV MGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPFTFDDWGQGT LVT VSS (SEQ ID NO: 344)
- 10 BMS3h-56-29
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYELMWVRQAPGKGLERVSAINPQGRTRYADSV MGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPFMFDDRGQGT LVT VSS (SEQ ID NO: 345)
- 15 BMS3h-56-30
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMMWVRQAPGKGLERVSAINPQGRTRYADSV MGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPFTFDDWGQGT LVT VSS (SEQ ID NO: 346)
- 20 BMS3h-56-31
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMMWVRQAPGKGLERVSAINPQGRTRYADSV MGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPFMFDDRGQGT LVT VSS (SEQ ID NO: 347)
- 25 BMS3h-56-32
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGRTRYADSV MGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPFTFDDWGQGT LVT VSS (SEQ ID NO: 348)
- 30 BMS3h-56-33
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGRTRYADSV MGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPFMFDDRGQGT LVT VSS (SEQ ID NO: 349)
- 35 BMS3h-56-202
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGRTRYADSV KGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPTYFSDRGQGT LVT VSS (SEQ ID NO: 350)
- 40 BMS3h-56-203
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGRTRYADSV KGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPFFFEWGQGT LVT VSS (SEQ ID NO: 351)
- 45 BMS3h-56-204
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGRTRYADSV KGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPTYFKDWGQGT LVT VSS (SEQ ID NO: 352)
- 50 BMS3h-56-205
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGRTRYADSV KGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPFYFSEWGQGT LVT VSS (SEQ ID NO: 353)
- 55 BMS3h-56-206
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGRTRYADSV KGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPFMFEDWGQGT LVT VSN (SEQ ID NO: 354)
- 60 BMS3h-56-207
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGRTRYADSV KGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPFFFEWGQGT LVT VSS (SEQ ID NO: 355)

- 5 BMS3h-56-208
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMDSLR AEDTAVYYCAKLPFYFSEWGQGLTVTVSS (SEQ ID NO: 356)
- 10 BMS3h-56-209
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPYGNLIYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPFTFEDWGQGLTVTVSS (SEQ ID NO: 357)
- 15 BMS3h-56-210
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPPGTLTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPFTFEDRGQGLTVTVSS (SEQ ID NO: 358)
- 20 BMS3h-56-211
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGLTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPFTFEDWGQGLTVTVSS (SEQ ID NO: 359)
- 25 BMS3h-56-212
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPMGGFTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPFTFEDWGQGLTVTVSS (SEQ ID NO: 360)
- 30 BMS3h-56-213
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGSHYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPFTFEDWGQGLTVTVSS (SEQ ID NO: 361)
- 35 BMS3h-56-214
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPSGGLTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPFTFDDRQGLTVTVSS (SEQ ID NO: 362)
- 40 BMS3h-56-215
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPHGSLTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPFTFDDWGQGLTVTVSS (SEQ ID NO: 363)
- 45 BMS3h-56-216
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPAGRLTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPFTFEDWGQGLTVTVSS (SEQ ID NO: 364)
- 50 BMS3h-56-217
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGSLTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPFTFEDWGQGLTVTVSS (SEQ ID NO: 365)
- BMS3h-56-218
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPFTFDDWGQGLTVTVSS (SEQ ID NO: 366)
- BMS3h-56-219
EVQLLESGGGLVQPGGSLRLSCADSGFTFPVEMWWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKLPFTFEDWGQGLTVTVSS (SEQ ID NO: 367)
- 50 BMS3h-56-220

- EVQLLES GGGVLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPYGGLTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLVTVSS (SEQ ID NO: 368)
- 5 BMS3h-56-221
EVQLLES GGGVLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGNHTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLVTVSS (SEQ ID NO: 369)
- 10 BMS3h-56-222
EVQLLES GGGVLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPHGGYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLVTVSS (SEQ ID NO: 370)
- 15 BMS3h-56-223
EVQLLES GGGVLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPPGMLTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLVTVSS (SEQ ID NO: 371)
- BMS3h-56-224
EVQLLES GGGVLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGLTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLVTVSS (SEQ ID NO: 372)
- 20 BMS3h-56-225
EVQLLES GGGVLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLVTVSS (SEQ ID NO: 373)
- 25 BMS3h-56-226
EVQLLES GGGVLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPSGGLTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLVTVSS (SEQ ID NO: 374)
- 30 BMS3h-56-227
EVQLLES GGGVLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPSGGLTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLVTVSS (SEQ ID NO: 375)
- BMS3h-56-228
EVQLLES GGGVLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPSGTLTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLVTVSS (SEQ ID NO: 376)
- 35 BMS3h-56-229
EVQLLES GGGVLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPYGSLTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLVTVSS (SEQ ID NO: 377)
- 40 BMS3h-56-230
EVQLLES GGGVLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLVTVSS (SEQ ID NO: 378)
- 45 BMS3h-56-231
EVQLLES GGGVLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGGTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLVTVSS (SEQ ID NO: 379)
- 50 BMS3h-56-232
EVQLLES GGGVLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGSHYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGLVTVSS (SEQ ID NO: 380)

- BMS3h-56-233
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPWGTLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 381)
- 5 BMS3h-56-234
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPNRGLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFADWGQGT LVTVSS (SEQ ID NO: 382)
- 10 BMS3h-56-235
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPWGQLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 383)
- 15 BMS3h-56-236
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPHGGLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 384)
- 20 BMS3h-56-237
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPAGMLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 385)
- 25 BMS3h-56-238
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPHGTLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 386)
- 30 BMS3h-56-239
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPWGSLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 387)
- 35 BMS3h-56-240
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPYGGLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 388)
- 40 BMS3h-56-241
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPAGFLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 389)
- 45 BMS3h-56-242
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPYGGLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 390)
- 50 BMS3h-56-243
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPWGGFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 391)
- 55 BMS3h-56-244
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPWGGLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 392)
- 60 BMS3h-56-245
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPYGGLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 393)

- 5 BMS3h-56-246
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGTLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGT LVTVSS (SEQ ID NO: 394)
- 10 BMS3h-56-247
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFEDWGRGT LVTVSS (SEQ ID NO: 395)
- 15 BMS3h-56-248
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPYGNLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 396)
- 20 BMS3h-56-249
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPHGGFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGT LVTVSS (SEQ ID NO: 397)
- 25 BMS3h-56-250
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPAGFYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 398)
- 30 BMS3h-56-251
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPAGGLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFDDWGQGT LVTVSS (SEQ ID NO: 399)
- 35 BMS3h-56-252
EVQLLES GGGGLVQPGGSLRLSCAASGFAFRDYEMWWVRQAPGKGLERVSAINPHGSLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFTFEDWGQGT LVTVSS (SEQ ID NO: 400)
- 40 BMS3h-56-253
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPAGGYTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYHCAKLPFTFEDWGQGT LVTVSS (SEQ ID NO: 401)
- 45 BMS3h-56-254
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFWFTEWGQGT LVTVSS (SEQ ID NO: 402)
- 50 BMS3h-56-255
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFMFSDRGQGT LVTVSS (SEQ ID NO: 403)
- BMS3h-56-256
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFLFQEWGQGT LVTVSS (SEQ ID NO: 404)
- BMS3h-56-257
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPTRFEDWGQGT LVTVSS (SEQ ID NO: 405)
- 50 BMS3h-56-258

- EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFYFHEWGQGLTVTVSS (SEQ ID NO: 406)
- BMS3h-56-259
5 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCGKEPFRDYWGQGLTVTVSS (SEQ ID NO: 407)
- BMS3h-56-260
10 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPTFFKDWGQGLTVTVSS (SEQ ID NO: 408)
- BMS3h-56-261
15 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPTFFQEWGQGLTVTVSS (SEQ ID NO: 409)
- BMS3h-56-262
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPLFHD RGQGLTVTVSS (SEQ ID NO: 410)
- 20 BMS3h-56-263
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPLFHDWGQGLTVTVSS (SEQ ID NO: 411)
- BMS3h-56-264
25 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPLFGFSEWGQGLTVTVSS (SEQ ID NO: 412)
- BMS3h-56-265
30 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPLFQDWGQGLTVTVSS (SEQ ID NO: 413)
- BMS3h-56-266
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPTFFHEWGQGLTVTVSS (SEQ ID NO: 414)
- 35 BMS3h-56-267
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPHYFKDWGQGLTVTVSS (SEQ ID NO: 415)
- 40 BMS3h-56-268
EVQLLESGGGLVQSGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPHYFEWGQGLTVTVSS (SEQ ID NO: 416)
- BMS3h-56-269
45 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPRFSDRGQGLTVTVSS (SEQ ID NO: 417)
- BMS3h-56-270
50 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMMWVRQAPGKGLERVSAINPQGTRITYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPTLFQDWGQGLTVTVSS (SEQ ID NO: 418)

- BMS3h-56-271
EVQLLES GGG LVQP GGS LRLSCAASGFTFRDYEMWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFYFQEWGQGT LVT VSN (SEQ ID NO: 419)
- 5 BMS3h-56-272
EVQLLES GGG LVQP GGS LRLSCAASGFTFRDYEMWVRQAPGKGLERVSAINPQGTRTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFWFQEWGQGT LVT VSS (SEQ ID NO: 420)
- 10 BMS3h-56-273
EVQLLES GGG LVQP GGS LRLSCAASGFTFRDYEMWVRQAPGKGLERVSAINPWGSLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFYFQEWGQGT LVT VSS (SEQ ID NO: 421)
- 15 BMS3h-56-274
EVQLLES GGG LVQP GGS LRLSCAASGFTFRDYEMWVRQAPGKGLERVSAINPWGSLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFWFQEWGQGT LVT VSN (SEQ ID NO: 422)
- 20 BMS3h-56-275
EVQLLES GGG LVQP GGS LRLSCAASGFTFRDYEMWVRQAPGKGLERVSAINPWGSLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFYFQEWGQGT LVT VSS (SEQ ID NO: 423)
- 25 BMS3h-56-276
EVQLLES GGG LVQP GGS LRLSCAASGFTFRDYEMWVRQAPGKGLERVSAINPWGSLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFFQEWGQGT LVT VSS (SEQ ID NO: 424)
- 30 BMS3h-56-277
EVQLLES GGG LVQP GGS LRLSCAASGFTFRDYEMWVRQAPGKGLERVSAINPWGSLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFFQEWGQGT LVT VSS (SEQ ID NO: 425)
- 35 BMS3h-56-278
EVQLLES GGG LVQP GGS LRLSCAASGFTFRDYEMWVRQAPGKGLERVSAINPWGGFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFYFQEWGQGT LVT VSS (SEQ ID NO: 426)
- 40 BMS3h-56-279
EVQLLES GGG LVQP GGS LRLSCAASGFTFRDYEMWVRQAPGKGLERVSAINPWGGFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFFQEWGQGT LVT VSN (SEQ ID NO: 427)
- 45 BMS3h-56-280
EVQLLES GGG LVQP GGS LRLSCAASGFTFRDYEMWVRQAPGKGLERVSAINPWGGFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFYFQEWGQGT LVT VSS (SEQ ID NO: 428)
- 50 BMS3h-56-281
EVQLLES GGG LVQP GGS LRLSCAASGFTFRDYEMWVRQAPGKGLERVSAINPWGGFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFFQEWGQGT LVT VSS (SEQ ID NO: 429)
- 55 BMS3h-56-282
EVQLLES GGG LVQP GGS LRLSCAASGFTFRDYEMWVRQAPGKGLERVSAINPWGGFTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFFQEWGQGT LVT VSS (SEQ ID NO: 430)
- 60 BMS3h-56-283
EVQLLES GGG LVQP GGS LRLSCAASGFTFRDYEMWVRQAPGKGLERVSAINPWGGLTYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKLPFYFQEWGQGT LVT VSS (SEQ ID NO: 431)

- 5 BMS3h-56-284
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWVRQAPGKGLERVSAINPWGGLTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYHCAKLPMFFEDWGQGLTVTSN (SEQ ID NO: 432)
- 10 BMS3h-56-285
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWVRQAPGKGLERVSAINPWGGLTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYCAKLPMFFHEWGQGLTVTVSS (SEQ ID NO: 433)
- 15 BMS3h-56-286
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWVRQAPGKGLERVSAINPWGGLTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYCAKLPMFFQEWGQGLTVTVSS (SEQ ID NO: 434)
- 20 BMS3h-56-287
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWVRQAPGKGLERVSAINPWGGLTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYCAKLPMFFHEWGQGLTVTVSS (SEQ ID NO: 435)
- 25 BMS3h-56-288
EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWVRQAPGKGLERVSAINPWGGLTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYHCAKLPMFFEDWGQGLTVTVSS (SEQ ID NO: 436)
- 30 BMS3h-106-1
EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYHMQWVRAPGKGLEWVSMIDADGLGTYADPVKGRFTISRDN SKNTL
YLQMNSLR AKDTAVYVCARPGPQFGQFDYLGQGLTVTVSS (SEQ ID NO: 437)
- 35 BMS3h-106-2
EVQLFESGGGLVQTGGSLRLSCAASGFTFSTYHMQWVRAPGKGLEWVSMIDADGLGTYADPVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYVCVKPGPQFGQYDYWGQGLTVTVSS (SEQ ID NO: 438)
- 40 BMS3h-107-1
EVQLLESGGGLVQPGGSLRLSCSASGFTFSGYDMQWVRAPGKGLEWVSTISASGVYTYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYCAKYPNRFALNSFDYRGRGLTVTVSS (SEQ ID NO: 439)
- 45 BMS3h-107-2
EVQLLESGGGLVQPGGSLRLSCAASGFTFSGYDMQWVRAPGRGLEWVSTISASGVYTYTDSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYCYKYPNRFARNNFDYWGQGLTVTVSS (SEQ ID NO: 440)
- 50 BMS3h-131-1
DILMTQSPSSLSASVGDRTITCRANSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSRFSGSGSDFTLTISSLQ
PEDFATYYCVQNAVWPGTFSQGTKVEIKR (SEQ ID NO: 441)
- 55 BMS3h-131-2
DIQMTQSPSSLSASVGDRTITCRADSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSRFSGSGSDFTLTISSLQ
PEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO: 442)
- 60 BMS3h-131-3
DIQMTVSPSSLSASVGDRTITCRADSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSRFSGSGSDFTLTISSLQ
PEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO: 443)
- 65 BMS3h-131-4

- DIQMTQSPSSLSASVGDRVITITCRANSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO: 444)
- BMS3h-131-5
5 DIQMTQSPSSLSASVGDRVITITCRANSSILWALAWYQQKPGKAPKLLIESSTGLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO: 445)
- BMS3h-131-6
10 DIQMTVSPSSLSASVGDRVITITCRANSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO: 446)
- BMS3h-131-7
15 DIQMTQSPSSLSASVGDRVITITCRADSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCVQNAVWPGTFDQGTKVEIKR (SEQ ID NO: 447)
- BMS3h-131-8
20 DIQMTQSPSSLSASVGDRVITITCRANSSILWALAWYQQKPGKAPELLIESSSGLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO: 448)
- BMS3h-131-9
25 DIQMTQSPSSLSASVGDRVITITCRANSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCVQNAVWPGTFGQGTKVENKR (SEQ ID NO: 449)
- BMS3h-131-10
30 DIQMTQSPSSLSASVGDRVITITCRANSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO: 450)
- BMS3h-131-11
35 DIQMTQSPSSLSASVGDRVITITCRANSSILWALAWYQQKPGKAPKLLIESSSGLQSGIPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO: 451)
- BMS3h-131-12
40 DIQMTQSPSSLSASVGDRVITITCRANSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO: 452)
- BMS3h-131-13
45 DIQMTQSPSSLSASVGDRVITITCRANSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO: 453)
- BMS3h-131-14
50 DIQMTQSPSSLSASVGDRVITITCRANSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSRFSGSGSGTDFTLTISGLQ
PEDFATYYCVQNAVWPGTFDQGTKVEIKR (SEQ ID NO: 454)
- BMS3h-131-15
DIQMTQSPSSLSASVGDRVITIPCRANSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO: 455)
- BMS3h-193-1
DIQMAQSPSSLSASVGDRVITITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISSLQ
50 PEDFATYYCHQYASPLTLGQGTKVEIKR (SEQ ID NO: 456)

- BMS3h-193-2
DIQMTQSPSSLSASVGDSVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYASPLTFGQGTNVEIKR (SEQ ID NO: 457)
- 5 BMS3h-193-3
DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFAAYYCHQYESPPLTFGQGTKEIKR (SEQ ID NO: 458)
- BMS3h-193-4
10 DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKEIKR (SEQ ID NO: 459)
- BMS3h-193-5
15 DIQMTQSPSSLSASVGERVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDSATYYCHQYASPLTLGQGTKEIKR (SEQ ID NO: 460)
- BMS3h-193-6
20 DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYASPLTLGQGTKEIKR (SEQ ID NO: 461)
- BMS3h-193-7
DIQITQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKEIKR (SEQ ID NO: 462)
- 25 BMS3h-193-8
DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKEIKR (SEQ ID NO: 463)
- BMS3h-193-9
30 DIQITQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTEFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKEIKR (SEQ ID NO: 464)
- BMS3h-193-10
35 DIQMSQSPSTLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKEIKR (SEQ ID NO: 465)
- BMS3h-193-11
40 DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKEIKR (SEQ ID NO: 466)
- BMS3h-193-12
DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKEIKR (SEQ ID NO: 467)
- 45 BMS3h-193-13
DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKEIKR (SEQ ID NO: 468)
- BMS3h-193-14
50 DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKEIKR (SEQ ID NO: 469)

- 5 BMS3h-193-15
DIQMTQSPSSLSASVGDRVTITCRASRTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCHPYESPPLTFGQGTKVEIKR (SEQ ID NO: 470)
- BMS3h-193-16
DIQMTQSPSSLSASVGDRVTITCRASQAIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCHQYASPLTLGQGTKVEIKR (SEQ ID NO: 471)
- 10 BMS3h-193-17
NIQMTQSPSSLSASVGDRVTITCRASQAIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 472)
- 15 BMS3h-193-18
DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 473)
- 20 BMS3h-193-19
DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTEFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 474)
- 25 BMS3h-193-20
DIQMTQTPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVVEIKR (SEQ ID NO: 475)
- BMS3h-193-21
DIQMTQSPSSLSASVGDSVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 476)
- 30 BMS3h-193-22
HIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 477)
- 35 BMS3h-193-23
DVQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLSRLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCHQYASPLTFGQGTKVEIKR (SEQ ID NO: 478)
- 40 BMS3h-193-24
DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVVEIKR (SEQ ID NO: 479)
- 45 BMS3h-193-25
DIQMTQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 480)
- BMS3h-193-26
DIQMTQSPSSLSASVGDRVTITCRASQPIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 481)
- 50 BMS3h-193-27

- DIQMTQSPSSLSASVGDRTITCRASQTIGRRLNWYQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 482)
- BMS3h-193-28
5 DIQMTQSPSSLSASVGDRTITCRASQSIERRLNWYQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIIR (SEQ ID NO: 483)
- BMS3h-193-29
10 DIQMTQSPSSLSASVGDRTITCRASQTIERRLNWYQKPGKAPKLLIYLATRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 484)
- BMS3h-193-30
15 DIQMTQSPSSLSASVGDRTITCRASQSIERRLNWYQKPGKAPKLLIYLASRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 485)
- BMS3h-193-2501
DIQMTQSPSSLSASVGDRTITCRASQTIERRLNWYQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQFHPPLTFGQGTKVEIKR (SEQ ID NO: 486)
- 20 BMS3h-193-2502
DIQMTQSPSSLSASVGDRTITCRASFIDRRLNWYQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 487)
- BMS3h-193-2503
25 DIQMTQSPSSLSASVGDRTITCRASSTIGRRLNWYQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 488)
- BMS3h-193-2504
30 DIQMTQSPSSLSASVGDRTITCRASSQIGRRLNWYQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 489)
- BMS3h-193-2505
35 DIQMTQSPSSLSASVGDRTITCRASERIGRRLNWYQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 490)
- BMS3h-193-2506
DIQMTQSPSSLSASVGDRTITCRASQQIGRRLNWYQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 491)
- 40 BMS3h-193-2507
DIQMTQSPSSLSASVGDRTITCRASQPIARRLNWYQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 492)
- BMS3h-193-2508
45 DIQMTQSPSSLSASVGDRTITCRASGNIGRRLNWYQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 493)
- BMS3h-193-2509
50 DIQMTQSPSSLSASVGDRTITCRASRNIDRRLNWYQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFTLTISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 494)

- BMS3h-193-2510
DIQMTQSPSSLSASVGDRTITCRASQSIGRRNLNWKQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFLTITISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 495)
- 5 BMS3h-193-2511
DIQMTQSPSSLSASVGDRTITCRASQNIQTRNLNWKQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFLTITISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 496)
- 10 BMS3h-193-2512
DIQMTQSPSSLSASVGDRTITCRASEVIGRRNLNWKQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFLTITISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 497)
- 15 BMS3h-193-2513
DIQMTQSPSSLSASVGDRTITCRASEATIGRRNLNWKQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFLTITISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 498)
- 20 BMS3h-193-2514
DIQMTQSPSSLSASVGDRTITCRASQIARRNLNWKQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFLTITISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 499)
- 25 BMS3h-193-2515
DIQMTQSPSSLSASVGDRTITCRASLNIGRRNLNWKQKPGKAPRLLIYLATRLQSGVPSRFSGSGSGTDFLTITISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 500)
- 30 BMS3h-193-2516
DIQMTQSPSSLSASVGDRTITCRASQTIERRNLNWKQKPGKAPRLLIYLSKQLQSGVPSRFSGSGSGTDFLTITISLQ
PEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 501)
- 35 BMS3h-198-1
EVQLLESGGGLVQPGGSLRLSCAASGSTIAGYEMMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRRAEDTAVYYCARDPYSFDYWGQGLTVTVSS (SEQ ID NO: 502)
- 40 BMS3h-198-2
EVQPLESGGGLVQPGGSLRLSCAASGFTFAGYEMMWVRQAPGKGLERISATISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRRAEDTAVYYCARDPYSFDYWGQGLTVTVSS (SEQ ID NO: 503)
- 45 BMS3h-198-3
EVQLLESGGGLVQPGGSLRLSCAATGSTFAGYEMMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRRAEDTAVYYCARDPYSFDYWGQGLTVTVSS (SEQ ID NO: 504)
- 50 BMS3h-198-4
EVQLLESGGGLVQPGGSLRLSCAASGLTFAGYEMMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRRAEDTAVYHCARDPYSFDYWGQGLTVTVSS (SEQ ID NO: 505)
- 55 BMS3h-198-5
EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRRAEDTAVYHCAKEPYSFDYWGQGLTVTVSS (SEQ ID NO: 506)
- 60 BMS3h-198-6
EVQLLESGGGLVQPGGSLRLSCAASGSTFAGYEMMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRPEDTAVYYCVKDPYSFDYWGQGLTVTVSS (SEQ ID NO: 507)

- 5 BMS3h-198-7
EVQLLESGGGLVQPGGSLRLSCAASGSIAGYEMWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCARDPYSFDYWGGQGLTVTVSS (SEQ ID NO: 508)
- 10 BMS3h-198-8
EVQLLESGGGLVQPGGSLRLSCAASGSIAGYEMWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKDPYSFDYWGGQGLTVTVSS (SEQ ID NO: 509)
- 15 BMS3h-198-9
EVQLLESGGGLVQPGGSLRLSCAASGSIAGYEMWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKEPYSFDYWGGQGLTVTVSS (SEQ ID NO: 510)
- 20 BMS3h-198-10
EVQLLESGGGLVQPGGSLRLSCAASGSIAGYEMWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKDPYSFDYWGGQGLTVTVSS (SEQ ID NO: 511)
- 25 BMS3h-198-11
EVQLLESGGGLVQPGGSLRLSCAASGSIAGYEMWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCARDPYSFDYWGGQGLTVTVSS (SEQ ID NO: 512)
- BMS3h-198-12
EVQLLESGGGLVQPGGSLRLSCAASGSIAGYEMWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKDPYSFDYWGGQGLTVTVSS (SEQ ID NO: 513)
- 30 BMS3h-198-13
EVQLLESGGGLVQPGGSLRLSCAASGSIAGYEMWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKEPYSFDYWGGQGLTVTVSS (SEQ ID NO: 514)
- 35 BMS3h-198-14
EVQLLESGGGLVQPGGSLRLSCAASGSIAGYEMWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDTKNTL
YLQMNSLRAEDTAVYYCAKDPYSFDYWRQGLTVTVSS (SEQ ID NO: 515)
- 40 BMS3h-198-15
EVQLLESGGGLVQPGGSLRLSCAASGSIAGYEMWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCARDPYSFDYWGGQGLTVTVSS (SEQ ID NO: 516)
- 45 BMS3h-198-16
EVQLLESGGGLVQPGGSLRLSCAASGSIAGYEMWVRQAPGKGLERISAIISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCAKDPYSFDYWGGQGLTVTVSS (SEQ ID NO: 517)
- BMS3h-198-17
EVQLLESGGGLVQPGGSLRLSCAASGSIAGYEMWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCARDPYSFDYWGGQGLTVTVSS (SEQ ID NO: 518)
- 50 BMS3h-198-18
EVQLLESGGGLVQPGGSLRLSCAASGLTIFAGYEMWVRAPGKGLERVAISGSGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLRAEDTAVYYCARDPYSFDYWGGQGLTVTVSS (SEQ ID NO: 519)
- BMS3h-198-19

- EVQLLES GGGGLVQPGGSLRLSCAASGFTFAGYELWVRQAPGKGLERVSAISGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLR AEDTAVYYCARDPYSFDYRGQGLTVTVSS (SEQ ID NO: 520)
- BMS3h-198-20
5 EVQLLES GGGGLVQPGGSLRLSCAAPGFTFAGYEMWVRQAPGKGLERVSAISGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLR AEDTAVYYCAKEPYSFDYWGQGLTVTVSS (SEQ ID NO: 521)
- BMS3h-198-21
10 EVQLLES GGGGLVQPGGSLRLSCAASGLTFAGYEMWVRQAPGKGLERVSAISGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLR AEDTAVYYCARDPYSFDYWGRGTLTVTVSS (SEQ ID NO: 522)
- BMS3h-198-22
15 EVQLLES GGGGLVQPGGSLRLSCAASGFTFAGYEMWVRQAPGKGLERVSAISGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLR AEDTAVYYCAKEPYSYDYWGHTLTVTVSS (SEQ ID NO: 523)
- BMS3h-198-23
20 EVQPLESGGGGLVQPGGSLRLSCAASGFTFAGYEMWVRQAPGKGLERVSAISGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLR AEDTGVYYCARDPYSFDYWGQGLTVTVSS (SEQ ID NO: 524)
- BMS3h-198-24
25 EVQLLES GGGGLVQPGGSLRLSCAASGFTFAGYEMWVRQAPGKGLERVSAISGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLR AEDTAVYYCAKEPYSFDSWGQGLTVTVSS (SEQ ID NO: 525)
- BMS3h-198-25
25 EAQLLES GGGGLVQPGGSLRLSCAASGLTFAGYEMWVRQAPGKGLERVSAISGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLR AEDTAVYYCARDPYSFDYWGQGLTVTVSS (SEQ ID NO: 526)
- BMS3h-198-26
30 EVQLLES GGGGLVQPGGSLRLSCAASGSTFAGYEMWVRQAPGKGLERVSAISGGSTYYADSVKGRFISRDDSKNTL
YLQMNSLR AEDTAVYYCAKEPYSFDHWGQGLTVTVSS (SEQ ID NO: 527)
- BMS3h-198-27
35 EVQLLES GGGGLVQPGGSLRLSCAASGSTFAGYEMWVRQAPGKGLERVSAISGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLR AEDTAVYYCARDPYSFDYWGQGLTVTVSS (SEQ ID NO: 528)
- BMS3h-198-28
EVQLLES GGGGLVQPGGSLRLSCAASGFTFAGYEMWVRQAPGKGLERVSAISGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLR AEDTAVYYCAKDPYSFDNWGQGLTVTVSS (SEQ ID NO: 529)
- BMS3h-198-29
40 EVQLLES GGGGLVQPGGSLRLSCAASGFTFAGYEMWVRQAPGKGLERVSAISGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLR AEDTAVYYCAKEPYSFDHRGQGLTVTVSS (SEQ ID NO: 530)
- BMS3h-198-30
45 EVQLLES GGGGLVQPGGSLRLSCAASGYTFAGYEMWVRQAPGKGLERVSAISGGSTYYADSVKGRFTISRDDSKNTL
YLQMNSLR AEDTAVYYCAKEPYSFDHRGQGLTVTVSS (SEQ ID NO: 531)
- BMS3h-198-31
50 EVQLLES GGGGLVQPGGSLRLSCAASGFTFAGYEMWVRQAPGKGLERVSAISGGSTYYADSVKGRFTISRDNKNTL
YLQMNSLR AEDTAVYYHCAKEPYSYDYWGQGLTVTVSS (SEQ ID NO: 532)

- BMS3h-198-32
EVQLLES GGG LVQP GGS LRLSCAASGFTFAGYEMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKDPYSFDNWGGGTLVTVSS (SEQ ID NO: 533)
- 5 BMS3h-198-33
EVQLLES GGG LVQP GGS LRLSCAASGFTFAGYEMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDS KNTL
YLQMNSLRAEDTAVYYCAKEPYSYDYWGQGLVTVSS (SEQ ID NO: 534)
- 10 BMS3h-198-34
EVQLLES GGG LVQP GGS LRLSCAASGFTFAGYEMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDS KNTL
YLQMNSLRAEDTAVYYCAKDPYSFDNWGGGTLVTVSS (SEQ ID NO: 535)
- 15 BMS3h-198-35
EVQLLES GGG LVQP GGS LRLSCAASGFTFAGYEMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDS KNTL
YLQMNSLRAEDTAVYYCAKEPYSYDYWGQGLVTVSS (SEQ ID NO: 536)
- 20 BMS3h-198-36
EVQLLES GGG LVQP GGS LRLSCAASGFTFAGYEMWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDS KNTL
YLQMNSLRAEDTAVYYCAKDPYSFDNWGGGTLVTVSS (SEQ ID NO: 537)
- 25 BMS3h-198-37
EVQLLES GGG LVQP GGS LRLSCAASGFTFAGYELWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDS KNTL
YLQMNSLRAEDTAVYYCAKDPYSFDYRGQGLVTVSS (SEQ ID NO: 538)
- 30 BMS3h-198-38
EVQLLES GGG LVQP GGS LRLSCAASGFTFAGYELWVRQAPGKGLERVSATISGSGGSTYYADSVKGRFTISRDDS KNTL
YLQMNSLRAEDTAVYYCARDPYSFDYWGQGLVTVSS (SEQ ID NO: 539)
- 35 BMS3h-202-1
EVQLLES GGG LVQP GGS LRLSCAASGFTFPTAEMLVVRKAPGKGLEWVSSISASGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPVS YVATFDYWGQGLVTVSS (SEQ ID NO: 540)
- 40 BMS3h-202-2
EVQLLES GGG LVQP GGS LRLSCAASGFTFPTAEMLVVRQAPGKGLEWVSSISASGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPVS YVATFDYWGQGLVTVSS (SEQ ID NO: 541)
- 45 BMS3h-202-3
EVQLLES GGG LVQP GGS LRLSCAASGFTFPTAEMVVRKAPGMGLEWVSSISASGGYTYADSVKGRFTISRDN SKNML
YLQMNSLRAEDTAVYYCAKEPVS YVATFDYWGQGLVTVSS (SEQ ID NO: 542)
- 50 BMS3h-202-4
EVQLLES GGG LVQP GGS LRLSCAASGFTFPTAEMVVRQAPGKGLEWVSSISASGGSTYYADSVKGRFISRDDS KNTL
YLQMNSLRAEDTAVYYCAKEPVS YVATFDYWGHALVTVSS (SEQ ID NO: 543)
- 55 BMS3h-202-5
EVQLLES GGG LVQP GGS LRLSCAASGFTFPTAEMLVVRQAPGKGLEWVSSISASGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLRAEDTAVYYCAKEPVS YVATFDYWGQGLVTVSS (SEQ ID NO: 544)
- 60 BMS3h-202-6
EAQLLES GGG LVQP GGS LRLSCAASGFTFPTAEMVVRQAPGKGLEWISSISASGGSTYYADSVKGRFTISRDN SKNTL
YLQNLNSLRAEDTAVYYCAKEPVS YVATFDYWGRTLVTVSS (SEQ ID NO: 545)

- BMS3h-202-7
EVQLLES GGGVLVQPGGSLRLSCAASGFTFPTAEMLWVRQAPGKGLEWVSSISASGGSTYYADSVKGRFTISRDN SKSTL
YLQMNSLR AEDTAVYYCAKEPVSYVATFDYWGP GALVTVSS (SEQ ID NO: 546)
- 5 BMS3h-202-8
EVQLLES GGGVLVQPGGSLRLSCAASGFTFPTAEMLWVRQAPGKGLEWVSSISASGGSTYYADSVKGRFTISRDN SKNTL
FLQMNSLR AEDTAVYYCAKEPVSYVATFDYWGGT LVTVSS (SEQ ID NO: 547)
- 10 BMS3h-202-9
EVQLLES GGGVLVQPGGSLRLSCAASGFTFPTAEMLWVRQAPGKGLEWVSSISASGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKEPVSYVATFDYWGP GALVTVSS (SEQ ID NO: 548)
- 15 BMS3h-202-10
EVQLLES GGGVLVQPGGSLRLSCAASGFTFPTAEMLWVRQAPGKGLEWVSSISASGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDTAVYYCAKEPVVYVATFDYWGGT LVTVSS (SEQ ID NO: 549)
- 20 BMS3h-202-11
EVQLLES GGGVLVQPGGSLRLSCAASGFTFPTAEMLWVRQAPGKGLEWVSSISASGGSTYYADSVKGRFTISRDN SKNTL
YLQMNSLR AEDAAYYYCAKEPVSYVATFDYWGGT LVTVSS (SEQ ID NO: 550)
- 25 BMS3h-217-1
NIQMTQSPSSLSASVGDRTITCRASHFIGTLLTWYQHKGKAPKLLITYGSLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 551)
- 25 BMS3h-217-2
DIQMTQSPSSLSASVGDRTITCRASHFIGTLLSWYQQKPRKAPKLLITYGSLQSGVPSRFSGSGSGTDFTLTISSLH
PEDFATYYCGQGVLPPTFGQGTKVEIKR (SEQ ID NO: 552)
- 30 BMS3h-217-3
DIQMTQSPSSLTASVGDRTITCRASHFIGTLLSWYQQKPGKAPKLLVITYGSLQSGVPSRFSGSGSGTDFTLTISNLQ
PEDFATYYCGQGVLPPTFGQGTKVENIR (SEQ ID NO: 553)
- 35 BMS3h-217-4
DIQMTQSPSSLSASVGDRTITCRASHFIATLLSWYQQKPGKAPKLLITYGSLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCGQGVLPPTFGQGTKVEIKR (SEQ ID NO: 554)
- 40 BMS3h-217-5
DIQMTQSPSFLSASVGDRTITCRASHFIATLLSWYQQKPGKAPKLLITYGSLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCGQGVLPPTFGQGTKVEIKR (SEQ ID NO: 555)
- 45 BMS3h-217-6
DIQMTQSPSSLSASVGDRTITCRASHFIGTLLSWYQQKPGKATKLLITYGSLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCGQGVLPPTFGQGTKVEIKR (SEQ ID NO: 556)
- 50 BMS3h-217-7
DIQMTQSPSSLSASVGDRTITCRASHFIGSLLSWYQHKGKAPKLLITYGSLQSGVPSRFSGSGSGTDFTLTISSLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 557)
- 50 BMS3h-217-8

- DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQHKPGKAPKLLITYGSLQSGVPSRFSGSGSGTDFLTISLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 558)
- BMS3h-217-9
5 DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQHKPGKAPKLLITYGSLQSGVPSRFSGSGSGTDFLTISLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 559)
- BMS3h-217-10
10 DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQHKPGKAPKLLITYGSLQSGVPSRFSGSGSGTEFTLTISLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 560)
- BMS3h-217-11
15 DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQHKPGKAPKLLITYGSLQSGVPSRFSGSGSGTEFTLTISLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 561)
- BMS3h-217-12
NIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQHKPGKAPKLLITYGSLQSGVPSRFSGSGSGTDFLTISLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 562)
- BMS3h-217-13
20 DIQMTQSPSSLSASVGDRVTINCRASHFIGTLLSWYQHKPGKAPKLLITYGSLQSGVPSRFSGSGSGTDFLTISLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 563)
- BMS3h-217-14
25 DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQKPGKATKLLITYGSLQSGVPSRFSGSGSGTDFLTISLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 564)
- BMS3h-217-15
30 DIQMTQSPSSLYASVGDRVTITCRVSHFIGTLLSWYQKPGKAPKLLITYGSLQSGVPSRFSGSGSGTDFLTISLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 565)
- BMS3h-217-16
DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQKPRKAPKLLITYGSLQSGVPSRFSGSGSGTDFLTISLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 566)
- BMS3h-217-17
35 DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQKPGKAPKLLITYGSLQSGVPSRFSGSGSGTDFLTISLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 567)
- BMS3h-217-18
40 DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQKPGKAPKLLITYGSLQSGVPSRFSGSGSGTDFLTISLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 568)
- BMS3h-217-19
45 DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQKPGKAPKLLITYGSLQSGVPSRFSGSGSGTDFLTISLQ
PEDFATYYCGQGVLPATFGQGTKVENKR (SEQ ID NO: 569)
- BMS3h-217-20
50 DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQKPGKAPKLLITYGSLQSGVPSRFSGSGSGTDFLTISLQ
PEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 570)

- BMS3h-217-21
DIQMTQAPSSLSASVGDRVTITCRASHFIGTLLSWYQLKPGKAPKLLITYGSLQSGVPSRFSGSGSGTDFLTIISSLQ
PEDFATYYCGQVLWPATFGQGTKVEIKR (SEQ ID NO: 571)
- 5 BMS3h-217-22
DIQMTQSPSSLSASVGDRVTITCRASHFIGSLLSWYQQKPGKAPKLLITYGSLQSGVPSRFSGSGSGTDFLTIISSLQ
PEDFATYYCGQVLWPATFGQGTKVEIKR (SEQ ID NO: 572)
- 10 BMS3h-217-23
DIQMTQSPSSLSASVGDRVTITCRASHFIGSLLSWYQQKPGKAPKLLITYGSLQSGVPSRFSGSGSGTDFLTIISSLQ
PEDFATYYCGQVLWPATFGQGTKVEIKR (SEQ ID NO: 573)
- 15 BMS3h-217-24
DILMTQSPSSLSASVGDRVTITCRASHFIGSLLSWYQQKPGKAPKLLITYGSLQSGVPSRFSGSGSGTDFLTIISSLQ
PEDFATYYCGQVLWPATFGQGTKVEIKR (SEQ ID NO: 574)
- 20 BMS3h-217-25
DIQMTQSPSSLSASVGDRVTITCRASHFIGTLVSWYQQKPGKAPKLLITYGSLQSGVPSRFSGSGSGTDFLTIISSLQ
PEDFATYYCGQVLWPATFGQGTKVEIKR (SEQ ID NO: 575)
- 25 BMS3h-217-26
DIQMTQSPSSLSASVGDRVTITCRASHFIGTLVSWYQQKPGKAPKLLITYGSLQSGVPSRFSGSGSGTDFLTIISSLQ
PEDFATYYCGQVLWPATFGQGTKVEIKR (SEQ ID NO: 576)
- 30 BMS3h-217-27
DIQMTQSPSSLSASVGDRVTITCRASHFIGTLVSWYQQKPGKAPKLLITYGSLQSGVPSRFSGSGSGTDFLTIISSLQ
PEDFATYYCGQVLWPATFGQGTKVEIKR (SEQ ID NO: 577)
- 35 BMS3h-217-28
DIQMTQSPSSLSASVGDRVTITCRASHFIGTLVSWYQQKPGKAPKLLITYGSLQSGVPSRFSGSGSGTDFLTIISSLQ
PEDFATYYCGQVLWPATFGQGTKVEIKR (SEQ ID NO: 578)
- 40 BMS3h-217-29
DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQQKPGKAPKLLITYGSLQSGVPSRFSGSGSGTDFLTIISSLQ
PEDFATYYCGQVLWPATFGQGTKVEIKR (SEQ ID NO: 579)
- 45 BMS3h-217-30
DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQLKPGKAPKLLITYGSLQSGVPSRFSGSGSGTDFLTIISSLQ
PEDFATYYCGQVLWPATFGQGTKVEIKR (SEQ ID NO: 580)
- 50 BMS3h-217-31
DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQQKPGKAPKLLITYGSLQSGVPSRFSGSGSGTDFLTIISSLQ
PEDFATYYCGQVLWPATFGQGTKVEIKR (SEQ ID NO: 581)
- 55 BMS3h-217-32
DIQMTQSPSSLSASVGDRVITCRASHFIGTLLSWYQQKPGKAPKLLITYGSLQSGVPSRFSGSGSGTDFLTIISSLQ
PEDLATYYCGQVLWPATFGQGTKVEIKR (SEQ ID NO: 582)
- 60 BMS3h-217-33
DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQQKPGKAPKLLITYGSLQSGVPSRFSGSGSGTDFLTIISSLQ
PEDFATYYCGQVLWPATFGQGTKVEIKR (SEQ ID NO: 583)

- 5 BMS3h-217-34
DIQMTQSPSSLSASVGDRVITICRASHFIGTLLSWYQQKPGKAPKLLITYGSLQSGVPSRFSGSGGTFTLTIGSLQ
PEDFATYYCGQGVLPATFGGQTKVEIKR (SEQ ID NO: 584)
- BMS3h-217-35
DIQMTQSPSSLSASVGDRVITICRASHFIGTLLSWYQQKPGKATKLLITYGSLQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQGVLPPTFGGQTKVEIKR (SEQ ID NO: 585)
- 10 BMS3h-217-2301
DIQMTQSPSSLSASVGDRVITICRASHFIASLLSWYQVKPGKAPKLLITYGSLQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQGVLPATFGGQTTVEIKR (SEQ ID NO: 586)
- 15 BMS3h-217-2302
DIQMTQSPSSLSASVGDRVITICRASHFIAQLLSWYQVKPGKAPKLLITYGSLQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQGVLPATFGGQTTVEIKR (SEQ ID NO: 587)
- BMS3h-217-2303
DIQMTQSPSSLSASVGDRVITICRASHFIAQLLSWYQVKPGKAPKLLITYGSLQSGVPSRFSGSGGTDFLTITISLQ
20 PEDFATYYCGQGVLPATFGGQTTVEIRR (SEQ ID NO: 588)
- BMS3h-217-2304
DIQMTQSPSSLSASVGDRVITICRASHFIASLLSWYQVKPGKAPKLLITYGSLQSGAPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQGVLPATFGGQTTVEIKR (SEQ ID NO: 589)
- 25 BMS3h-217-2305
DIQMTQSPSSLSASVGDRVITICRASHFIGSLLSWYQVKPGKAPKLLITWASYLQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQGVLPATFGGQTTVEIKR (SEQ ID NO: 590)
- 30 BMS3h-217-2306
DIQMTQSPSSLSASVGDRVITICRASHFIGSLLSWYQVKPGKAPKLLITWSSYLQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQGVLPATFGGQTTVEIKR (SEQ ID NO: 591)
- BMS3h-217-2307
35 DIQMTQSPSSLSASVGDRVITICRASHFIGSLLSWYQVKPGKAPKLLITWSSYLQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQGVLPATFGGQTTVEIKR (SEQ ID NO: 592)
- BMS3h-217-2308
DIQMTQSPSSLSASVGDRVITICRASHFIGSLLSWYQVKPGKAPKLLITWGSWLQSGVPSRFSGSGGTDFLTITISLQ
40 PEDFATYYCGQGVLPATFGGQTTVEIKR (SEQ ID NO: 593)
- BMS3h-217-2309
DIQMTQSPSSLSASVGDRVITICRASHFIGSLLSWYQVKPGKAPKLLITWASWLQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQGVLPATFGGQTTVEIKR (SEQ ID NO: 594)
- 45 BMS3h-217-2310
DIQMTQSPSSLSASVGDRVITICRASHFIGSLLSWYQVKPGKAPKLLITWSSWLQSGVPSRFSGSGGTDFLTITISLQ
PEDFATYYCGQGVLPATFGGQTTVEIKR (SEQ ID NO: 595)
- 50 BMS3h-217-2311

	DIQMTQSPSSLSASVGDRVTITCRASHWIAQLLSWYQVKPGKAPKLLITYGSLIQSGVPSRFSGSGSGTDFLTIISSLQ PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 596)
5	BMS3h-217-2312 DIQMTQSPSSLSASVGDRVTITCRASHIIFIGSLLRWYQVKPGKAPKLLITYGSLIQSGVPSRFSGSGSGTDFLTIISSLQ PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 597)
10	BMS3h-217-2313 DIQMTQSPSSLSASVGDRVTITCRASHRIAQLLSWYQVKPGKAPKLLITYGSLIQSGVPSRFSGSGSGTDFLTIISSLQ PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 598)
15	BMS3h-217-2314 DIQMTQSPSSLSASVGDRVTITCRASHYIASLLSWYQVKPGKAPKLLITYGSLIQSGVPSRFSGSGSGTDFLTIISSLQ PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 599)
20	BMS3h-217-2315 DIQMTQSPSSLSASVGDRVTITCRASHFIGSLLSWYQVKPGKAPKLLIRFGSLLQSGVPSRFSGSGSGTDFLTIISSLQ PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 600)
25	BMS3h-217-2316 DIQMTQSPSSLSASVGDRVTITCRASHFIGSLLSWYQVKPGKAPKLLITYKSYLQSGVPSRFSGSGSGTDFLTIISSLQ PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 601)
30	BMS3h-217-2317 DIQMTQSPSSLSASVGDRVTITCRASHFIGSLLSWYQVKPGKAPKLLITWGSYLQSGVPSRFSGSGSGTDFLTIISSLQ PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 602)
35	BMS3h-217-2318 DIQMTQSPSSLSASVGDRVTITCRASHFIGWPLSWYQVKPGKAPKLLITYGSLIQSGVPSRFSGSGSGTDFLTIISSLQ PEDSATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 603)
40	BMS3h-217-2319 DIQMTQSPSSLSASVGDRVTITCRASHWIAQLLSWYQVKPGKAPKLLITYGSLIQSGVPSRFSGSGSGTDFLTIISSLQ PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 604)
45	BMS3h-217-2320 DIQMTQSPSSLSASVGDRVTITCRASHFIGWPLSWYQVKPGKAPKLLITYGSLIQSGVPSRFSGSGSGTDFLTIISSLQ PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 605)
	BMS3h-217-2321 DIQMTQSPSSLSASVGDRVTITCRASHFIGSLLNMYQVKPGKAPKLLITYGSLIQSGVPSRFSGSGSGTDFLTIISSLQ PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 606)
	BMS3h-217-2322 GIQMTQSPSSLSASVGDRVTITCRASHFIGSLLSWYQVKPGKAPKLLITYGSLQSGVPSRFSGSGSGTDFLTIISSLQ PEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 607)

TABLE 4

Human Anti-CD40 Variable Domain Encoding Nucleotide Sequences

- BMS3h-56-201
 5 GAGGTGCAGCTGTTGGAGTCCGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTCAGGAGT
 GGGGTACAGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 608)
- 10 BMS3h-56-258
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
 15 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTCACGAGT
 GGGGTACAGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 609)
- BMS3h-37
 20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTCTCTGG
 TGATGGTTATCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTATTTGACTACT
 GGGGTACAGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 610)
- BMS3h-38
 25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTCGGGATTATGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
 TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCGTTTCGTTTACTACT
 30 GGGGTACAGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 611)
- BMS3h-41
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTCAGTATGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTTCGGG
 35 TAATGGTGCTAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCGCTTAGGTTTACTACT
 GGGGTACAGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 612)
- BMS3h-43
 40 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTACAGCCTCCGGAT
 TCACCTTTCAGTATGAGATGCTGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTAG
 GCGTGGTTTTACTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCGATTACGTATGCTATGA
 GGATATGCGCGTTTTGACTACTGGGTACAGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 613)
- BMS3h-56
 45 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTATTTTACTACT
 50 GGGGTACAGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 614)

- BMS3h-106
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
 TCACCTTTTCGACTTATCATATGCAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCAATGATTGATGC
 GGATGGTCTTGGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATCCAAGAACACGCTG
 5 IATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGTCCGCAGTTTGGTCAGT
 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 615)
- BMS3h-107
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCTCCGGAT
 10 TCACCTTTTCGGGGTATGATATGCAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTAGTGC
 GTCGGGTGTTTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCACTCCCGGACAATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATCCTAATCGTTTTCGCTTA
 ATAATTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 616)
- BMS3h-131
 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAATA
 GTTCTATTTTGTGGGCGTTAGCTTGGTACCAGCAGAAACCAGGGAAGCCCTAAGCTCCTGATCGAGAGTTCTTCCGG
 TTTGCAAAAGTGGGGTCCCATCACGTTTCACTGGCAGTGGATCTGGGACAGATTCACTCTACCATCAGCAGCTGCAA
 CCTGAAGATTTTGTACGTACTACTGTGTTAGAATGCGGGTTGGCCTGTCAGTTCCGCCAAGGGACCAAGGTGGAAA
 20 TCAAACGG (SEQ ID NO: 617)
- BMS3h-193
 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
 AGACGATTGAGCGTCGTTAAATTGGTATCAGCAGAAACCAGGGAAGCCCTAAGCTCCTGATCTATCTGCTTCCCG
 25 TTTGCAAAAGTGGGGTCCCATCACGTTTCACTGGCAGTGGATCTGGGACAGATTCACTCTACCATCAGCAGCTGCAA
 CCTGAAGATTTTGTACGTACTACTGTCTAGTATGCGAGTCCACCTTTGACGTTCCGGCAAGGGACCAAGGTGGAAA
 TCAAACGG (SEQ ID NO: 618)
- BMS3h-198
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
 30 TCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
 TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACGATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATCCTTATAGTTTGTACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 619)
- BMS3h-202
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
 TCACCTTTCCGACTGCTGAGATGGTGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCCGG
 TAGTGGTGGTTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATCCAAGAACACGCTG
 40 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGGTGGTTATGTGGCGA
 CGTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 620)
- BMS3h-217
 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
 ATTTTATTGGTACTCTGTATCTTGGTACCAGCAGAAACCAGGGAAGCCCTAAGCTCCTGATCACTTATGGTTCCTT
 GTTGCAAAAGTGGGGTCCCATCACGTTTCACTGGCAGTGGATCTGGGACAGATTTCACTCTACCATCAGCAGCTGCAA
 CCTGAAGATTTTGTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTCCGCCAAGGGACCAAGGTGGAAA
 45 TCAAACGG (SEQ ID NO: 621)
- BMS3h-1

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTCCGAAGAATGAGATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTGAGTC
 GGATGGTCAAGCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGCGAAAAATCGGATTCCTGATCTTGTGT
 5 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 622)

BMS3i-2
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTGATGCTGGGGCTATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGATAA
 10 GGAGGGTCTGTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGGTAGGATTCTGGGCTGGTTT
 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 623)

BMS3h-3
 15 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTGGTGATGCGCGATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTACAGCC
 TATGGGTGATGGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCGTATTCTACTCTTCAGT
 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 624)

BMS3h-4
 20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTGAGGATTCGCCTATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTACTTC
 GAATGGTTATGAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 25 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCGTATTCTACTCTTCATT
 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 625)

BMS3h-5
 30 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTGATGAGCATGATATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTGGTCC
 GGATGGTTTTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCGTATTCTACTCTTCATT
 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 626)

BMS3h-6
 35 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTGGTGAGTATCATATGCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTACTCC
 TCTTGGTACGCTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 40 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCGTATTCTCTGCTTACGT
 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 627)

BMS3h-7
 45 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTGGTACGAATGCGATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGAGTGGGTCTCAAGGATTTCCGCC
 GGGTGGTGATTATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATTACTGTGCGAAAGGGCGTGTCCGGATCTGCTTT
 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 628)

BMS3h-8
 50 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTCCGTCTGAGGAGATGCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTTCCGCC

TGATGGTGTAAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAATGAACAGCCTGCGTGCCGAGGACGCCGGTATATTACTGTGCGAAAGGCGTGTTCGGATCTGCTTT
TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 629)

5 BMS3h-9
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCTGAGGATGATATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTGCGGT
TGATGGTATCGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGGTAAGGTTCCGTCTCTTCATT
10 TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 630)

BMS3h-10
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAGGACGATGGATATGCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTACGGG
15 TGATGGTATGAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAATGAACAGCCTGCGTGCCGGGACACCGGGTATATTACTGTGCGAAAGGGTGACTCCGGATTGACTT
TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 631)

BMS3h-11
20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAGGCGTGATGATATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTAATGC
TGGGGGTGTGCATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAAGGGTGACTCCGGATTGACTT
25 TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 632)

BMS3h-12
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGATGATGATTCTATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGGATTTCGAG
30 TGATGGTGCAGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGGGTGACTCCGGATTGACTT
TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 633)

BMS3h-13
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
35 TCACCTTTACTGAGGAGGATATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTGATAG
TGTGGTGGAGGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGGGTGACTCCGGATTGACTT
TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 634)

BMS3h-14
40 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCTGATTCCGGCGATGAGTTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGGATTGATAA
TCCTGGTCAGCATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAAGGTACTGTTCTACGCTGGAGT
45 TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 635)

BMS3h-15
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGGCAGCATAGTATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTGATGG
50 TGGGGGTATAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG

TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGAGGTTCCCTCGTCTTCATT
TTGACTACTGGGGTCAGGGAAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 636)

BMS3h-16

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGGTCAGGAGCCTATGACTTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGATTGCGTA
TAATGGTGGTGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAAGAACACGCG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATTACTCCTAATTTGACTT
10 TTGACTACTGGGGTCAGGGAAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 637)

BMS3h-17

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGAAGATTATCCGATGTCTTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAATGC
TACGGGTCTTATTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAAGAACACGCTG
15 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGTTATTCCTCATTGTGATG
TTGACTACTGGGGTCAGGGAAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 638)

BMS3h-18

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
20 TCACCTTTTGTGATTATGATATGAGTTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTACTGG
TACTGGTAATAGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGTGGTCCGTTCTTGGTCTT
TTGACTACTGGGGTCAGGGAAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 639)

BMS3h-19

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGAAGCTGATGCGATGACGTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTAATGT
GGATGGTGATCGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTACTGTTCTACGCTGGAGT
30 TTGACTACTGGGGTCAGGGAAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 640)

BMS3h-21

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGATCGGGCGGATATGACGTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTTCGGG
35 GGAGGGTAAGTGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATGGTTCCTAATTTGGTTT
TTGACTACTGGGGTCAGGGAAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 641)

BMS3h-22

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
40 TCACCTTTTCAATGGGAGCCGATGTCTTGGGTCGCGCAGGCTCCGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAATTC
TTCTGGTTGGGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATGGTTCCTAATTTGGTTT
TTGACTACTGGGGTCAGGGAAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 642)

BMS3h-24

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGTGATGAGCCGATGACTTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTCCTCC
TGAGGGTGCTCCGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAAGAACACGCTG
50 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATTACTCCTAATTTGACTT
TTGACTACTGGGGTCAGGGAAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 643)

- BMS3h-26
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCATAATCATGATATGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTAGTCG
5 GGGTGGTCTTCAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATTGTGCCGGATCTGCATT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 644)
- BMS3h-27
10 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAATGAGTATCCTATGTCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTAATGG
GGATGGTGCTAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATTATTCGGCTATGCAAT
15 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 645)
- BMS3h-28
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGGGATGTGCTATGTCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTGATCC
TTATGGTTCTAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
20 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTATTATGCTAGTCTTACTT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 646)
- BMS3h-29
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
25 TCACCTTTGCGGATTATGATATGTCCTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTCGGC
GCTTGGTGCTACTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTAGGATTCCGGATCTGCATT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 647)
- BMS3h-30
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAAGCGTTATTATGACTTGGGTCCGCCAGGCTCCAGGGAAGGATCTAGAGTGGGTCTCAGGTATTGTTCC
TTCTGGTAATAGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
30 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTAGGATTCCGGATCTGCATT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 648)
- BMS3h-31
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCTGATTATGATATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTTCCTCC
40 GACGGGTGGGCAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTATTATCCGATTGTTCTT
TTTCTCCGTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 649)
- BMS3h-32
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
45 TCACCTTTTAAAGTATTGGATGGGTGGGCCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGATTC
GCATGGTGCTGGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGTCGAGGACACCGCGGTATATTACTGTGCGAAAGGTGCTCTAAGTTTATGACTA
CGTATACGTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 650)
- BMS3h-33

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGTCTTATCCGATGCAATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGATTC
GAGGGGTTCCGTTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTCATAGTTGGACGTTTGACT
5 ACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 651)

BMS3h-34
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCGAATAGTAATATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTATATCC
10 GGATGGTGGGTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGCGTATTCCTACTCTTCATT
TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 652)

BMS3h-35
15 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGGCGAGGAGGATGGGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGATGA
TATTGGTCGTAGGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGCGCAGGGGTGTGTTGTTGT
20 TTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 653)

BMS3h-36
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGGATTATAGGATGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTCTAC
TTCTGGTGAGCTGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATCCAAGAACACGCTG
25 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGCGCGGGTCAGTTTTTGACT
ACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 654)

BMS3h-39
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
30 TCACCTTTCCGAGTATGAGATGGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTTCCGG
TGAGGGTCGGGCTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGGCTGTTGTTTTGACTACT
GGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 655)

BMS3h-40
35 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCGACTTATGAGATGCTTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCTTC
TTCTGGTAATTATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATCCAAGAACACGCTG
40 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGCGCTGATGTTTGACTACT
GGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 656)

BMS3h-42
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
45 TCACCTTTGATACTGAGGAGATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTAGTCC
TAATGGTGCTTTTACATTCTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGCTATTCTGTTTGACTACT
GGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 657)

BMS3h-44
50 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTCATTATGATAGGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTATGAG

- TGCTGGTCTGAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAAAGTGCTAGTCGATTTTTGACT
ACTGGGGTCAGGGAAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 658)
- 5 BMS3h-45
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAGGAGTTATGAGATGGCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTAGTAC
TCTGGGTACGAAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAAATCTTCTACTCATATTTTTGACT
10 ACTGGGGTCAGGGAAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 659)
- BMS3h-46
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTATAGGTATGAGATGGCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTTCTGTC
15 GTCTGGTTGGACGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAAGTGATGCTCATATTTTTGACT
ACTGGGGTCAGGGAAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 660)
- BMS3h-47
20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTATGCTTATGAGATGGCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCGGA
TGATGGTACGCGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGATCTGGGGCAGGGTTTGACT
25 ACTGGGGTCAGGGAAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 661)
- BMS3h-48
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCTGATCATGCGATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTGGTCC
30 GTCTGGTGAGGCGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGATCGTATTCCTAATCTGTGT
TTGACTACTGGGGTCAGGGAAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 662)
- BMS3h-49
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
35 TCACCTTTGAGTCTCAGGATATGTCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTCC
GAATGGTTGGGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAAGATAGGTCTGATTTTGACTACT
GGGGTCAGGGAAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 663)
- BMS3h-50
40 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGGGATTATGATATGTGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTCTGTC
TCCGGGTGGTGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGCTGTCTCAAGGGTTTGACT
45 ACTGGGGTCAGGGAAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 664)
- BMS3h-51
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
50 TCACCTTTCCGGTTTATTGGATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGATCC
GCAGGGTGGGATGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCTCGCACAATTCCAAGAACACGCTG

TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGCGCGTATTCTAATTTGGAGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 665)

BMS3h-52

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGAGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTAGTGCTTATGATATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTTAGAGTGGGTCTCAGGTATTGCGCA
GACGGGTTCTTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCAICICCCGCGACAAIICCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGCTAAGATTCCGAATTTGGTTT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 666)

BMS3h-53

10 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTGCGGATAGTGAGATGATGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGCGCA
TAATGGTGGGCATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTG
15 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTGGTCATCCTCAGCAGACTG
AGGCTTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 667)

BMS3h-54

20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTGCTACTTATGATATGATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGATTTCCTC
GAATGGTGGAGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATCAGACGCATTTTGACTACT
GGGGTCAGGGAACCTGTGTCACCGTCTCGAGC (SEQ ID NO: 668)

BMS3h-55

25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTAGTGTTTATGATATGAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCCTC
TTGCGGTACGTATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTG
30 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATCCTAAGAATTTTGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 669)

BMS3h-57

35 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTTCTCATGAGGATATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTCC
GAATGGTGGGATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACGTAAGGAGTAAGTTTGACT
ACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 670)

BMS3h-58

40 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTGAGAAGTATATTATGGGTGGGCCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGATTA
TTGGGGTCAGCATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACGTAAGTATCTTATCTCTGCG
45 AGTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 671)

BMS3h-59

50 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTTCTGATTATGCGATGGGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGAGTGGGTCTCAACGATTTCGTA
TGTGGGTATTATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGCTCTGCGGGGGAGGCGT
TTACGGAGCGTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 672)

- BMS3h-60
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTCCGTATATGATGCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGAGGT
5 TAATGGTAATAGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAATGGGTTGGTTCGAAGACGCTGT
CGGATAAGAGTTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 673)
- BMS3h-61
10 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTACGACGGAGATGGCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGGTAG
TGCTGGTGGTGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAATTTGGTGGCATCCTCAGGGTC
15 AGTTTACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 674)
- BMS3h-62
20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCTAGGGAGTGGATGGCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTACGCTG
TATGGGTCAGACTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
25 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAATTTCTCGGAATAAGGGGTTTT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 675)
- BMS3h-63
25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTACGAGTGAGTATATGGGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTACAGAG
GTATGGTAGTACGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAATTTCTCGGAATAAGGGGTTTT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 676)
- BMS3h-70
30 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCGGTGTATAGTATGCACTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTACTCC
TAATGGTACTCGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
35 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAACTCTTGGTCGGGGTTCTTATC
CTGGTGTTGATTTTACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 677)
- BMS3h-71
40 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCCGAGTTATGATATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCAGCTATTTCACGGC
GGATGGTACTGTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGTTCTATTCCGATGCTTACGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 678)
- BMS3h-72
45 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCGACTTATGATATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTTCCTCC
TAATGGTACTGGTATATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAATTCAGAGTGTTCATCATGCTG
50 TTTTGTACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 679)
- BMS3h-73

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGAATTATGAGATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTGCGCC
GCATGGTCGGCTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGGTCAGATTCCGATGCTTGATT
5 TTGACTACTGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 680)

BMS3h-74
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGCATTATATGATGATGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTCTCA
10 TTTTGGTGATATTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAATGATATGGTGATGAAGAATG
GGGGGTTGACTACTGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 681)

BMS3h-75
15 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGAGGTATGATATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTGATTC
GCGGGGTTGGTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTTGGTGCCGATCTGAGGT
TTGACTACTGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 682)

BMS3h-76
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCGAATGCGCAGATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTGATGC
TATGGGTGATGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
25 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTAAGGTTCCGAGTATTGACT
ACTGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 683)

BMS3h-77
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
30 TCACCTTTGCGAATGCGCAGATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTGATGC
TATGGGTGATGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGGTTATTCCGGCGTTTGACT
ACTGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 684)

BMS3h-78
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
35 TCACCTTTGAGAATGATCGGATGCATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTCTGC
TACTGGTGGTGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACAGACGGGTACGAATCGTTTTG
40 ACTACTGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 685)

BMS3h-79
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
45 TCACCTTTAATCAGCCTTATATGTCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTGATGC
TTCCGGTGGTACTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACCGCGGTATATTACTGTGCGAAAGATCGTATTCTTAATCTTGTT
TTGACTACTGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 686)

BMS3h-80
50 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGATAATGAGAATATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGTATTGATGG

TGGGGTTATAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGGCAGGTTCTTGAGCTGCTGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 687)

5 BMS3h-81
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGTTTCGTGCAATATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTATGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGGTCGGATTCTACGTTGGTGT
10 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 688)

BMS3h-82
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGTTTCGTGCAATATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
15 TAGTGGTGGTAGCACATACTATGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGGTCGATTCTTAATCTTGTGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 689)

BMS3h-83
20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCTGATGATTCGATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
TGCTGGTAGTTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGGTCGATTCTTCTTCTGGAGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 690)

25 BMS3h-84
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGTTTCGGATACTATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
GACTGGTGGTGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
30 TATCTGCAATGAACAGCCTGCGTGCCGGGACACCGGGTATATTACTGTGCGAAAGGCTATTCTTGATCTTCAGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 691)

BMS3h-85
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
35 TCACCTTTGATGAGGAGGAGATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
TGGTGGTCATGAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGGTCGATTCTTCTTGGAGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 692)

40 BMS3h-86
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGATAATGAGAATATGACTTGGGTCCGCCAGGCTCCAGGGAAGGATCTAGAGTGGGTCTCAGGATTACTGA
GAGGGGTGATGTGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
45 TATCTGCAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGGTCGATTCTTCTACGCTGGAGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 693)

BMS3h-87
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGATGAGGAGGAGATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
50 TGGTGGTCATGAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG

TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGGTAAGTCTTCTACGCTGGAGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 694)

BMS3h-88

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTTCATGAGACGGAGATGACGTGGGTCCGCCAGGC'CCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAATCG
GCTGGGTCAAGGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCAGGAACACGC 16
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGGTAAGGATTCTGGGCTGGTTT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 695)

10

BMS3h-89

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTTCTGATGATTTCGATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAATGA
TGCTGGTAGTTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCAGGAACACGCTG
15 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGGTAAGTCTTCTACGCTGGAGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 696)

BMS3h-90

20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTTGATAATGAGGAATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGATTACTGA
GAGGGGTGATGTGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCAGGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGGTCGGATTCTACGTTGGTGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 697)

25 BMS3h-91

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTTCTGATGATTTCGATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAATGA
TGCTGGTAGTTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCAGGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGGTAAGTCTTCTAATTTGACTT
30 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 698)

BMS3h-92

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTTCTGATGAGCCGATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTTCTCC
35 TGAGGGTGCTCCGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCAGGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGGCTTATCTCTGATCTTCAGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 699)

BMS3h-93

40 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTTCAGGATAGTGATATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTGCTGC
GCCTGGTGGTAGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCAGGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGATCGTATTCCTAATCTTAGGT
45 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 700)

BMS3h-94

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTTGTTCGGATACTATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTGATGG
GACTGGTGGTGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCAGGAACACGCTG
50 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGGTCAGTTCTCTGAGCTGCTGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 701)

- BMS3h-95
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCAGGATAGTGATATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTGCTGC
5 GCCTGGTGGTAGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATCGTATTCCTAATCTGTGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 702)
- BMS3h-96
10 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCGCCGGAT
TCACCTTTGATCTGGCGGAGATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTGATGA
GGATGGTGGTCTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACGCCGCGGTATATTACTGTGCGAAAGGTGTTATTCCGCTCTGACTT
15 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 703)
- BMS3h-97
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTACTGATAAGCATATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGATTTCGCC
20 TGATGGTACGTATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACGCCGCGGTATATTACTGTGCGAAAGGTGTTATTCCGCTCTGACTT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 704)
- BMS3h-98
25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCTGAGGATGATATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTGCGGT
TGATGGTATCGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTACCGAGGACGCCGCGGTATATTACTGTGCGAAAGGAGACGCCATCTTGTGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 705)
- BMS3h-99
30 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCGCCGGAT
TCACCTTTGATCTGGCGGAGATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTGATGA
GGATGGTGGTCTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
35 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACGCCGCGGTATATTACTGTGCGAAAGGTGAGGTTCTGCTTTGGTTT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 706)
- BMS3h-100
40 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGGATTGATGATGCTGTTGGGTCCGCCAGGCGCCAGGGAAGGGTCTAGAGTGGGTCTCAGGATTGATCC
TGGGGGTGCTCAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACGCCGCGGTATATTACTGTGCGAAAGGGTGACTCCGGATTGACTT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 707)
- BMS3h-101
45 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGCATGCGGATATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTGATAA
TAGTGGTCAGTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACGCCGCGGTATATTACTGTGCGAAAGGGTGACTCCGGATTGACGT
50 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 708)
- BMS3h-102

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAGTGAGGCGGAGATGAATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGTATTACGAC
GGATGGTGATTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGTATTCCTACTCTTCATT
5 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 709)

BMS3h-103
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCAGGAT
TCACCTTTGATGATAGTGATATGACTTGGGTCCGCCAGGCTCCAGGGAAGAGTCTAGAGTGGGTCTCATATATTCCGGG
10 TGATGATGATGAGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCGGATTCTGATCTTGTGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 710)

BMS3h-108
15 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAATGTGGCGGATATGCAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTCC
GAATGGTTGGGATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCGTCTACGGAGGGGCCGA
20 CTGCTTTTACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 711)

BMS3h-109
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGGCGTATGATATGGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATGGATTCTGCG
TCATGGTTTCGTTTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
25 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATGGCCTTATAAGTTTACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 712)

BMS3h-110
30 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGGAGTGGGTCTATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGATTGGTAG
TAATGGTGCGGATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATGGTTCCTAATTTGGTTT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 713)

BMS3h-111
35 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAATCGTTTGTATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATCGTATTCTAATCTTGTGT
40 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 714)

BMS3h-112
45 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGGGAGAGTGATATGAAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTCC
GAATGGTTGGGATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCTCCTTCTTCGCTTAAAGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 715)

BMS3h-139
50 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGATAGTAGTGAGATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGAGAA

TCAGGGTGGTGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATCGTATTCTTAATCTTGTGT
TTGACTACTGGGGTCAGGGAAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 716)

5 BMS3h-140
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGATGCGTATCTATGTATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATGGATTGCTTC
GGGTGGTGGTGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACGTACGAAGAATTTGACTACT
10 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 717)

BMS3h-141
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTATGAGTTATCTATGGCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGGATTACTTC
15 TAATGGTAATCGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATCGACTGGGGCTAATAGTAGGA
ATTTTACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 718)

BMS3h-142
20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGGGGTATCTGATGTCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGCGGC
TAATGGTATGCAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCCGAGGGGTATTGGGATG
25 GGGATTTTACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 719)

BMS3h-143
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTATGAGTCTACGATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTTCGGCA
TCCGGGTGAGTTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
30 TATCTGCAAAATGAACAGCCTGCGTGCCGGGGACACCGCGGTATATTACTGTGCGAAAGGGCTTATCTGATCTTCAGT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 720)

BMS3h-144
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
35 TCACCTTTGCGATGTATAGTATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGCGCC
GCCGGGTGGTAGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACAGTCGCTGACGGGGTATAGTA
GGTCTTTTACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 721)

BMS3h-145
40 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCGAGAAATCCGATGTCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTCTGCG
GAATGGTGTCTTACATCTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATATAGTCAGCAGCCGGGTGCTG
45 GGTGTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 722)

BMS3h-146
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCTAATTATCATATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTCTGGA
50 TAGTGGTAAGCAGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG

TATCTCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTAGGATTCCGCTCTCTCTTT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 723)

BMS3h-147

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTGCGCAGTATCATATGCGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTATGA
TATTGGTAGTAATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCAATCCTCCGCGACAAATCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGGGGCGGGGAGTTTTT
CTTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 724)

BMS3h-148

10 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTTCTTCGTATGATATGAAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTAGTGC
GTCTGGTGTGTTTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCGCGACAAATCCAAGAACACGCTG
15 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACGGGAGCATGCGGGTCAGCCGC
CTTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 725)

BMS3h-149

20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTAATGGTTATGCTATGAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACATTATATGC
TAATGGTAAGTATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCGCGACAAATCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGACTCTTGTCTTAATT
ATTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 726)

BMS3h-150

25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTATGATTATGATATGAAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTACTGC
GCTTGGTAAGAAGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCGCGACAAATCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATAGTGTAAATATCCTCTTA
30 ATCTTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 727)

BMS3h-151

35 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTCCGATTATACGATGGCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGAGTGGGTCTCATCTATTACGTC
GCCTGGTIGGCGGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCGCGACAAATCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATATGGGGATGGTCTTCTTTGA
CTTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 728)

BMS3h-167

40 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTAGTGTACGCCGATGCTTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCATTTGGGGA
TGAGGGTCAGGAGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCGCGACAAATCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGTGACTCCGGATTGACTT
45 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 729)

BMS3h-168

50 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTAGTAGTAGTTGATGCTTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCATTTGGGTG
TGATGGTCCGAGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCGCGACAAATCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGTATTCCTACTCTTCATT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 730)

- BMS3h-169
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTAATCCTGGTGAGATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGATGG
5 GTCTGGTTCCTTGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGGGCGTATTCCTACTCTTCATT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 731)
- BMS3h-170
10 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCTGAGTCTATGATGGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGGGTA
TCCTGGTGCTACTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGGTGGTAGTCGGGATGATAATT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 732)
- 15 BMS3h-171
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTCAGCATAGTATGCAATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTGT
TCCGGGTCCGAAGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
20 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTCTTAGGGATTTCGCTCCGG
GTGATAGTAAGAGTTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 733)
- BMS3h-197
25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTTCGCTGCTATGGATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTAATGA
TATGGGTCTAATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTCTTAGGGATTTCGCTCCGG
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 734)
- 30 BMS3h-199
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTTATGATAGGATGGCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGATGG
TCCTGGTGGGGCTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
35 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTGGTTCCTGATTGTTG
ACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 735)
- BMS3h-200
40 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTGAGTATGAGATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTGATCC
GTTTGGTTCTGAGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTGGTTCCTGATTGAAAT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 736)
- 45 BMS3h-201
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGATAAGTATGTTATGGGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTGGTAG
TTATGGTGGGGCTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTCTACTCTTAGTGCGACTA
AGTTTACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 737)
- 50

- BMS3h-203
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGGATTATGTGATGGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTGCGCA
TCGGGGTGATATTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
5 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACGTAGGCGCTTAGTGATTATC
GGTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 738)
- BMS3h-204
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
10 TCACCTTTGGGCAGTTTGATATGTATTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTAGTCC
GGCTGGTACTGGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGGGGATCGGTCTAGTCTTT
TTGACTACAGGGGTGAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 739)
- BMS3h-205
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
15 TCACCTTTAAGGATACGGGTATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTCTAG
TTATGGTCGTGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTGAATGCGGCGCTGGGTTTTG
20 ACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 740)
- BMS3h-206
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
25 TCACCTTTGGTCCGATCCGATGAGTTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAATGC
GCCGGGTACGAGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACAGATGTCTAGTGGGGTTTTG
ACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 741)
- BMS3h-207
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
30 TCACCTTTTGAATCAGGATATGACTTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGATAG
TTCTGGTCAGCTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTAAGTCTCTTGGCGGGTTTG
35 ACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 742)
- BMS3h-208
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGAGCCTCCGGAT
TCACCTTTCTGAGTCTGATATGAAGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTCC
GAATGGTTGGGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
40 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACCGGCTCAGGTTCTGTTGACT
ACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 743)
- BMS3h-209
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
45 TCACCTTTGAGCAGTATGTGATGGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGGTAC
GTCGGGTAAGTATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAACGTAGGTCTCTGACTCGGGTTC
ATTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 744)

- BMS3h-210
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTGGTGTGGAGCATATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTACGGG
 TGATGGTGATCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
 5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAACGGTTTCGTGGAATGGTCTGT
 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 745)
- BMS3h-211
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 10 TCACCTTTGCGTGGTATAATATGGGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCAAGGATTGCTCC
 GTCTGGTATTATTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGGGTTCGTGGTAAGTTTGACT
 ACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 746)
- BMS3h-212
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 15 TCACCTTTTGAATTATGAGATGAGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCTTC
 GGCTGGTACTGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAACAGTCGCTTAATTTTGACTACT
 20 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 747)
- BMS3h-213
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGAGCCTCCGGAT
 25 TCACCTTTGATGAGGAGCCGATGACTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAATTATTGATCC
 GGGTGGTGGGGCGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATCTAATAGTATGTTTGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 748)
- BMS3h-214
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 30 TCACCTTTTCTGCGTATCCTATGCAATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTGCTTC
 TTCGGGTATTACGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTTACTCGGCTGCAATTTCTCTG
 CGCAGTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 749)
- BMS3h-215
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 35 TCACCTTTGCTGATTATGCGATGGGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGGATTTCTCC
 TGAGGGTTCTAGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
 40 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATTCGGCCGTATGCGTCGAAGT
 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 750)
- BMS3h-230
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 45 TCACCTTTAGGCCGTATGATATGGGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCTCA
 TCAGGGTAATCGGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATGTCTCATATTTTGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 751)

- BMS3h-231
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCGCTATAATATGTGGTGGGCCCGCCAGGCTCCAGGGAAGGGTTAGAGTGGGTCTCATGGATTAATTC
GACTGGTTCTCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAAATTGGCATCGGGGAGGTTTG
ACTACTGGGTGAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 752)
- BMS3h-232
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
10 TCACCTTTGATAGGTATCGGATGGGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTAAATCG
GCTGGGTGAGAGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTGAAGAAGCATAAGTTTGACT
ACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 753)
- BMS3h-233
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
15 TCACCTTTGCGCATTATAATATGCGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTACGAA
GACTGGTTTCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGTGAACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTGAAGAAGCATAAGTTTGACT
20 ACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 754)
- BMS3h-234
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTAGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
25 TCACCTTTTATCCTTATAGTATGCAATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGAGTGGGTCTCAACTATTGATGG
TAGTGGTATGTTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTGAAGAAGCATAAGTTTGACT
ACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 755)
- BMS3h-235
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
30 TCACCTTTCCGCTTTATGGGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATATATTGGGCC
TTATGGTCATACTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
GTATGGTGCTCATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
35 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAAAGCGGAAGAAGTGGTGGTGGT
ACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 756)
- BMS3h-236
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
40 TCACCTTTCTAGGTATCGGATGAGTTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTACTCC
GTATGGTGCTCATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATGGTAAGTGGTATTTTGACT
ACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 757)
- BMS3h-237
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
45 TCACCTTTAATGAGTATGCGATGAGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGATCG
TCTGGGTCTTCATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTGGGCTTTTACGTTTGACT
ACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 758)

- BMS3h-238
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTGAGCGGTATAATATGCGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGATCG
 GCTGGGTCTTGCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATCCAAGAACACGCTG
 5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAMGCGGGTCTGTGGTCTTTGACT
 ACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 759)
- BMS3h-239
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 10 TCACCTTTGGTATTTATGATATGAAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCGTC
 GTCGGGTACTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATCCTCAGCCTTATCCTTTG
 ACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 760)
- BMS3h-240
 GAGGTGCAGCTATTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTTGGGTGATGATATGCGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCGTC
 GACTGGTGTGCAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATCCAAGAACACGCTG
 15 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATCCGCTGCTGGTGGTTG
 20 ACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 761)
- BMS3h-241
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTTCGACTTATGATATGATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTTCTCC
 25 TAATGGTACTGGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCCGCAAGTGAATGACTGAGT
 TTGACTACCGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 762)
- BMS3h-243
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 30 TCACCTTTGAGAAGGAGGATATGGGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTACATATTTCTCC
 GAATGGTTATGCGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGTCTAGTTTTGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 763)
- BMS3h-244
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTAGTGCTACTCCGATGGAGTGGGCCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACTATTTCTGA
 40 GAGTGGTTATAGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGAATTCGACTACTGTTTTG
 ACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 764)
- BMS3h-245
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 45 TCACCTTTAATACGGTGGATATGGAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTCC
 GAATGGTTGGGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTCCGCATCGGGCGTTTGACT
 ACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 765)

- BMS3h-246
GAGGTGCAGCTGTTGGAGTCTGGGGGGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGGAIAAGGAGATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGATTGATGC
TTTGGGTGATTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGGATGGTTCTCTGCTGAAGT
TTGACTACTGGGTGAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 766)
- BMS3h-247
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
10 TCACCTTTAGTGATCATTGATGATGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGATATTGAGCC
GCATGGTGTTCATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAATCCTACTTTTGACTACTGGGGT
AGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 767)
- BMS3h-248
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
15 TCACCTTTTCGCCGCACTACTATGCATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGATTGGTCC
GGATGGTACTACTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAACGTTCTGATAGTTGGGATCGTG
20 GGTGGAGCTTGACTACTGGGGTCAAGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 768)
- BMS3h-249
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTATGCTTCGGATATGAAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTCC
25 GAATGGTTGGGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGCTGATTATATCATTTCTT
TTGACTACTGGGGTCAAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 769)
- BMS3h-250
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
30 TCACCTTTTCGCATTATAATATGCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTACGAA
GACTGGTTTTTCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGTGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGCGGGCAGTTTGATTTTGACT
ACTGGGGTCAAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 770)
- BMS3h-251
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCGCATTATCATATGGTTGGGCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGTTATTGGGCC
35 GAGGGGTATTTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAATCGCCTTCGCGTCATAGGTTTG
40 ACTACTGGGGTCAAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 771)
- BMS3h-252
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
45 TCACCTTTAATGAGTATGCGATGAGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGATCG
TCTGGGTCTTCATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGTGGGCCTTTACGTTTGACT
ACTGGGGTCAAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 772)

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- BMS3h-273
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGGGCGGTTGATATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTTCGCC
TAGTGGTTCTGCTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCGTGTGCCGGATCTTGGTT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 780)
- BMS3h-274
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
10 TCACCTTTGATAGTTATGCGATGGGGTGGGCCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTGGGGC
TAAGGGTTTGTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGCTAGGGGTAAGTTTGACT
ACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 781)
- BMS3h-275
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
15 TCACCTTTACTCGGTATCAGATGGGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGTTATTAAATGT
TTGGGGTTTCAGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGCTAGGGGTAAGTTTGACT
20 GGGGTTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 782)
- BMS3h-276
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGGAATTATAGTATGATGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTATTC
25 TGCTGGTACGTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGTTCGATTAGGTTGTTTGACT
ACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 783)
- BMS3h-279
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
30 TCACCTTTGGTGCATGATATGGGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATGGATTTC
GAATGGTTATGATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGTGTGAAGTTTGACTACT
35 GGGGTTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 784)
- BMS3h-282
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGTTTGGTATGAGATGGCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTACGGC
40 TGATGGTGAGCAGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGCTTCGTATGCTCTTGTGTATC
CTCCTGAGGAGTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 785)
- BMS3h-287
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
45 TCACCTTTACGAATTATAGGATGCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTGATGA
TCTGGGTGTGTCGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGAGGCTTAAGAATAGTCAGC
CGACGGATTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 786)

- BMS3h-292
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGATCAGGCTCATATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATTTATTAATCC
TTCGGGTTATTATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTTCGCTTAGTCCGCTCTCTT
TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 787)
- BMS3h-293
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
10 TCACCTTTGAGACTGGTCCAGATGGGTTGGGCCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAATATTGATGG
GTCTGGTACGTATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTACGCAGAATTATCGGTTG
ACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 788)
- BMS3h-296
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
15 TCACCTTTGGTGCTTATCCGATGTATTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTCATAA
GGATGGTAGGATTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACAGGGTACGCCGGTTGATGGGT
20 TTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 789)
- BMS3h-297
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
25 TCACCTTTCTGATGAGGATGACGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTGAGAC
TGGTGGTACGGTGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGATGGGTCTGGTACATGGC
AGACCTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 790)
- BMS3h-298
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
30 TCACCTTTGATAGTCTGGGTATGGGTTGGGCCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATATATTCGGGC
TGAGGGTGCTTATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATATCTTGGGATTCTGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 791)
- BMS3h-299
GAGGTGCAGCTGTTGGAATCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
35 TCACCTTTAGTGAGTCGTATATGGAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGATCA
TATTGGTGGTGGGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
40 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATGATGGTCTGGTGGGTCTA
TGTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 792)
- BMS3h-300
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
45 TCACCTTTTCTGGTGGGTATATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGGGGC
TAGTGGTGGTATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACAGGGGGTAGGTTAGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 793)

- BMS3h-301
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTGATGAGGGGCATATGGGGTGGGTCCGCCAGGCTCCAGGGAAGGATCTAGAGTGGGTCTCATATATTGGGAG
TCTGGGTTTGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATCCAGAACACGCTG
5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAACGGGAGTTTAGTAATGGGGGT
TTGACTACTGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 794)
- BMS3h-302
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
10 TCACCTTTAAGACTAGTCTATGTATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGATCG
GACTGGTGGGCATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATCCAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAACAGGCTCTGCTTACTGATGCGA
AGCGTTTTGACTACTGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 795)
- BMS3h-303
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
15 TCACCTTTTGATGGTCCGGATATGGTTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTCC
GAGTGGTCTGGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATCCAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAACGTTCTATGCGGCATCAGCCGT
20 ATTTGACTACTGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 796)
- BMS3h-304
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGTAATGATCCGATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGATTGGTCG
25 GGAGGGTGATTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATCCAGAACACGCTG
IATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGATTCTATGCGGCATCAGCCGT
TTGACTACTGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 797)
- BMS3h-305
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
30 TCACCTTTGATGAGACTTATATGAAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTGGGGC
GTCGGGTGCTGATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATCCAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAATTTACGCATCTGAATGGTCGGT
TTGACTACTGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 798)
- BMS3h-306
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGGGGGTGGCCTATGGGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGATAT
35 TGATGGTGCTCCGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATCCAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAAGAGGAGGCGGGTTCTTGGTCTT
TTGACTACTGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 799)
- BMS3h-307
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
45 TCACCTTTAGTGATCAGCGATGTGGTGGGCCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATTTATTCAGGG
TGATGGTGGTTTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATCCAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAACCTAGTAAGCCGTTTGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 800)

- BMS3h-308
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTGAGACTGGTCAGATGGGTTGGGCCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAATATTGATGG
 GTCTGGTACGTATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
 5 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGTGCGGAATTTGCTTTTG
 ACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 801)
- BMS3h-309
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 10 TCACCTTTAGTGGGCATGATATGTCTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTCC
 TCATGGTACGCATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATTAGGGGTTGGATTGGTC
 ATGATACGCAGCCTTTTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 802)
- BMS3h-310
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 15 TCACCTTTGAGAGTAAGGATATGCTTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCGTG
 GGATGGTACTCATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTGGGTGGGTTCTTGGCAGT
 20 TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 803)
- BMS3h-311
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 25 TCACCTTTGCGGATCGTGATATGGTTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGGGGC
 GTCGGGTACGTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTGGGACGGGTCTACTGATT
 TGTGGGATTTTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 804)
- BMS3h-312
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 30 TCACCTTTGATGATGAGAAGATGCTTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTGT
 GAGTGGTCTGCATACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGGAGGCGGGTCTTGGTCTT
 35 TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 805)
- BMS3h-313
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 40 TCACCTTTGGGAGGAGAGGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGATATTTCGGC
 TTCGGGTGGGACTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGGAGGCGGGTCTTGGTCTT
 TTGACTACTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 806)
- BMS3h-37-1
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCTCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 45 TCACCTTTGAGTGGTATGAGATGCAAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTCTGG
 TGATGGTTATCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCATGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTATTTTGACTACA
 GGGGTCCGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 807)

- BMS3h-37-2
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGTGGTATGAGATGCACTGGGTCCGCCGGGCTCCAGGGAAGGGCTAGAGTGGGTCTCAGCGATTTCTGG
TGATGGTTATCGTACATACTACGCAGACTCCGTGAAAGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
5 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTATTTGACTACT
GGGGTCGGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 808)
- BMS3h-37-3
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
10 TCACCTTTGAGTGGTATGAGATGCACTGGGTCCGCCGGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTTCTGG
TGATGGTTATCGTACATACTACGCAGACTCCGTGAAAGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTATTTGACTACC
GGGTTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 809)
- BMS3h-37-4
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
15 TCACCTTTGAGTGGTATGAGATGCACTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTTCTGG
TGATGGTTATCGTACATACTACGCAGACTCCGTGAAAGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTATTTGACTACT
20 GGGTTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 810)
- BMS3h-37-5
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
25 TCACCTTTGAGTGGTATGAGATGCACTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTTCTGG
TGATGGTTATCGTACATACTACGCAGACTCCGTGAAAGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTATTTGACTACA
GGGTTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 811)
- BMS3h-37-6
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
30 TCACCTTTGAGTGGTATGAGATGCACTGGGTCCGCCGGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTTCTGG
TGATGGTTATCGTACATACTACGCAGACTCCGTGAAAGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTATTTGACTACT
GGGGTCGGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 812)
- BMS3h-37-7
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
35 TCACCTTTGAGTGGTATGAGATGCACTGGGTCCGCCGGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTTCTGG
TGATGGTTATCGTACATACTACGCAGACTCCGTGAAAGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
40 TATCTGCAAATGACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTATTTGACTACT
GGGGTCGGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 813)
- BMS3h-37-8
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
45 TCACCTTTGAGTGGTATGAGATGCACTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTTCTGG
TGATGGTTATCGTACATACTACGCAGACTCCGTGAAAGGCCGGTTACCATCTCAGCGACAATCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTATTTCACTACT
GGGGTCGGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 814)

- BMS3h-37-9
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGTAGCCTCCGGAT
TCACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCAGGCTCCAGGGAATGGTCTAGAGTGGATCTCAGCGATTTCTGG
TGATGGTTATCGTACATACTACGCAGACTCCGTGAAAGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTATTTTGACTACT
GGGGTCGGGGAACCTGGTCAACCGTCTCGAGC (SEQ ID NO: 815)
- BMS3h-37-10
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCTGGAT
10 TCACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATATCTGG
TGATGGTTATCGTACATACTACGCAGACTCCGTGAAAGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
TATCTGCTAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTATTTTGACTACT
GGGGTCGGGGAACCTCGTCAACCGTCTCGAGC (SEQ ID NO: 816)
- BMS3h-37-11
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTTCTGG
TGATGGTTATCGTACATACTACGCAGACTCCGTGAAAGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTATTTTGACTACA
20 GGGGTCGGGGAACCTGGTCAACCGTCTCGAGC (SEQ ID NO: 817)
- BMS3h-37-12
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCATGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCGATTTCTGG
25 TGATGGTTATCGTACATACTACGCAGACTCCGTGAAAGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTATTTTGACTACA
GGGGTCGGGGAACCTGGTCAACCGTCTCGAGC (SEQ ID NO: 818)
- BMS3h-37-201
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCCAGGGAAGGGATAGAGTGGGTCTCAATGATTTCCGG
GGATGGTTATCGTACATACTACGCAGACTCCGTGAAAGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTATTTTGACTACT
GGGGTCGGGGAACCTGGTCAACCGTCTCGAGC (SEQ ID NO: 819)
- BMS3h-37-202
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCCAGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGG
TGACGGTTGGCGCACATACTACGCAGACTCCGTGAAAGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
40 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTATTTTGACTACT
GGGGTCGGGGAACCTGGTCAACCGTCTCGAGC (SEQ ID NO: 820)
- BMS3h-37-203
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGGGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCCAGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGG
TGATGGTTATCGTACATACTACGCAGACTCCGTGAAAGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTGCTCTACTTTGACTACT
GGGGTCGGGGAACCTGGTCAACCGTCTCGAGC (SEQ ID NO: 821)

- BMS3h-37-204
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGTGGTATGAGATGCACTGGGTCCGCCGGGCTCCAGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGG
TGATGGTTATCGTACATACTACGCAGACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACACGCTG
5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTGGGGTCTTTGACTACT
GGGGTCGGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 822)
- BMS3h-37-205
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
10 TCACCTTTGAGTGGTATGAGATGCACTGGGTCCGCCGGGCTCCAGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGG
TGATGGTTATCGTACATACTACGCAGACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGTTGGAGTATTTGACTACT
GGGGTCGGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 823)
- BMS3h-37-206
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
15 TCACCTTTGAGTGGTATGAGATGCACTGGGTCCGCCGGGCTCCAGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGG
TGATGGTTATCGTACATACTACGCAGACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGTTGGAGTATTTGACTACT
20 GGGGTCGGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 824)
- BMS3h-37-207
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
25 TCACCTTTGAGTGGTATGAGATGCACTGGGTCCGCCGGGCTCCAGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGG
TGATGGTTATCGTACATACTACGCAGACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTGGCCTCTTTGACTACT
GGGGTCGGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 825)
- BMS3h-37-208
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
30 TCACCTTTGAGTGGTATGAGATGCACTGGGTCCGCCGGGCTCCAGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGG
TGATGGTTATCGTACATACTACGCAGACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTCTTGACTTTGACTACT
35 GGGGTCGGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 826)
- BMS3h-37-209
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
40 TCACCTTTGAGTGGTATGAGATGCACTGGGTCCGCCGGGCTCCAGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGG
TGATGGTTATCGTACATACTACGCAGACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGTTGGAGTCTTTGACTACT
GGGGTCGGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 827)
- BMS3h-37-210
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
45 TCACCTTTGAGTGGTATGAGATGCACTGGGTCCGCCGGGCTCCAGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGG
TGATGGTTATCGTACATACTACGCAGACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTGCAGTTCTTTGACTACT
GGGGTCGGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 828)

- BMS3h-37-211
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCCAGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGG
TGATGGTTATCGTACATACTACGCAGACTCCGTGAAAGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
5 1ATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCTGCTCTTCTTGACTACT
GGGGTCGGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 829)
- BMS3h-37-212
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACGGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
10 TCACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCCAGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGG
TGATGGTTATCGTACATACTACGCAGACTCCGTGAAAGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGTTGGAGTTCTTTGACTACT
GGGGTCGGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 830)
- BMS3h-37-213
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
15 TCACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCCAGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGG
TGATGGTTATCGTACATACTACGCAGACTCCGTGAAAGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGTTGCTCTTTCTTGACTACC
20 GGGGTCGGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 831)
- BMS3h-37-214
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCATCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCCAGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGG
25 TGATGGTTATCGTACATACTACGCAGACTCCGTGAAAGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAACTTGGAGTATTTTGACTACT
GGGGTCGGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 832)
- BMS3h-37-215
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
30 TCACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCCAGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGG
TGATGGTTATCGTACATACTACGCAGACTCCGTGAAAGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGTTGCGAGTTCTTTGACTACT
35 GGGGTCGGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 833)
- BMS3h-38-1
GAGGTGCAGCTGTTGGGGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAAGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
40 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCCGTTTCGTTTTGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 834)
- BMS3h-38-2
GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGAGCCTCCGGAT
45 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGTACAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAAGGCCGGTTCACCACTCCCGGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 835)

- BMS3h-38-3
 GAGGTGCAGCTGTTGGCTCTGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTGAGGAGGAGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGCTAGAGTGGATCTCAGCTATTAGTGG
 AAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTTACCATCTCCCGCACAATTCCAAGAACACGCTG
 5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGGGAAAGAGCCGTTTCGTTTTGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 836)
- BMS3h-38-4
 GAGGTGCAGCTGTTGGATCCTGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 10 TCACCTTTGGGAAGGAGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGCTAGAGTGGGTCTCATCTATTAGTGG
 TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTTACCATCTCCCGCACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGGGAAAGAGCCGTTTCGTTTTGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 837)
- BMS3h-38-5
 GAGGTGCAGCTGTTGGGCTCTGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTGAGGAGGAGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGCTAGAGTGGGTCTCAGCTATTAGTGG
 TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTTACCATCTCCCGCACAATTCCAAGAACACGCTG
 15 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGGGAAAGAGCCGTTTCGTTTTGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 838)
- BMS3h-38-6
 GAGGTGCAGCTGTTGAGCCTGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 25 TCACCTTTGAGGAGGAGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGCTAGAGTGGGTCTCAGCTATTAGTGG
 TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTTACCATCTCCCGCACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAAGAGCCGTTTCGTTTTGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 839)
- BMS3h-38-7
 GAGGTGCAGCTGTTGGATCCTGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 30 TCACCTTTGGGAAGGAGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGCTAGAGTGGGTCTCATCTATTAGTGG
 TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTTACCATCTCCCGCACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAAGAGCCGTTTACGTTTTGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 840)
- BMS3h-38-8
 GAGGTGCAGCTGTTGAGTCTGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTGAGGAGGAGAGATGATCTGGGTCCGCCAGGCTCTGGGAAGGGCTAGAGTGGATCTCAGCTATTAGTGG
 TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTTACCATCCACCGCACAATTCCAAGAACACGCTG
 40 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAAGAGCCGTTTCGTTTTGACTACA
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 841)
- BMS3h-38-9
 GAGGTGCAGCTGTTGGATCCTGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 45 TCACCTTTGGGAAGGAGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGCTAGAGTGGGTCTCATCTATTAGTGG
 TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTTACCATCTCCCGCACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAAGAGCCGTTTACGTTTTGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 842)

- BMS3h-38-10
 GAGGTGCAGCTGTTGGATTCTGGGGGAGGCTTTGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGATCTCAGCTATTAGTGG
 TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATCCAAGAACACGCTG
 5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATTACTGTGCGAAAGAGCCGTTTCGTTTTGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 843)
- BMS3h-38-11
 GAGGTGCAGCTGTTGGATCCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 10 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGATCTCAGCTATTAGTGG
 TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATTACTGTGGGAGAGAGCCGTTTCGTTTTGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 844)
- BMS3h-38-12
 GAGGTGCAGCTGTTGGAGTCTGGGGAAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 15 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
 TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCAGCGACAATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATTACTGTGGGAAAGAGCCGTTTCGTTTTGACTACT
 20 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 845)
- BMS3h-38-13
 GAGGTGCAGCAGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 25 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
 TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATTACTGTGGGAAAGAGCCGTTTCGTTTTGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 846)
- BMS3h-38-201
 GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 30 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGTACGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
 TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATTACTGTGGGAAAGAGCCGTTCTACTACGACTACT
 35 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 847)
- BMS3h-38-202
 GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGTACGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
 TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATCCAAGAACACGCTG
 40 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATTACTGTGGGAAAGAGCCGTTCTACTTCGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 848)
- BMS3h-38-203
 GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 45 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGTACGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
 TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATTACTGTGGGAAAGAGCCGTTCTCTACGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 849)

- BMS3h-38-204
GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGCGCAGCCTCCGGAT
TCACCTTTCCCAAGGAGGAGATGATTTGGGTCCGTCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATCCAAGAACACGCTG
5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 850)
- BMS3h-38-205
GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGCGCAGCCTCCGGAT
10 TCACCTTTTTCGCGCCGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 851)
- BMS3h-38-206
GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGCGCAGCCTCCGGAT
15 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAG
GCCCGGTACGAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
20 GGGGTCAAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 852)
- BMS3h-38-207
GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGCGCAGCCTCCGGAT
25 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTCG
GATGGGTTTCAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 853)
- BMS3h-38-208
GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGCGCAGCCTCCGGAT
30 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTCG
GTGGGGTTCAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
35 GGGGTCAAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 854)
- BMS3h-38-209
GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGCGCAGCCTCCGGAT
40 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTCG
CCTCGGTTGGAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 855)
- BMS3h-38-210
GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGCGCAGCCTCCGGAT
45 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGTCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTCG
CTGGGGTTCAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 856)

- BMS3h-38-211
 GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGAT
 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGTCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAG
 GCAGGGTGGGAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGTGACAATTCCAAGAACACGCTG
 5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 857)
- BMS3h-38-212
 GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGAT
 10 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGT
 GTCCGGTTGGAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 858)
- BMS3h-38-213
 GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGAT
 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGT
 GTGGGGTTGGAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
 20 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 859)
- BMS3h-38-214
 GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGAT
 25 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGT
 GAACGGTCTGAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 860)
- BMS3h-38-215
 GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGAT
 30 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGT
 GCTGGGTTGGAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 861)
- BMS3h-38-216
 GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGAT
 40 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGT
 GTTGGGTTGGAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 862)
- BMS3h-38-217
 GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGAT
 45 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGT
 CAGGGGTTACAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 863)

- BMS3h-38-218
GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGAT
TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGTACGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAG
GCACGGTTGGAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCGCGACAATTCCAAGAACACGCTG
5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 864)
- BMS3h-38-219
GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGAT
10 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCGAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAAGCATTAGCAG
GAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 865)
- BMS3h-38-220
GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGAT
15 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCGAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTCG
GATCGGTAAACAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
20 GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 866)
- BMS3h-38-221
GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGAT
25 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCGAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
GCACGGTTGGAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 867)
- BMS3h-38-222
GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGAT
30 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCGAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTTCGAG
GTGGGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 868)
- BMS3h-38-223
GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGAT
35 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGTACGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCGCGACAATTCCAAGAACACGCTG
40 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCATGTATGACTACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 869)
- BMS3h-38-224
GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGAT
45 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGTACGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTCCGCTACGACTACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 870)

- BMS3h-38-225
 GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGAT
 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGTACGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
 TAGTGGTGGTGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATCCAAGAACACGCTG
 5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 871)
- BMS3h-38-226
 GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGAT
 10 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGTACGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
 TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTGTTACTATGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 872)
- BMS3h-38-227
 GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGAT
 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGTACGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
 TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATCCAAGAACACGCTG
 15 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCCAIGTACTATGACTACT
 20 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 873)
- BMS3h-38-228
 GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGAT
 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAG
 25 GAACGGTTTCAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 874)
- BMS3h-38-229
 GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGAT
 30 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTCG
 CACGGGTGGGAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 875)
- BMS3h-38-230
 GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGAT
 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTCG
 35 GGAGGGTGGGAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATCCAAGAACACGCTG
 40 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 876)
- BMS3h-38-231
 GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGAT
 45 TCCCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTCG
 GCAGGGTTGGAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 877)

- BMS3h-38-232
GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGCGCAGCCTCCGGAT
TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAG
GGGCGGTGGGAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 878)
- BMS3h-38-233
GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGCGCAGCCTCCGGAT
10 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAG
CAGCGGTTACAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 879)
- BMS3h-38-234
GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGCGCAGCCTCCGGAT
15 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAG
GAACGGTAGGAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
20 GGGGTACAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 880)
- BMS3h-38-235
GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGCGCAGCCTCCGGAT
25 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAG
GAACGGTTACAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 881)
- BMS3h-38-236
GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGCGCAGCCTCCGGAT
30 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAG
GAAGGGTAGCAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
35 GGGGTACAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 882)
- BMS3h-38-237
GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGCGCAGCCTCCGGAT
40 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAG
GGGCGGTTGGAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 883)
- BMS3h-38-238
GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGCGCAGCCTCCGGAT
45 TCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAG
CTCGGGTTACAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 884)

- BMS3h-38-239
 GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGAT
 TCACCTTTGAGGAGGAGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAG
 GAACGGTATGAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATCCAAGAACACGCTG
 5 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 885)
- BMS3h-38-240
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGAT
 10 TCACCTTTGAGGAGGAGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAG
 GAACGGTATGAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 886)
- BMS3h-41-1
 GAGGTGCAGCTGTTGGAGTCTGGGGAAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTACTGAGCATGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGAGTGGGTCTCATCTATTTCCGGG
 TAATGGTGCTAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTTAGGTTTGACTACT
 20 GGGGCCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 887)
- BMS3h-41-2
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 CCACCTTTACTGAGTATGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGAGTGGATCTCATCTATTTCCGGG
 25 TAATGGTGCTAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTCTGTGCGAAAGAGCCGCTTAGGTTTGACTACA
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 888)
- BMS3h-41-3
 GAGGTGCAGCTGTTGGAGCCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 30 TCACCTTTACTGAGTATGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTATGAGTGGGTCTCATCTATTTCCGGG
 TAATGGTGCTAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATCCAAGAACATGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTTAGGTTTGACTACT
 GGGGTCAGGGTACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 889)
- BMS3h-41-4
 GAGGTGCAGCTGTTGGATTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCACTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTACTGAGTATGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGAGTGGGTCTCATCTATTTCCGGG
 TAATGGTGCTAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATCCAAGAACACGCTG
 40 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTTAGGTTTGACTACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 890)
- BMS3h-41-5
 GAGGTGCAGCTGTTGGGGTCAGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 45 TCACCTTTACTGAGTATGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGAGTCTGAGTGGGTCTCATCTATTTCCGGG
 TAATGGTGCTAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTTAGGTTATGACGACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 891)

- BMS3h-41-6
GAGGTGCAGCGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTTCAGCCTCCGGAT
TCACCTTTAATGAGTATGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTTCGGG
TAATGGTGCTAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTTAGGTTTGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 892)
- BMS3h-41-7
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTTCAGCCTCCGGAT
10 TCACCTTTTCTGAGTATGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTTCGGG
TAATGGTGCTAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTTAGGTTTGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 893)
- BMS3h-41-8
GAGGTGCAGCTGTTGGAGCCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTTCAGCCTCCGGAT
15 TCACCTTTTCTGAGTCTGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTTCGGG
AAATGGTGCTAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTTAGGTTTGACTACT
20 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 894)
- BMS3h-41-9
GAGGTGCAGCTGTTGGAGCCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTTCAGCCTCCGGAT
25 TCACCTTTTCTGAGTATGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTTCGGG
TAATGGTGCTAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTTAGGTTTGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 895)
- BMS3h-41-10
GAGGTGCAGCTGTTGGAGTCTGGGGTAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTTCAGCCTCCGGAT
30 TCACCTTTTCTGAGTATGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTTCGGG
TAATGGTGCTAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTTAGGTTTGACAACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 896)
- BMS3h-41-11
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTTCAGCCTCCGGAT
35 TCACCTTTTCTGAGTATGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTTCGGG
TAATGGTGCTAATACATACTACGCAGACTCCGTGAAGGGCCGGTTCTCCGTCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTTAGGTTTGACTACT
40 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 897)
- BMS3h-41-12
GAGGTGCAGCGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTTCAGCCTCCGGAT
45 TCACCTTTTCTGAGTATGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTTCGGG
TAATGGTGCTAATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTTAGGTTTGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 898)

- BMS3h-41-13
GAGGTGCAGCTGTTGGAGTCTGCGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGACGCTCCGGAT
TCACCTTTGCTGAGTATGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCATCAATTTCCGGG
TAATGGTGCTAATACTACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
5 TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTTAGGTTTGACTACT
GGGGTCAGGGAGCCCTGGTCAACGCTCTCGAGC (SEQ ID NO: 899)
- BMS3h-41-14
GAGGTGCAGCTGTTGGAGCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCTGCGTCTCTCCTGTGACGCTCCGGAT
10 TCACCTTTACTGAGTATGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCCGGG
TAATGGTGCTAATACTACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTTAGGTTTGACAACT
GGGGTCAGGGAACCTGGTCAACGCTCTCGAGC (SEQ ID NO: 900)
- BMS3h-43-1
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCTCTGCGTCTCTCCTGTACAGCCTCCGGAT
15 TCACCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTAG
ACGTGGTTTTACTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCCGATTACGTATGATTGA
20 GGTATGCGCGTTTTGACTACTCGGGTCAGGGAACCTGGTCAACGCTCTCGAGC (SEQ ID NO: 901)
- BMS3h-43-2
GAGGAGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTACAGCCTCCGGAT
TCACCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTAG
25 ACGTGGTTTTACTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCCGATTACGTATGCTACGA
GGTATGCGCGTTTTGACTACTGGGGTCAGGGAACCTGGTCAACGCTCTCGAGC (SEQ ID NO: 902)
- BMS3h-43-3
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTACAGCCTCCGGAT
30 TCACCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTAG
GCGTGGTTTTACTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCCGATTACGTATGATGA
GGTATGCGCGTTTTGACTACTGGGGTCAGGGAACCTGGTCAACGCTCTCGAGC (SEQ ID NO: 903)
- BMS3h-43-4
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTACAGCCTCCGGAT
TCACCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTAG
GCGTGGTTTTACTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
40 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCCGATTACGTATGATGA
GGTATGCGCGTTTTGACAACTGGGGTCAGGGAACCTGGTCAACGCTCTCGAAC (SEQ ID NO: 904)
- BMS3h-43-5
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTACAGCCTCCGGAT
45 TCACCTTTAATACGTATGAGATGTCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGGTAG
GCGTGGTTTTACTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCCGATTACGTATGATTGA
GGTATGCGCGTTTTGACTACTCGGGTCAGGGAACCTGGTCAACGCTCTCGAGC (SEQ ID NO: 905)

BMS3h-43-6

GAGGTGCAGCTGATGGAGTCAGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTACAGCCTCCGGAT
TCTCCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCCAGGGAAAGGTCTAGAGTGGGTCTCAGGTATTAGTAG
GCGTGGTTTACTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAAGAGCCGATTACGTATGATATGA
GGTATGCGCGTTTGGACTACTGGGGTCGGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 906)

BMS3h-43-7

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTGCAGCCTGGGGGGTCCCTGCGTCTCTCCTGTACAGCCTCCGGAT
10 TCGCCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCCAGGGAAGGGACTAGAGTGGGTCTCAGGTATTAGTAG
GCATGGTTTACTACGACTACGCAGACTCCGTGAAGGGCCGGTTACCGTCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAAGAGCCGATTACGTATGATATGC
GGTATGCGCGTTTGGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 907)

BMS3h-43-8

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTACAGCCTCCGGAT
15 TCACCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTAG
GCGTGGTTTACTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTCTGTGCGAAAGAGCCGATTACGTATGATATGA
20 GGTATGCGCGTTTGGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 908)

BMS3h-43-9

GAGGTGCAGCTGTTGGAGTCTGGGGGGGCTTGGTTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTACAGCCTCCGGGT
25 TCACCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTAG
GCGTGGTTTACTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAAGAGCCGATTACGTATTCTATGA
GGTATGCGCGTTTGGACTACTGGGTCTGGGAACCATGGTCACCGTCTCGAGC (SEQ ID NO: 909)

BMS3h-43-10

GAGGTGCAGCTGCTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTACAGCCTCCGGAT
30 TCACCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTAG
GCGTGGTTTACTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAAGAGCCGATTACGTATGATATGA
35 GGTATGCGCGTTTGGACTACAGTGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 910)

BMS3h-43-11

GAGGTGCAGCTGTTGGAGTCTGGAGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTACAGCCTCCGGAT
40 TCACCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTAG
GCATGGTTTACTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAAGAGCCGATTACGTATGATATGA
GGTATGCGCGTTTGGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 911)

BMS3h-43-12

GAGGTGCAGCTGTTGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTACAGCCTCCGGAT
45 TCACCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTAG
GCGTGGTTTACTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAAGAGCCGATTACGTATGATATGA
GGTATGCGCGTTTGGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 912)

- BMS3h-43-13
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGATCCCTGCGTCTCTCCTGTACAGCCTCCGGTT
 TCACCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTAG
 GCGTGGTTTTACTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
 5 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTAIATTAATCTGTGCGAAAGAGCCGATTACGTATGATATGA
 GGTATGCGCGTTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 913)
- BMS3h-43-14
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTCGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTACAGCCTCCGGAT
 10 TCTCCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTAG
 GCGTGGTTTTACTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCCGATTACGTATGATATGA
 GGTATGCGCGTTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGGGC (SEQ ID NO: 914)
- BMS3h-43-15
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAACCTGGGGGGTCCCTGCGTCTCTCCTGTACAGCCTCCGGAT
 15 TCACCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTAG
 GCGTGGTTTTACTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCCGATTACGTATGATATGA
 20 GGTATGCGCGTTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 915)
- BMS3h-56-1
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGACGCTCCGGAT
 TCACCTTTTCGGGATTATGAGATGTCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 25 GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTCCGTTTACTTTTGAGGACT
 GGGGTGAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 916)
- BMS3h-56-2
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGACGCTCCGGAT
 30 TCACCTTTTCGGGATTATGAGATGTCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTCCGTTTACTTTTGACGACT
 GGGGTGAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 917)
- BMS3h-56-3
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGACGCTCCGGAT
 TCACCTTTTCGGGATTATGAGATGTCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
 40 TATCTGCAAATGAACAGCCTGCGTGACAGGATACCGCGGTATATTACTGTACGAAACTCCGTTTATTTTGAATACT
 GGGGTGAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 918)
- BMS3h-56-4
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGACGCTCCGGAT
 45 TCACCTTTTCGGGATTATGAGATGTCGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTCCGTTTATGTTTGACGACC
 GGGGTGAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 919)

- BMS3h-56-5
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGATGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
5 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGACGACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 920)
- BMS3h-56-6
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
10 TCTCCTTTCGGGATTATGAGATGTGGTGGTACCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTATTTTGACAAC
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 921)
- BMS3h-56-7
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
15 TCACCTTTCGGGATTATGAGATGTGGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTATTTTGACGACT
20 GGGGTCCGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 922)
- BMS3h-56-8
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCGGCGTCTCTCCTGTGCAGCCTCCGGAT
25 TCACCTTTCGGGATTATGAGATGTGGTGGTCCGCCAGGCTCCGGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTATTTTGAGGACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 923)
- BMS3h-56-9
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTATCCTGTGCAGCCTCCGGAT
30 TCACCTTTCGGGATTATGAGATGTGGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGATGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
35 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTATGTTGACGACC
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 924)
- BMS3h-56-10
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
40 TCACCTTTCGGGATTATGAGATGTGGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTATGTTGACGACC
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 925)
- BMS3h-56-11
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
45 TCACCTTTCGGGATTATGAGATGTGGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGAGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTATGTTGACGACC
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 926)

- BMS3h-56-12
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGATACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTTGAACTTCCGTTTATTTTCTGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 927)
- BMS3h-56-13
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGATACAGCCTGGGGGGTCCCTGCGTCTATCCTGTGCAGCCTCCGGAT
10 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGATGATACCGCGGTATATCACTGTACGAAACTCCGTTTATTTTCTGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 928)
- BMS3h-56-14
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGATACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
15 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTA
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTATTTTCTGACTCCA
20 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 929)
- BMS3h-56-15
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGATACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
25 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTCTGAGGACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 930)
- BMS3h-56-16
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGATACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
30 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGATGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTCTGAGGACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 931)
- BMS3h-56-17
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGATACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
35 TCCTCTTTTCGGGATTATGAGATGTGGTGGTACCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTCTGAGGACT
40 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 932)
- BMS3h-56-18
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGATACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
45 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACATGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTCTGAGGACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 933)

- BMS3h-56-19
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATCACTGTGCGAAACTCCGTTTACTTTTGAGGACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 934)
- BMS3h-56-20
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
10 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTACGAAACTCCGTTTACTTTTGAGGACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 935)
- BMS3h-56-21
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
15 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTTTGAACACTCCGTTTACTTTTGAGGACT
20 GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 936)
- BMS3h-56-22
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTATCCTGTGCAGCCTCCGGAT
TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
25 GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGATGATACCGCGGTATATCACTGTACGAAACTCCGTTTATTTTGAATACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 937)
- BMS3h-56-23
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
30 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGATGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAACCTTATAGTTTGACTCCT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 938)
- BMS3h-56-24
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
35 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGATGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
40 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATCACTGTGCGAAAGAACCTTATAGTTATGACTACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 939)
- BMS3h-56-25
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
45 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCGGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGATGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTCCGTTTACTTTTGAGGACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 940)

- BMS3h-56-26
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTATCCTGTGCAGCCTCCGGAT
 TCACCTTTCCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GCAGGGTACGCGTACATACTACGCAGACTCCGTGATGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 5 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACTGCGGTATATTACTGTGCGAAACTTCCGTTTATGTTGACGACC
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 941)
- BMS3h-56-27
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTATCCTGTGCAGCCTCCGGAT
 10 TCACCTTTCCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GCAGGGTACGCGTACATACTACGCAGACTCCGTGATGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACTGCGGTATATTACTGTGCGAAACTTCCGTTTATGTTGACGACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 942)
- BMS3h-56-28
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 15 TCACCTTTGCTGGGTATGAGTTGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GCAGGGTACGCGTACATACTACGCAGACTCCGTGATGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACTGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTGACGACT
 20 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 943)
- BMS3h-56-29
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 25 TCACCTTTGCTGGGTATGAGTTGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GCAGGGTACGCGTACATACTACGCAGACTCCGTGATGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACTGCGGTATATTACTGTGCGAAACTTCCGTTTATGTTGACGACC
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 944)
- BMS3h-56-30
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 30 TCACCTTTGCTGGGTATGAGATGTGGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GCAGGGTACGCGTACATACTACGCAGACTCCGTGATGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACTGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTGACGACT
 35 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 945)
- BMS3h-56-31
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTGCTGGGTATGAGATGTGGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 40 GCAGGGTACGCGTACATACTACGCAGACTCCGTGATGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACTGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTGACGACC
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 946)
- BMS3h-56-32
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 45 TCACCTTTCCGGGATTATGAGATGTGGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAATCC
 GCAGGGTACGCGTACATACTACGCAGACTCCGTGATGGGCCGGTTACCACTCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACTGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTGACGACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 947)

- BMS3h-56-33
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTATCCTGTGCAGCCTCCGGAT
TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGATGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACTGCGGTATATTACTGTGCGAAACTTCCGTTTATGTTGACGACC
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 948)
- BMS3h-56-202
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
10 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGACCTACTTTTCCGACC
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 949)
- BMS3h-56-203
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
15 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTCTTTGAGGAGT
20 GGGGTACAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 950)
- BMS3h-56-204
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
25 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGACGTACTTTAAGGACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 951)
- BMS3h-56-205
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
30 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTCCGAGT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 952)
- BMS3h-56-206
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
35 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
40 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGATGTTCTTTGAGGACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAAC (SEQ ID NO: 953)
- BMS3h-56-207
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
45 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTCCGTTTCCGAGT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 954)

- BMS3h-56-208
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTCGGGATTATGAGATGTGGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
 5 TATCTGCAAAATGACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTCCGAGT
 GGGGTACAGGAACCTGGTCAACGCTCTCGAGC (SEQ ID NO: 955)
- BMS3h-56-209
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 10 TCACCTTTCGGGATTATGAGATGTGGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GTACGGTAACCTCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
 GGGGTACAGGAACCTGGTCAACGCTCTCGAGC (SEQ ID NO: 956)
- BMS3h-56-210
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTCGGGATTATGAGATGTGGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GCCCGGTACCTTGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACC
 20 GGGGTACAGGAACCTGGTCAACGCTCTCGAGC (SEQ ID NO: 957)
- BMS3h-56-211
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTCGGGATTATGAGATGTGGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 25 GTGGGGTGGCTTGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
 GGGGTACAGGAACCTGGTCAACGCTCTCGAGC (SEQ ID NO: 958)
- BMS3h-56-212
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 30 TCACCTTTCGGGATTATGAGATGTGGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GATGGGTGGGTTCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
 GGGGTACAGGAACCTGGTCAACGCTCTCGAGC (SEQ ID NO: 959)
- BMS3h-56-213
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTCGGGATTATGAGATGTGGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GTGGGGTTCGCACACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
 40 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
 GGGGTACAGGAACCTGGTCAACGCTCTCGAGC (SEQ ID NO: 960)
- BMS3h-56-214
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 45 TCACCTTTCGGGATTATGAGATGTGGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GTCCGGTGGGCTGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
 GGGGTACAGGAACCTGGTCAACGCTCTCGAGC (SEQ ID NO: 961)

- BMS3h-56-215
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCACGGTTCGTTGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGACGACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 962)
- BMS3h-56-216
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
10 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GGCCGGTTCGTTGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 963)
- BMS3h-56-217
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
15 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GTGGGGTAGCTTGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
20 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 964)
- BMS3h-56-218
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
25 TCACCTTTCGGGACTACGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGACGACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 965)
- BMS3h-56-219
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGACTCCGGAT
30 TCACCTTTCGGCCGTGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
35 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 966)
- BMS3h-56-220
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
40 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GTACGGTGGGCTGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGACGACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 967)
- BMS3h-56-221
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
45 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GTGGGGTAACACACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 968)

- BMS3h-56-222
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GCACGGTGGCTACACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
 5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 969)
- BMS3h-56-223
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 10 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GCCCGGTATGCTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 970)
- BMS3h-56-224
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 15 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GTGGGGTCAGTTGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
 20 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 971)
- BMS3h-56-225
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 25 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GTGGGGTGGCTACACATACTACGCAGACTCCGTGAAGGGCCGATTACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 972)
- BMS3h-56-226
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 30 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GTCGGGTGGGTGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
 35 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 973)
- BMS3h-56-227
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 40 GTCGGGTGGGTGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 974)
- BMS3h-56-228
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 45 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GTCGGGTACGCTCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 975)

- BMS3h-56-229
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GTACGGTTTCGTTGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACACGCTG
5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGACGACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 976)
- BMS3h-56-230
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
10 TCACCTTTCCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GTGGGGTGGCTACACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 977)
- BMS3h-56-231
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
15 TCACCTTTCCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTGGGCTGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
20 GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 978)
- BMS3h-56-232
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
25 GTGGGGTTCACACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGACGACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 979)
- BMS3h-56-233
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
30 TCACCTTTCCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GTGGGGTACCTTGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGACGACT
35 GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 980)
- BMS3h-56-234
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
40 GAACGGTTCGGCTGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGACGACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 981)
- BMS3h-56-235
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
45 TCACCTTTCCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GTGGGGTCACTGACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGACGACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 982)

- BMS3h-56-236
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCACGGTGGCTCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATCCAAGAACACGCTG
5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGACGACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 983)
- BMS3h-56-237
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
10 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGAGCGGGTCTCAGCTATTAATCC
GGCGGGTATGTTGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGACGACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 984)
- BMS3h-56-238
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
15 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCACGGTACCTTGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
20 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 985)
- BMS3h-56-239
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
25 GTGGGGTTCGTTGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGACGACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 986)
- BMS3h-56-240
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
30 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GTACGGTGGCTGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
35 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 987)
- BMS3h-56-241
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCGGGATTACGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GGCCGGTTCTTGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATCCAAGAACACGCTG
40 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 988)
- BMS3h-56-242
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
45 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGAGCGGGTCTCAGCTATTAATCC
GTACGGTGGCTGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 989)

- 8MS3h-56-243
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GTGGGGTGGGTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 990)
- BMS3h-56-244
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
10 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GTGGGGTGGGTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 991)
- BMS3h-56-245
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
15 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GTACGGTGGGCTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
20 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 992)
- BMS3h-56-246
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
25 GTGGGGTACGTTGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 993)
- BMS3h-56-247
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
30 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GTGGGGTACGTTGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 994)
- BMS3h-56-248
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
35 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GTACGGTAACCTGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
40 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 995)
- BMS3h-56-249
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
45 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCACGGTGGGTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 996)

- BMS3h-56-250
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GGCCGGTTTCTACACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGACGACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 997)
- BMS3h-56-251
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
10 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GGCCGGTGGCTCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGACGACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 998)
- BMS3h-56-252
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
15 TCGCCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCACGGTTCCCTCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
20 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 999)
- BMS3h-56-253
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCGTTGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
25 GGCCGGTGGGTACACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTGAGGACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1000)
- BMS3h-56-254
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
30 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTGGTTTACGGAGT
35 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1001)
- BMS3h-56-255
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
40 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTCCGAGC
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1002)
- BMS3h-56-256
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
45 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTGTTCAGGAGT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1003)

- BMS3h-56-257
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGACAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGACGCGTTTGAGGACT
GGGGTCAGGGAACCTTGGTACCGTCTCGAGC (SEQ ID NO: 1004)
- BMS3h-56-258
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
10 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGACAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTACAGAGT
GGGGTCAGGGAACCTTGGTACCGTCTCGAGC (SEQ ID NO: 1005)
- BMS3h-56-259
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
15 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGACAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCCGTTTCTGTTATGACTACT
20 GGGGTCAGGGAACCTTGGTACCGTCTCGAGC (SEQ ID NO: 1006)
- BMS3h-56-260
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
25 GCAGGGTACGCGTACATACTACGACAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGACGTTCTTTAAGGACT
GGGGTCAGGGAACCTTGGTACCGTCTCGAGC (SEQ ID NO: 1007)
- BMS3h-56-261
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
30 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGACAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTCTTTTACGAGT
35 GGGGTCAGGGAACCTTGGTACCGTCTCGAGC (SEQ ID NO: 1008)
- BMS3h-56-262
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
40 GCAGGGTACGCGTACATACTACGACAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGAGTTGTTTACGAGC
GGGGTCAGGGAACCTTGGTACCGTCTCGAGC (SEQ ID NO: 1009)
- BMS3h-56-263
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
45 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGACAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGAGCTCTTTGAGGACT
GGGGTCAGGGAACCTTGGTACCGTCTCGAGC (SEQ ID NO: 1010)

- BMS3h-56-264
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATCTGTGCGAAACTTCCGTTTGGGTTTCCGAGT
 GGGGTACAGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 1011)
- BMS3h-56-265
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 10 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAACTTCCGAGTTGTTTCAGGACT
 GGGGTACAGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 1012)
- BMS3h-56-266
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 15 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAACTTCCGTTTTCCTTTCACGAGT
 20 GGGGTACAGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 1013)
- BMS3h-56-267
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 25 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAACTTCCGCACTACTTTAAGGACT
 GGGGTACAGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 1014)
- BMS3h-56-268
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGTCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 30 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAACTTCCGTTTACTTTGAGGAGT
 35 GGGGTACAGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 1015)
- BMS3h-56-269
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 40 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAACTTCCGTTTAGGTTTCCGACC
 GGGGTACAGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 1016)
- BMS3h-56-270
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 45 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAACTTCCGACGCTTTTCAGGACT
 GGGGTACAGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 1017)

- BMS3h-56-271
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTCCGAGT
GGGGTCAGGGAACCTGGTACCGTCTCGAAC (SEQ ID NO: 1018)
- BMS3h-56-272
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
10 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTGGTTTCAGGAGT
GGGGTCAGGGAACCTGGTACCGTCTCGAGC (SEQ ID NO: 1019)
- BMS3h-56-273
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
15 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GTGGGGTTCGTTGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTCAGGAGT
20 GGGGTACAGGGAACCTGGTACCGTCTCGAGC (SEQ ID NO: 1020)
- BMS3h-56-274
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
25 GTGGGGTTCGTTGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGATGTTCTTTGAGGACT
GGGGTCAGGGAACCTGGTACCGTCTCGAAC (SEQ ID NO: 1021)
- BMS3h-56-275
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
30 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GTGGGGTTCGTTGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTCAGGAGT
35 GGGGTACAGGGAACCTGGTACCGTCTCGAGC (SEQ ID NO: 1022)
- BMS3h-56-276
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
40 GTGGGGTTCGTTGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTCTTTTCAGGAGT
GGGGTCAGGGAACCTGGTACCGTCTCGAGC (SEQ ID NO: 1023)
- BMS3h-56-277
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
45 TCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GTGGGGTTCGTTGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTCTTTTCAGGAGT
GGGGTCAGGGAACCTGGTACCGTCTCGAGC (SEQ ID NO: 1024)

- BMS3h-56-278
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GTGGGGTGGGTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTACGGAGT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1025)
- BMS3h-56-279
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 10 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GTGGGGTGGGTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGATGTTCTTTGAGGACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAAC (SEQ ID NO: 1026)
- BMS3h-56-280
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GTGGGGTGGGTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 15 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTACCGAGT
 20 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1027)
- BMS3h-56-281
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 25 GTGGGGTGGGTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTACCGAGT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1028)
- BMS3h-56-282
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 30 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GTGGGGTGGGTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTACCGAGT
 35 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1029)
- BMS3h-56-283
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GTGGGGTGGGTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 40 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTACGGAGT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1030)
- BMS3h-56-284
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 45 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
 GTGGGGTGGGTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGATGTTCTTTGAGGACT
 GGGGTCAGGGAACCTGGTCACCGTCTCGAAC (SEQ ID NO: 1031)

- BMS3h-56-285
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GTGGGGTGGGTTGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAACTCCGTTTTTACTTTCACGAGT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 1032)
- BMS3h-56-286
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
10 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GTGGGGTGGGTTGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAACTCCGTTTTTCTTTTCAGGAGT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 1033)
- BMS3h-56-287
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
15 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GTGGGGTGGGTTGACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAACTCCGTTTTTCTTTTCAGGAGT
20 GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 1034)
- BMS3h-56-288
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
25 TCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCC
GCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAACTCCGATGTTCTTTGAGGACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 1035)
- BMS3h-106-1
GAGGTGCAGCTGTTGGAGACTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
30 TCACCTTTTCGACTTATCATATGCAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCAATGATTGATGC
GGATGGTCTTGGGACATACTACGCAGACCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAGACCGGGTCCGCAATTTGGTCAGT
TTGACTACTTGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 1036)
- BMS3h-106-2
GAGGTGCAGCTGTTTGGAGTCTGGGGGAGGCTTGGTACAGACTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
35 TCACCTTTTCGACTTATCATATGCAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCAATGATTGATGC
GGATGGTCTTGGGAAATACTACGCAGACCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
40 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAACCGGGTCCGCAATTTGGTCAGT
ATGACTACTGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 1037)
- BMS3h-107-1
GAGGTGCAGCTGTTGGAGTCAAGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGGCTCTCCTGTTTCAGCTTCCGGAT
45 TCACCTTTTCGGGATTGATATGCAGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAACGATTAGTGC
GTCGGGTGTTTATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAAATATCCTAATCGTTTTGCGCTTA
ATAGTTTTGACTACAGGGTTCGGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 1038)

- BMS3h-107-2
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCTTCCGGAT
TCACCTTTTCGGGGTATGATATGCAGTGGGTCCGCCAGGCTCCAGGGAGGGGTCTAGAGTGGGTCTCAACGATTAGTGC
GTCGGGTGTTTATACATACTACACAGACTCCGTGAAGGGCCGGTTCACACCTCCCGGACAATCCAAGAACACGCTG
5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTACGAAATATCAAAATCGTTTTGCGGTA
ATAATTTGACTACTGGGTACGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1039)
- BMS3h-131-1
GACATCCTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAATA
10 GTTCTATTTTGTGGGCGTTAGCTTGGTACCAGCAGAAACCAGGGGAAGCCCTAAGCTCCTGATCGAGAGTTCTTCCGG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGTTTCAAGATGCGGTTTGGCTGGTACGTTACGCCAAGGGACCAAGGTGGAAA
TCAAACGG (SEQ ID NO: 1040)
- 15 BMS3h-131-2
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGACAGACA
GTTCTATTTTGTGGGCGTTAGCTTGGTACCAGCAGAAACCAGGGAAAGCCCTAAGCTCCTGATCGAGAGTTCTTCCGG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGTTTCAAGATGCGGTTTGGCTGGTACGTTACGCCAAGGGACCAAGGTGGAAA
20 TCAAACGG (SEQ ID NO: 1041)
- BMS3h-131-3
GACATCCAGATGACCGTGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGACAGATA
GTTCTATTTTGTGGGCGTTAGCTTGGTACCAGCAGAAACCAGGGAAAGCCCTAAGCTCCTGATCGAGAGTTCTTCCGG
25 ATTGCAAAGCGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGTTTCAAGATGCGGTTTGGCTGGTACGTTACGCCAAGGGACCAAGGTGGAAA
TCAAACGG (SEQ ID NO: 1042)
- 30 BMS3h-131-4
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAATA
GTTCTATTTTGTGGGCGTTAGCTTGGTACCAGCAGAAACCAGGGAAAGCCCTAAGCTCCTGATCGAGAGTTCTTCCGG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGTTTCAAGATGCGGTTTGGCTGGTACGTTACGCCAAGGGACCAAGGTGGAAA
35 TCAAACGG (SEQ ID NO: 1043)
- BMS3h-131-5
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAATA
GTTCTATTTTGTGGGCGTTAGCTTGGTACCAGCAGAAACCAGGGAAAGCCCTAAGCTCCTGATCGAGAGTTCTTCCGG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
40 CCTGAAGATTTTGTACGTACTACTGTGTTTCAAGATGCGGTTTGGCTGGTACGTTACGCCAAGGGACCAAGGTGGAAA
TCAAACGG (SEQ ID NO: 1044)
- 45 BMS3h-131-6
GACATCCAGATGACCGTGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAATA
GTTCTATTTTGTGGGCGTTAGCTTGGTACCAGCAGAAACCAGGGAAAGCCCTAAGCTCCTGATCGAGAGTTCTTCCGG
ATTGCAAAGCGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGTTTCAAGATGCGGTTTGGCTGGTACGTTACGCCAAGGGACCAAGGTGGAAA
TCAAACGG (SEQ ID NO: 1045)

- BMS3h-131-7
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAGATA
GTTCTATTTGTGGGCGTTAGCTTGGTACCAGCAGAAACAGGGAAAGCCCCAAGCTCCTGATCGAGAGTTCTTCCGG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
5 CCTGAAGATTTGCTACGTACTACTGTGTTTCAAGATGCGGTTTGGCCTGGTACGTTTCGACCAAGGGACCAAGGTGGAAA
TCAAACGG (SEQ ID NO: 1046)
- BMS3h-131-8
GACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAATA
10 GTTCTATTTGTGGGCGTTAGCTTGGTACCAGCAGAAACAGGGAAAGCCCCAAGCTCCTGATCGAGAGTTCTTCCGG
TCTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTGCTACGTACTACTGTGTTTCAAGATGCGGTTTGGCCTGGTACGTTTCGGCCAAGGGACCAAGGTGGAAA
TCAAACGG (SEQ ID NO: 1047)
- BMS3h-131-9
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCGAATA
15 GTTCTATTTGTGGGCGTTAGCTTGGTACCAGCAGAAACAGGGAAAGCCCCAAGCTCCTGATCGAGAGTTCTTCCGG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTGCTACGTACTACTGTGTTTCAAGATGCGGTTTGGCCTGGTACGTTTCGGCCAAGGGACCAAGGTGGAAA
20 ACAAACGG (SEQ ID NO: 1048)
- BMS3h-131-10
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAATA
25 GTTCTATTTGTGGGCGTTAGCTTGGTACCAGCAGAAACAGGGAAAGCCCCAAGCTCCTGATCGAGAGTTCTTCCGG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCCGAAGATTTGCTACGTACTACTGTGTTTCAAGATGCGGTTTGGCCTGGTACGTTTCGGCCAAGGGACCAAGGTGGAAA
TCAAACGG (SEQ ID NO: 1049)
- BMS3h-131-11
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAATA
30 GTTCTATTTGTGGGCGTTAGCTTGGTACCAGCAGAAACAGGGAAAGCCCCAAGCTCCTGATCGAGAGTTCTTCCGG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTGCTACGTACTACTGTGTTTCAAGATGCGGTTTGGCCTGGTACGTTTCGGCCAAGGGACCAAGGTGGAAA
35 TCAAACGG (SEQ ID NO: 1050)
- BMS3h-131-12
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAATA
40 GTTCTATTTGTGGGCGTTAGCTTGGTACCAGCAGAAACAGGGAAAGCCCCAAGCTCCTGATCGAGAGTTCTTCCGG
ATTGCAAAGCGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTGCTACGTACTACTGTGTTTCAAGATGCGGTTTGGCCTGGTACGTTTCGGCCAAGGGACCAAGGTGGAAA
TCAAACGG (SEQ ID NO: 1051)
- BMS3h-131-13
GACATCCTGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAATA
45 GTTCTATTTGTGGGCGTTAGCTTGGTACCAGCAGAAACAGGGAAAGCCCCAAGCTCCTGATCGAGAGTTCTTCCGG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTGCTACGTACTACTGTGTTTCAAGATGCGGTTTGGCCTGGTACGTTTCGGCCAAGGGACCAAGGTGGAAA
TCAAACGG (SEQ ID NO: 1052)

- BMS3h-131-14
GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAATA
GTTCTATTTTGTGGGCGTTAGCTTGGTACCAGCAGAAACCAGGGAAAGCCCTAAGCTCCTGATCGAGAGTTCTTCCGG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGAAAGTGGAACTGGGACAGATTTCACCTCACCATCAGCGGTCTGCAA
5 CCTGAAGATTTTGTACGTACTACTGTGTTTCAAGATGCGGTTTGGCCTGGTACGTTGACCAAGGGACCAAGGTGGAA
TCAAACGG (SEQ ID NO: 1053)
- BMS3h-131-15
GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGCATCTGTAGGAGACCGTGTACCATCCCTTGCCGGGCAAATA
10 GTTCTATTTTGTGGGCGTTAGCTTGGTACCAGCAGAAACCAGGGAAAGCCCTAAGCTCCTGATCGAGAGTTCTTCCGG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGCACTGGGACAGATTTCACCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGTTTCAAGATGCGGTTTGGCCTGGTACGTTGCGCAAGGGACCAAGGTGGAGA
TCAAACGG (SEQ ID NO: 1054)
- BMS3h-193-1
GACATCCAGATGAGCCAGTCTCCATCCTCCCTGCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
AGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCTAAGCTCCTGATCTATCTTGCTTCCCG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTATCAGTATGCGAGTCCACCTTTGACGTTAGGCCAAGGGACCAAGTGGAAA
15 TCAAACGG (SEQ ID NO: 1055)
- BMS3h-193-2
GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGCATCTGTAGGAGACAGTGTACCATCACTTGCCGGGCAAGTC
AGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCTAAGCTCCTGATCTATCTTGCTTCCCG
25 TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGCCATCAGTATGCGAGTCCACCTTTGACGTTGCGCAAGGGACCAAGTGGAAA
TCAAACGG (SEQ ID NO: 1056)
- BMS3h-193-3
GACATCCAGATGACCCAGTCTCCATCCTCCCTATCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
AGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCTAAGCTCCTGATCTATCTTGCTTCCCG
30 TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTGCGTACTACTGTATCAGTACGAGAGTCCACCTTTGACGTTTGGCCAAGGGACCAAGTGGAAA
TCAAACGG (SEQ ID NO: 1057)
- BMS3h-193-4
GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
GGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCTAAGCTCCTGATCTATCTTGCTTCCCG
35 TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTGCGCAAGGGACCAAGTGGAAA
40 TCAAACGG (SEQ ID NO: 1058)
- BMS3h-193-5
GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGCATCTGTAGGAGAACGTGTACCATCACTTGCCGGGCAAGTC
AGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCTAAGCTCCTGATCTATCTTGCTTCCCG
45 TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACCTCACCATCAGCAATCTGCAA
CCTGAAGATTTGCTACGTACTACTGTATCAGTATGCGAGTCCACCTTTGACGTTAGGCCAAGGGACCAAGTGGAAA
TCAAACGG (SEQ ID NO: 1059)

- BMS3h-193-6
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGCC
AGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGGGAAAGGCCCTAAGCTCCTGATCTATCTTGCTTCCCG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
5 CCTGAAGATTTTGCTACGTACTACTGTCTCATCAGTATGCGAGTCCACCTTTGACGTTAGGCCAAGGGACCAAAGTGAAAA
TCAAACGG (SEQ ID NO: 1060)
- BMS3h-193-7
GACATCCAGATAACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
10 AGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCTAAGCTCCTGATCTATCTTGCTTCCCG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTCTCATCAGTATGAGAGTCTCCTTTGACGTTTGGCCAAGGGACCAAAGTGAAAA
TCAAACGG (SEQ ID NO: 1061)
- BMS3h-193-8
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
15 AGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGGGAAAGGCCCTAAGCTCCTGATCTATCTTGCTTCCCG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTCTCATCAGTATGAGAGTCCACCTTTGACGTTTGGCCAAGGGACCAAAGTGAAAA
20 TCAAATGG (SEQ ID NO: 1062)
- BMS3h-193-9
GACATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTACCATCACTTGCCGGGCAAGTC
25 AGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGGGAAAGGCCCTAAGCTCCTGATCTATCTTGCTTCCCG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGAAATTCACCTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTCTCATCAGTATGAGAGTCCACCTTTGACGTTTGGCCAAGGGACCAAAGTGAAAA
TCAAACGG (SEQ ID NO: 1063)
- BMS3h-193-10
GACATCCAGATGTCCAGTCTCCATCCACCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
30 AGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGGGAAAGGCCCTAAGCTCCTGATCTATCTTGCTTCCCG
CTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTCTCATCAGTATGAGAGTCCACCTTTGATGTTTGGCCAAGGGACCAAAGTGAAAA
35 TCAAACGG (SEQ ID NO: 1064)
- BMS3h-193-11
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATTACTTGCCGGGCAAGTC
40 AGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCTAAGCTCCTGATCTATCTTGCTTCCCG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCAGAAGATTTTGCTACGTACTACTGTCTCATCAGTATGAGAGTCCACCTTTGACGTTTGGCCAAGGGACCAAAGTGAAAA
TCAAACGG (SEQ ID NO: 1065)
- BMS3h-193-12
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCCGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
45 AGACGATTGAGCGTCGTTTAACTGGTATCAGCAGAAACCAGGGAAAGCCCTAAGCTCCTGATCTATCTTGCTTCCCG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTCTCATCAGTATGAGAGTCCACCTTTGACGTTTGGCCAAGGGACCAAAGTGAAAA
TCAAACGG (SEQ ID NO: 1066)

- BMS3h-193-13
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTTTGCATCTGTAGGGGACCGTGTACCATCACTTGCCGGGCAAGTC
AGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACAGGGAAAGCCCCTAAGCTCCTGATCTATCTTGCTTCCCG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
5 CCTGAAGATTTTGCTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTGCGCCAAGGGACCAAAGTGGAAT
TCAAACGG (SEQ ID NO: 1067)
- BMS3h-193-14
GACATCCAGATGACCCAGTATCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
10 AGTCGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACAGGGAAAGCCCCTAAGCTCCTGATCTATCTTGCTTCCCG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTGCGCCAAGGGACTAAAGTGGAAT
TCAAACGG (SEQ ID NO: 1068)
- BMS3h-193-15
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
15 GGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACAGGGAAAGCCCCTAAGCTCCTGATCTATCTTGCTTCCCG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTGCGCCAAGGGACCAAAGTGGAAT
20 TCAAACGG (SEQ ID NO: 1069)
- BMS3h-193-16
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
25 AGGCGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACAGGGAAAGCCCCTAAGCTCCTGATCTATCTTGCTTCCCG
TTTGCAAAGTGGGGTCCCATCTCGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCAGAAAGATTTTGCTACGTACTACTGTATCAGTATGCGAGTCCACCTTTGACGTTGCGCCAAGGGACCAAAGTGGAAT
TCAAACGG (SEQ ID NO: 1070)
- BMS3h-193-17
AACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
30 AGGCGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACAGGGAAAGCCCCTAAGCTCCTGATCTATCTTGCTTCCCG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTGCGCCAAGGGACCAAAGTGGAAT
35 TCAAACGG (SEQ ID NO: 1071)
- BMS3h-193-18
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
40 AGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACAGGGAAAGCCCCTAAGCTCCTGATCTATCTTGCTTCCCG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTGCGCCAAGGGACCAAAGTGGAAT
TCAAACGG (SEQ ID NO: 1072)
- BMS3h-193-19
GACATCCAGATGACCCAGTCTCCATCCTCCCTTTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
45 AGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACAGGGAAAGCCCCTAAGCTCCTGATCTATCTTGCTTCCCG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTGCGCCAAGGGACCAAAGTGGAAT
TCAAACGG (SEQ ID NO: 1073)

- BMS3h-193-20
GACATCCAGATGACCCAGACTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
AGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGGGGAAAGCCCTAAGCTCCTGATCTATCTTGCTTCCCG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
5 CCTGAAGATTTTCCACGTACTACTGTCTCATCAGTATGAGAGTCCACCTTTGACGTTTGGCCAAGGGACCAAAGTGAAAA
TCAAACGG (SEQ ID NO: 1074)
- BMS3h-193-21
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGTGTACCATCACTTGCCGGGCAAGTC
10 AGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGGGGAAAGCCCTAAGCTCCTGATCTATCTTGCTTCCCG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCCGAAGATTTTGTACGTACTACTGTCTCATCAGTATGAGAGTCCACCTTTGACGTTTGGCCAAGGGACCAAAGTGAAAA
TCAAACGG (SEQ ID NO: 1075)
- BMS3h-193-22
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
15 AGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGGGGAAAGCCCTAAGCTCCTGATCTATCTTGCTTCCCG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTCTCATCAGTATGAGAGTCCACCTTTGACGTTTGGCCAAGGGACCAAAGTGAAAA
20 TCAAACGG (SEQ ID NO: 1076)
- BMS3h-193-23
GACGTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
25 AGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGGGGAAAGCCCTAAGCTCCTGATCTATCTTACTTCCCG
TTTGCAAAGCGGGTCCCATCACGTTTCAGTGGTAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTCTCATCAGTATGCGAGTCCACCTTTGACGTTTGGCCAAGGGACCAAAGTGAAAA
TCAAACGG (SEQ ID NO: 1077)
- BMS3h-193-24
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
30 AGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGGGGAAAGCCCTAAGCTCCTGATCTATCTTGCTTCCCG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTCTCATCAGTATGAGAGTCCACCTTTGACGTTTGGCCAAGGGACCAAAGTGTTAA
35 TCAAACGG (SEQ ID NO: 1078)
- BMS3h-193-25
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTACCATCACTTGCCGGGCAAGTC
40 AGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGGGGAAAGCCCTAAGCTCCTGATCTATCTTGCTTCCCG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTCTCATCAGTATGAGAGTCCACCTTTGACGTTTGGCCAAGGGACCAAAGTGAAAA
TCAAACGG (SEQ ID NO: 1079)
- BMS3h-193-26
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
45 AGCCGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGGGGAAAGCCCTAAGCTCCTGATCTATCTTGCTTCCCG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTCTCATCAGTATGAGAGTCCACCTTTGACGTTTGGCCAAGGGACCAAAGTGAAAA
TCAAACGG (SEQ ID NO: 1080)

- 5 BMS3h-193-27
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
AGACGATTGGGCGTCGTTTAAATTGGTATCAGCAGAAACAGGGAAAGCCCTAAGCTCCTGATCTATCTTGCTTCCCG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTCAICAGIAIGAGAGTCCACCTTTGACGTTTCGGCCAAGGGACCAAAGTGGAAA
TCAAACGG (SEQ ID NO: 1081)
- 10 BMS3h-193-28
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCACTCACTTGCCGGGCAAGTC
AGTCGATTGAGCGCCGTTTAAATTGGTATCAGCAGAAACAGGGAAAGCCCTAAGCTCCTGATCTATCTTGCTTCCCG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTCAICAGIAIGAGAGTCCACCTTTGACGTTTCGGCCAAGGGACCAAAGTGGAAA
TCATACGG (SEQ ID NO: 1082)
- 15 BMS3h-193-29
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTACCATCACTTGCCGGGCAAGTC
AGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCTGGGAAAGCCCTAAGCTCCTGATCTATCTTGCTACCCG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTCAICAGIAIGAGAGTCCACCTTTGACGTTTCGGCCAAGGGACCAAAGTGGAAA
20 TCAAACGG (SEQ ID NO: 1083)
- BMS3h-193-30
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
AGTCGATTGAGCGCCGTTTAAATTGGTATCAGCAGAAACAGGGAAAGCCCTAAGCTCCTGATCTATCTTGCTTCCCG
25 TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTCAICAGIAIGAGAGTCCCTCTTGACGTTTCGGCCAAGGGACCAAAGTGGAAA
TCAAACGG (SEQ ID NO: 1084)
- 30 BMS3h-193-2501
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTACCATCACTTGCCGGGCAAGTC
AGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCTGGGAAAGCCCTAAGCTCCTGATCTATCTTGCTACCCG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTCAICAGIAIGAGACCCACCTTTGACGTTTCGGCCAAGGGACCAAAGTGGAAA
35 TCAAACGG (SEQ ID NO: 1085)
- BMS3h-193-2502
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTACCATCACTTGCCGGGCAAGTC
TCCCCATTGACCGTCGTTTAAATTGGTATCAGCAGAAACCTGGGAAAGCCCTAAGCTCCTGATCTATCTTGCTACCCG
TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
40 CCTGAAGATTTTGCTACGTACTACTGTCAICAGIAIGAGAGTCCACCTTTGACGTTTCGGCCAAGGGACCAAAGTGGAAA
TCAAACGG (SEQ ID NO: 1086)
- BMS3h-193-2503
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTACCATCACTTGCCGGGCAAGTC
CCACCATTTGGCCGTCGTTTAAATTGGTATCAGCAGAAACCTGGGAAAGCCCTAAGCTCCTGATCTATCTTGCTACCCG
45 TTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTCAICAGIAIGAGAGTCCACCTTTGACGTTTCGGCCAAGGGACCAAAGTGGAAA
TCAAACGG (SEQ ID NO: 1087)

- BMS3h-193-2504
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTTACCATCACTTGCCGGGCAAGTT
CCCAGATTGGGCGTCGTTAAATTGGTACAGCAGAAACCAAGGAAAGCCCCTAGGCTCCTGATCTATCTTGCTACCCG
TTTGCAAAGTGGGGTCCCATCACGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
5 CCTGAAGATTTTGCTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTCCGGCAAGGGACCAAAGTGAAAA
TCAAACGG (SEQ ID NO: 1088)
- BMS3h-193-2505
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCATCACTTGCCGGGCAAGTG
10 AGCGGATTGGGCGTCGTTAAATTGGTATCAGCAGAAACCAAGGAAAGCCCCTAGGCTCCTGATCTATCTTGCTACCCG
TTTGCAAAGTGGGGTCCCATCACGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTCCGGCAAGGGACCAAAGTGAAAA
TCAAACGG (SEQ ID NO: 1089)
- BMS3h-193-2506
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCATCACTTGCCGGGCAAGTC
15 AGCAGATTGGCGCCGTTAAATTGGTATCAGCAGAAACCAAGGAAAGCCCCTAGGCTCCTGATCTATCTTGCTACCCG
TTTGCAAAGTGGGGTCCCATCACGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTCCGGCAAGGGACCAAAGTGAAAA
20 TCAAACGG (SEQ ID NO: 1090)
- BMS3h-193-2507
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCATCACTTGCCGGGCAAGTC
25 AGCGGATTGGCGCCGTTAAATTGGTACAGCAGAAACCAAGGAAAGCCCCTAGGCTCCTGATCTATCTTGCTACCCG
TTTGCAAAGTGGGGTCCCATCACGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTCCGGCAAGGGACCAAAGTGAAAA
TCAAACGG (SEQ ID NO: 1091)
- BMS3h-193-2508
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCATCACTTGCCGGGCAAGTC
30 GGAACATTGGCGTCGTTAAATTGGTACAGCAGAAACCAAGGAAAGCCCCTAGGCTCCTGATCTATCTTGCTACCCG
TTTGCAAAGTGGGGTCCCATCACGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTCCGGCAAGGGACCAAAGTGAAAA
35 TCAAGCGG (SEQ ID NO: 1092)
- BMS3h-193-2509
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCATCACTTGCCGGGCAAGTC
GGAACATTGACCGTCGTTAAATTGGTACAGCAGAAACCAAGGAAAGCCCCTAGGCTCCTGATCTATCTTGCTACCCG
40 TTTGCAAAGTGGGGTCCCATCACGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTCCGGCAAGGGACCAAAGTGAAAA
TCAAACGG (SEQ ID NO: 1093)
- BMS3h-193-2510
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCATCACTTGCCGGGCAAGTC
45 AGAGCATTGGCGTCGTTAAATTGGTACAGCAGAAACCAAGGAAAGCCCCTAGGCTCCTGATCTATCTTGCTACCCG
TTTGCAAAGTGGGGTCCCATCACGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTCCGGCAAGGGACCAAAGTGAAAA
TCAAACGG (SEQ ID NO: 1094)

- BMS3h-193-2511
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCATCACCTTGCCGGGCAAGTC
AGAACATTGGGACGCGTTTAAATTGGTACCAGCAGAAACCAGGGAAAGCCCTAGGCTCCTGATCTATCTTGCTACCCG
TTTGCAAAGTGGGGTCCCATCACGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
5 CCTGAAGATTTTGCTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTGCGCCAAGGGACCAAAGTGAAAA
TCAAACGG (SEQ ID NO: 1095)
- BMS3h-193-2512
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCATCACCTTGCCGGGCAAGTG
AGGTCAATTGGGCGTCGTTTAAATTGGTACCAGCAGAAACCAGGGAAAGCCCTAGGCTCCTGATCTATCTTGCTACCCG
10 TTTGCAAAGTGGGGTCCCATCACGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTGCGCCAAGGGACCAAAGTGAAAA
TCAAACGG (SEQ ID NO: 1096)
- BMS3h-193-2513
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCATCACCTTGCCGGGCAAGTG
AGGCGATTGGCCGTCGTTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCTAGGCTCCTGATCTATCTTGCTACCCG
15 TTTGCAAAGTGGGGTCCCATCACGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTGCGCCAAGGGACCAAAGTGAAAA
TCAAACGG (SEQ ID NO: 1097)
- BMS3h-193-2514
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCATCACCTTGCCGGGCAAGTA
CCAGCATTGGCGCTCGTTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCTAGGCTCCTGATCTATCTTGCTACCCG
20 TTTGCAAAGTGGGGTCCCATCACGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTGCGCCAAGGGACCAAAGTGAAAA
TCAAACGG (SEQ ID NO: 1098)
- BMS3h-193-2515
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCATCACCTTGCCGGGCAAGTT
TGAACATTGGGCGTCGTTTAAATTGGTACCAGCAGAAACCAGGGAAAGCCCTAGGCTCCTGATCTATCTTGCTACCCG
30 TTTGCAAAGTGGGGTCCCATCACGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTGCGCCAAGGGACCAAAGTGAAAA
TCAAACGG (SEQ ID NO: 1099)
- BMS3h-193-2516
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCATCACCTTGCCGGGCAAGTC
AGACGATTGAGCGTCGTTTAAATTGGTACCAGCAGAAACCAGGGAAAGCCCTAGGCTCCTGATCTATCTTGCTCGAA
40 GTTGCAAAGTGGGGTCCCATCACGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTATCAGTATGAGAGTCCACCTTTGACGTTGCGCCAAGGGACCAAAGTGAAAA
TCAAACGG (SEQ ID NO: 1100)
- BMS3h-198-1
GAGGTGCAGCTGTTGGAGTCTGGGGAGGCTTGTTGACCTGGGGGTCCTGCGTCTCTCTGTGCAGCTCCGGAT
45 CCACCATTTGCTGGGTATGAGATGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGTGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCGGTTCAACATCTCCCGAGACGATTCCAAGAACACGCTG
TATCTGCAATGAACAGCTGCGTGCCGAGGATACCGCGGTATTAATTGTGCGAGAGATCCTTATAGTTTTGACTACT
GGGGTCAGGGAACCTGGTCAACGCTCTCGAGC (SEQ ID NO: 1101)

- BMS3h-198-2
GAGGTGCAGCCGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGATCTCAGCTATTAGCGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACGATTCCAAGAACACGCTG
5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAGAGATCCTTAGTTTTGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1102)
- BMS3h-198-3
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTCGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCACCGGAT
10 CCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACGATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAGAGATCCTTAGTTATGACTACT
GGGGTCAGGGAACCTGGTCTCCGTCTCGAGC (SEQ ID NO: 1103)
- BMS3h-198-4
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAC
15 TCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACGATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGAGTATATCACTGTGCGAGAGATCCTTAGTTTTGACTACT
20 GGGGTCAAGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1104)
- BMS3h-198-5
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
25 TCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCTGTGAAGGGCCGGTTACCATCTCCCGCGACGATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATCACTGTGCGAAAGAACCTTAGTTATGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1105)
- BMS3h-198-6
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
30 CCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACGATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGTGAAAGATCCTTAGTTTTGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1106)
- BMS3h-198-7
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
35 CCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACGATTCCAAGAACACGCTG
40 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAGAGATCCTTAGTTTTGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1107)
- BMS3h-198-8
GAGGTGCAGCTGATGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
45 CCACCTTTGCTGGGTATGAGATGTGGTGGTACCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
AAGTGGTAGAAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACGATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGGGTATATTACTGTGCGAAAGATCCTTAGTTTTGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1108)

- BMS3h-198-9
GAGGTGCAGCTGCTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCTGGGTATGAGATGTGGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCAGCATCCAAGAACACGCTG
5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAACCTTATAGTTTTGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1109)
- BMS3h-198-10
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
10 CCACCATTTGCTGGGTATGAGATGTGGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCAGCATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATCCATATAGTTTTGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1110)
- BMS3h-198-11
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
15 TCACCTTTGCTGGGTATGAGATGTGGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCAGCATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATCCATATAGTTTTGACTACT
20 GGGGTCAGGGAACCTGGTCTCCGTCTCGAGC (SEQ ID NO: 1111)
- BMS3h-198-12
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
25 TCACCATTTGCTGGGTATGAGATGTGGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCCGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCAGCATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATCCATATAGTTTTGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1112)
- BMS3h-198-13
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
30 TCACCTTTGCTGGGTATGAGATGTGGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCACC CGCAGCATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATCCATATAGTTTTGACTACT
35 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1113)
- BMS3h-198-14
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCTGGGTATGAGATGTGGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCAGCATCCAAGAACACGCTG
40 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATCCATATAGTTTTGACTACT
GGCGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1114)
- BMS3h-198-15
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
45 CCACCTTTGCTGGGTATGAGGTGTGGTGGTCCGCCAGGCTCCAGGGAAGGGTCTGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCAGCATCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAGAGATCCATATAGTTTTGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1115)

- BMS3h-198-16
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
CCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGATCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACGATTCCAAGAACACGCTG
5 TATCTGAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATCCTTAGTTTTGACTACT
GGGGTCAGGGAACCTGGTACCGTCTCGAGC (SEQ ID NO: 1116)
- BMS3h-198-17
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
10 TCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACGATTCCAAGAACACGCTG
TATCTGCAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAGAGATCCTTAGTTTTGACTACT
GGGGTCAGGGAACCTGGTACCGTCTCGAGC (SEQ ID NO: 1117)
- BMS3h-198-18
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAC
15 TCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACGATTCCAAGAACACGCTG
TATCTGCAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAGAGATCCTTAGTTTTGACTACT
20 GGGGTCAGGGAACCTGGTACCGTCTCGAGC (SEQ ID NO: 1118)
- BMS3h-198-19
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAT
TCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
25 AAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACGATTCCAAGAACACGCTG
TATCTGCAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAGAGATCCTTAGTTTTGACTACT
GGGGTCAGGGAACCTGGTACCGTCTCGAGC (SEQ ID NO: 1119)
- BMS3h-198-20
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCCCGGAT
30 TCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACGATTCCAAGAACACGCTG
TATCTGCAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAACCTTAGTTTTGACTACT
GGGGTCAGGGAACCTGGTACCGTCTCGAGC (SEQ ID NO: 1120)
- BMS3h-198-21
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGAC
TCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
35 TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACGATTCCAAGAACACGCTG
TATCTGCAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAGAGATCCTTAGTTTTGACTACT
GGGGTCAGGGAACCTGGTACCGTCTCGAGC (SEQ ID NO: 1121)
- BMS3h-198-22
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCCGGGGGTCCCTGCGTCTCTCTGTGCCGCTCCGGAT
45 TCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGCGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACGATTCCAAGAACACGCTG
TATCTGCAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAACCTTAGTTATGACTACT
GGGGTCATGGAACCTGGTACTGTCTCGAGC (SEQ ID NO: 1122)

- BMS3h-198-23
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCTGGGTATGAGATGTGGTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAACACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCAGGATTCCAAGAACACGCTG
5 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGGGGTATATTACTGTGCGAGAGATCCTTATAGTTTTGACTACT
GGGGTCAGGGTACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1123)
- BMS3h-198-24
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
10 TCACCTTTGCTGGGTATGAGATGTGGTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCAGGATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAACCTTATAGTTTTGACTCT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1124)
- BMS3h-198-25
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
15 TAACCTTCGCTGGGTATGAGATGTGGTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGCGGTCTCAGCTATTAGTGG
TAGTGGCGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCAGGATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAACCTTATAGTTTTGACTACT
20 GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1125)
- BMS3h-198-26
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
CCACCTTTGCTGGGTATGAGATGTGGTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
25 TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCCATCTCCCGCAGGATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAACCTTATAGTTTTGACCACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1126)
- BMS3h-198-27
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
30 CCACCTTTGCTGGGTATGAGATGTGGTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCAGGATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAGAGATCCTTATAGTTTTGACTACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1127)
- BMS3h-198-28
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTGCTGGGTATGAGATGTGGTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCAGGATTCCAAGAACACGCTG
40 TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATCCTTATAGTTTTGACAACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1128)
- BMS3h-198-29
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAGAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
45 TCACCTTTGCTGGGTATGAGATGTGGTGGGTCGCGCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCAGGATTCCAAGAACACGCTG
TATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAACCTTATAGTTTTGACCACT
GGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1129)

- BMS3h-198-30
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
ACACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTG
5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAACCTTATAGTTTTGACCACC
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 1130)
- BMS3h-198-31
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
10 TCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCTGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAACCTTATAGTTATGACTACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 1131)
- BMS3h-198-32
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
15 TCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATCCTTATAGTTTGGACAACT
20 GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 1132)
- BMS3h-198-33
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
25 TCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCTGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAACCTTATAGTTATGACTACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 1133)
- BMS3h-198-34
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
30 TCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATCCTTATAGTTTGGACAACT
35 GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 1134)
- BMS3h-198-35
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
40 TCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCTGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAACCTTATAGTTATGACTACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 1135)
- BMS3h-198-36
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
45 TCACCTTTGCTGGGTATGAGATGTGGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGG
TAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATCCTTATAGTTTGGACAACT
GGGGTCAGGGAACCTTGGTCACCGTCTCGAGC (SEQ ID NO: 1136)

- BMS3h-198-37
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTGCTGGGTATGAGTTGTGGTGGTCCGCCAGGCCCCAGGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTG
 AAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACGATCCAAGAACACGCTG
 5 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGTATATTACTGTGCGAAAGATCCTTATAGTTTGTACTACC
 GGGGTCAAGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1137)
- BMS3h-198-38
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 10 TCACCTTTGCTGGGTATGAGTTGTGGTGGTCCGCCAGGCCCCAGGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTG
 AAGTGGTGGTAGCACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACGATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGTATATTACTGTGCGAAAGATCCTTATAGTTTGTACTACT
 GGGGTCAAGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1138)
- BMS3h-202-1
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTCCGACTGCTGAGATGCTGTGGTCCGCAAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCCGGC
 TAGTGGTGGTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
 15 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGTATATTACTGTGCGAAAGAGCCGGTGAGTTATGTGGCGA
 20 CGTTTGACTACTGGGGTCAAGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1139)
- BMS3h-202-2
 GAGGTGCAGCTGTTGGTGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTCCGACTGCTGAGATGTTGTGGTCCGCCAGGCTCCAGGGAAGGGTCCAGAGTGGGTCTCATCAATTTCCGGC
 25 TAGTGGTGGTTTACATACTATGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGTATATTACTGTGCGAAAGAGCCGGTGAGTTATGTGGCGA
 CGTTTGACTACTGGGGTCAAGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1140)
- BMS3h-202-3
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 30 TCACCTTTCCGACTGCTGAGATGTTGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCCGGC
 TAGTGGTGGTTATACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACATGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGTATATTACTGTGCGAAAGAGCCGGTGAGTTATGTGGCGA
 35 CGTTTGACTACTGGGGTCAAGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1141)
- BMS3h-202-4
 GAGGTGCAGCTGTTGGTGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 TCACCTTTCCGACTGCTGAGATGTTGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCCGGC
 40 TAGTGGTGGTTTACATACTACGCAGACTCCGTGAAGGGCCGGTTCTCATCTCCCGCGACGATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGTATATTACTGTGCGAAAGAGCCGGTGAGTTATGTGGCGA
 CGTTTGACTACTGGGGTCAAGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1142)
- BMS3h-202-5
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
 45 TCACATTTCCGACTGCTGAGATGTTGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCCGGC
 TAGTGGTGGTTTACATACTACGCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATCCAAGAACACGCTG
 TATCTGCAAAATGAACAGCCTGCGAGCCGAGGACACCGCGTATATTACTGTGCGAAAGAGCCGGTGAGTTATGTGGCAA
 CGTTTGACTACTGGGGTCAAGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1143)

- BMS3h-202-6
GAGGCGCAGCTGTTGGAGTCTGGGGGTGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
TCACCTTTCCGACTGCTGAGATGGTGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGATCTCATCTATTTCCGGC
TAGTGGTGGTTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCAGAAGACAGCTG
5 TATCTGCAATTGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGGTGAGTTATGTGGCGA
CGTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1144)
- BMS3h-202-7
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
10 TCACATTTCCGACTGCTGAGATGTTGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCCGGC
TAGTGGTGGTTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCAGAAGACAGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGGTGAGTTATGTGGCGA
CGTTTGACTACTGGGGTCCAGGAGCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1145)
- BMS3h-202-8
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
15 TCACCTTTCCGACTGCTGAGATGCTGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCCGGC
TAGTGGTGGTTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCAGAAGACAGCTG
TTTCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGGTGAGTTATGTGGCGA
20 CGTTTGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1146)
- BMS3h-202-9
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
25 TCACATTTCCGACTGCTGAGATGTTGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCCGGC
TAGTGGTGGTTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCAGAAGACAGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGGTGAGTTATGTGGCGA
CGTTTGACTACTGGGGTCCAGGAGCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1147)
- BMS3h-202-10
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
30 TCACCTTTCCGACTGCTGAGATGCTGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCCGGC
TAGTGGTGGTTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCAGAAGACAGCTG
TATTTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGGTGATTTATGTGGCGA
CGTTTGACTACTGGGGTCCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1148)
- BMS3h-202-11
GAGGTGCAGCTGTTGGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGAT
35 TCACCTTTCCGACTGCTGAGATGCTGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCCGGC
TAGTGGTGGTTCTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCAGAAGACAGCTG
TATCTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGGTGAGTTATGTGGCGA
40 CGTTTGACTACTGGGGTCCAGGGAACCTGGTCACCGTCTCGAGC (SEQ ID NO: 1149)
- BMS3h-217-1
AACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
45 ATTTTATTTGGTACTCTGTTAACTTGGTACCAGCATAAACAGGGAAGCCCTAAGCTCCTGATCACTTATGTTCCCTT
GTTGCAAAAGTGGGGTCCCATCACGTTTCACTGGGAGTGGATCTGGGACAGATTTCACTCTACCATCAGCAGTCTGCAA
CCTGAAGATTTGCTACGTACTACTGTGTCAGGGGGTGTGTGGCTGCGACGTTTGGCCAAGGGACCAAGGTGGAAA
TCAAACGG (SEQ ID NO: 1150)

- BMS3h-217-2
GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGTCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACACGGAAAGCCCTAAACTCCTGATCACTTATGGTTCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTACCATCAGCAGTCTGCAT
5 CCTGAAGATTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCTCCGACGTTCCGGTCAAGGGACCAAGGTGGAAA
TCAAACGG (SEQ ID NO: 1151)
- BMS3h-217-3
GACATCCAGATGACCCAGTCTCCGTCTCCCTGACTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
10 ATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACACGGGAAAGCCCTAAAGTCTCTGGTCACTTATGGTTCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTACCATCAGCAATCTGCAA
CCTGAAGATTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCTCTACGTTCCGGCAAGGGACCAAGGTGGAAA
ACATACGG (SEQ ID NO: 1152)
- BMS3h-217-4
GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGTCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
15 ATTTTATTGCTACTCTGTTATCTTGGTACCAGCAGAAACACGGGAAAGCCCTAAAGTCTCTGATCACTTATGGTTCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTACCATCAGCAGTCTGCAA
CCTGAAGATTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCTCCGACGTTCCGGCAAGGGACCAAGGTGGAAA
20 TCAAACGG (SEQ ID NO: 1153)
- BMS3h-217-5
GACATCCAGATGACCCAGTCTCCATCCTCCTGCTGTCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
25 ATTTTATTGCTACTCTGTTATCTTGGTACCAGCAGAAACACGGGAAAGCCCTAAAGTCTCTGATCACTTATGGTTCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTACCATCAGCAGTCTGCAA
CCTGAAGATTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCTCCGACGTTCCGGCAAGGGACCAAGGTGGAAA
TCAAACGG (SEQ ID NO: 1154)
- BMS3h-217-6
GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGTCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
30 ATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACACGGGAAAGCCCTAAAGTCTCTGATCACTTATGGTTCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTACCATCAGCAGTCTGCAA
CCTGAAGACTTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCCCCGACGTTCCGGCAGGGGACCAAGGTGGAAA
35 TCAAACGT (SEQ ID NO: 1155)
- BMS3h-217-7
GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGTCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
40 ATTTTATTGGTCTCTGTTATCTTGGTACCAGCATAAACACGGGAAAGCCCTAAAGTCTCTGATCACTTATGGTTCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTACCATCAGCAGTCTGCAA
CCTGAAGATTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTCCGGCAAGGGACCAAGGTGGAAA
TCAAACGG (SEQ ID NO: 1156)
- BMS3h-217-8
GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGTCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
45 ATTTTATTGGTACTCTGTTATCTTGGTACCAGCATAAACACGGGAAAGCCCTAAAGTCTCTGATCACTTATGGTTCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTACCATCAGCAGTCTGCAA
CCTGAAGATTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTCCGGCAAGGGACCAAGGTGGAAA
TCAAACGG (SEQ ID NO: 1157)

- BMS3h-217-9
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTGGTACTCTGTTATCTTGGTACCAGCATAAACAGGGAAAGCCCCAAGCTCCTGATCACTTATGGTTCCAT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
5 CCTGAAGATTTTGCAACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTTCGGCCAAGGGACCAAGGTGGAAA
TCAAACGG (SEQ ID NO: 1158)
- BMS3h-217-10
GACATCCAGATGACTCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTACCATCACTTGCCGGGCAAGTC
10 ATTTTATTGGTACTCTGTTATCTTGGTACCAGCATAAACAGGGAAAGCCCCAAGCTCCTGATCACCTATGGTTCCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGGTCAGGGAGTGTGTGGCTGCGACGTTTCGGCCAAGGGACCAAGGTGGAAA
TCAAACGG (SEQ ID NO: 1159)
- BMS3h-217-11
GACATCCAGATGACCCAGTCTCCATCCTCCCTGACTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
15 ATTTTATTGGTACTCTGTTATCTTGGTACCAGCATAAACAGGGAAAGCCCCAAGCTCCTGATCACTTATGGTTCCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTTCGGCCAAGGGACCAAGGTGGAAA
20 TCAAACGG (SEQ ID NO: 1160)
- BMS3h-217-12
AACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTGGTACTCTGTTATCTTGGTACCAGCATAAACAGGGAAAGCCCCAAGCTCCTGATCACTTATGGTTCCCTT
25 GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTTCGGCCAAGGGACCAAGGTGGAAA
TCAAACGG (SEQ ID NO: 1161)
- BMS3h-217-13
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCAATTGCCGGGCAAGTC
30 ATTTTATTGGTACTCTGTTATCTTGGTACCAGCATAAACAGGGAAAGCCCCAAGCTCCTGATCACTTATGGTTCCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTTCGGCCAAGGGACCAAGGTGGAAA
35 TCAAACGG (SEQ ID NO: 1162)
- BMS3h-217-14
GACATCCAGTTGACCCAGTACCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACAGGGAAAGCCCAAGCTCCTGATCACTTATGGTTCCCTT
40 GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGGTCAGGGGGTGTGTGGCTCCGACGTTTCGGCCAAGGGACCAAGGTGGAAA
TCAAACGG (SEQ ID NO: 1163)
- BMS3h-217-15
GACATCCAGATGACACAGTCTCCATCCTCCCTGTATGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGTAAAGTC
45 ATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACAGGGAAAGCCCAAGCTCCTGATCACTTATGGTTCCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCAGCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGGTCAGGGGGTGTGTGGCCCCGACGTTTCGGACAAGGGACCAAGGTGGAAA
TCAAACAG (SEQ ID NO: 1164)

- 5 BMS3h-217-16
GACATTCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACCAAGGAAAGCCCTAAGCTCCTGATCACTTATGGTTCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCTCCGACGTTGGCCAAGGGACCAAGGTGAAAA
TCAAACGG (SEQ ID NO: 1165)
- 10 BMS3h-217-17
GACATCCAGATTATCCAGTCTCCATCCTCCCTTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACCAAGGAAAGCCCTAAGCTCCTGATCACTTATGGTTCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCTCCGACGTTGGCCAAGGGACCAAGGTGAAAA
TCAAACGG (SEQ ID NO: 1166)
- 15 BMS3h-217-18
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTGGTACTCTGTTATCTTGGTACCAGCTGAAACCAAGGAAAGCCCTAAGCTCCTGATCACTTATGGTTCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTGGCCAAGGGACCAAGGTGAAAA
TCAAACGG (SEQ ID NO: 1167)
- 20 BMS3h-217-19
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTGGTACTCTGTTATCTTGGTACCAGCTGAAACCAAGGAAAGCCCTAAGCTCCTGATCACTTATGGTTCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTGGCCAAGGGACCAAGGTGAAAA
ACAAACGG (SEQ ID NO: 1168)
- 25 BMS3h-217-20
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTGGTACTCTGTTATCTTGGTACCAGCTTAAACCAAGGAAAGCCCTAAGCTCCTGATCACTTATGGTTCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTGGCCAAGGGACCAAGGTGAAAA
TCAAACGG (SEQ ID NO: 1169)
- 30 BMS3h-217-21
GACATCCAGATGACCCAGGCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTGGTACTCTGTTATCTTGGTACCAGCTGAAACCAAGGAAAGCCCTAAGCTCCTGATCACTTATGGTTCCTT
GTTGCAAGTGGGGTCCCATCACGTTTCAGTGGTGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTGGCCAAGGGACCAAGGTGAAAA
ACAAACGG (SEQ ID NO: 1170)
- 35 BMS3h-217-22
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACCAAGGAAAGCCCTAAGCTCCTGATCACTTATGGTTCCTT
GTTGCAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTGCTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTGGCCAAGGGACCAAGGTGAAAA
TCAAACGG (SEQ ID NO: 1171)
- 40
- 45

- BMS3h-217-23
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTGGTAGTCTGTTATCTTGGTACCAGGTGAAACCAGGGAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
5 CCTGAAGATTTTGCTACGTACTACTGTGGTCAGGGGGTGTCTGTGGCTGCGACGTTGCGCCAAGGGACAACGGTGAAAA
TCAAACGG (SEQ ID NO: 1172)
- BMS3h-217-24
GACATCCTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
10 ATTTTATTGGTAGTCTGTTATCTTGGTACCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTGGTCAGGGGGTGTCTGTGGCTGCGACGTTGCGCCAAGGGACCAAGGTGAAAA
TCAAACGG (SEQ ID NO: 1173)
- BMS3h-217-25
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
15 ATTTTATTGGTAGTCTGTTATCTTGGTACCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTGGTCAGGGGGTGTCTGTGGCTGCGACGTTGCGCCAAGGGACCAAGGTGAAAA
20 TCAAACGG (SEQ ID NO: 1174)
- BMS3h-217-26
GACATCCAGATGACCCAGTCTCCATCCTCTCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
25 ATTTTATTGGTAGTCTGTTATCTTGGTACCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTGGTCAGGGGGTGTCTGTGGCTGCGACGTTGCGCCAAGGGACCAAGGTGAAAA
ACAAACGG (SEQ ID NO: 1175)
- BMS3h-217-27
GACATCAAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
30 ATTTTATTGGTAGTCTGTTATCTTGGTACCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTGGTCAGGGGGTGTCTGTGGCTGCGACGTTGCGCCAAGGGACCAAGGTGAAAA
35 TCAAACGG (SEQ ID NO: 1176)
- BMS3h-217-28
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCAGGCAAGTC
40 ATTTTATTGGTAGTCTGTTATCTTGGTACCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTGGTCAGGGGGTGTCTGTGGCCCGCAGCTTCGGCCAAGGGACCAAGGTGAAAA
TCAAACGG (SEQ ID NO: 1177)
- BMS3h-217-29
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
45 ATTTTATTGGTAGTCTGTTATCTTGGTACCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTGGTCAGGGGGTGTCTGTGGCTGCGACGTTGCGCCAAGGGACCAAGGTGAAAA
TCAAACGG (SEQ ID NO: 1178)

- BMS3h-217-30
 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTTGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
 ATTTTATTGGTACTCTGTTATCTTGGTACCAGCTGAAACCAAGGAAAGCCCTAAGCTCCTGATCACTTATGGTTCCTG
 GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
 5 CCTGAAGATTTTGTACGTACTACTGTGGTCAGGGGGTGTGTGGCCTGCGACGTTCCGCCAAGGGACCAAGGTGGAAA
 TCAAACGG (SEQ ID NO: 1179)
- BMS3h-217-31
 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
 10 ATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACCGGGAAAGCCCTAAGCTCCTGATCACTTATGGTTCCTT
 GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATTTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
 CCTGAAGATTTTGTACGTACTACTGTGGTCAGGAGGTGCTGTGGCCTGCGACGTTCCGCCAAGGGACTAAGGTGGAAA
 TCAAACGG (SEQ ID NO: 1180)
- BMS3h-217-32
 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCTCCATCACTTGCCGGGCAAGTC
 15 ATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACCAAGGAAAGCCCTAAGCTCCTGATCACTTATGGTTCCTT
 GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATTTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
 CCTGAAGATCTTGTACGTACTACTGTGGTCAGGAGGTGCTGTGGCCTGCGACGTTCCGCCAAGGGACCAAGGTGGAAA
 20 TCAAACGG (SEQ ID NO: 1181)
- BMS3h-217-33
 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCAGGCAAGTC
 25 ATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACCAAGGAAAGCCCTAAGCTCCTGATCACTTATGGTTCCTT
 GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATTTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
 CCCGAAGATTTTGTACGTACTACTGTGGTCAGGAGGTGCTGTGGCCTGCGACGTTCCGCCAAGGGACCAAGGTGGAAA
 TCAAACGG (SEQ ID NO: 1182)
- BMS3h-217-34
 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
 30 ATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACCGGGAAAGCCCTAAGCTCCTGATCACTTATGGTTCCTT
 GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATTTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
 CCTGAAGATTTTGTACGTACTACTGTGGTCAGGGGGTGTGTGGCCTGCGACGTTCCGCCAAGGGACCAAGGTGGAAA
 35 TCAAACGG (SEQ ID NO: 1183)
- BMS3h-217-35
 GACATCCAGATGACCCAGTCAACATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
 ATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACCAAGGAAAGCCCTAAGCTCCTGATCACTTATGGTTCCTT
 GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
 40 CCTGAAGATTTTGTACGTACTACTGTGGTCAGGGGGTGTGTGGCCTCCGACGTTCCGCCAAGGGACCAAGGTGGAAA
 TCAAACGG (SEQ ID NO: 1184)
- BMS3h-217-2301
 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
 45 ACTTCATTGCCAGTCTGTTATCTTGGTACCAGGTGAAACCAAGGAAAGCCCTAAGCTCCTGATCACTTATGGTTCCTT
 GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
 CCTGAAGATTTTGTACGTACTACTGTGGTCAGGGGGTGTGTGGCCTGCGACGTTCCGCCAAGGGACCAAGGTGGAAA
 TCAAACGG (SEQ ID NO: 1185)

- BMS3h-217-2302
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTCAATTGCCAGCTGTTATCTTGGTACCAGGTGAAACAGGGAAAGCCCCAAGCTCCTGATCACTTATGGTTCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
5 CCTGAAGATTTTGTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTCCGGCAAGGGACAACGGTGAAAA
TCAAACGG (SEQ ID NO: 1186)
- BMS3h-217-2303
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
10 ATTTCAATTGCCAGCTGTTATCTTGGTACCAGGTGAAACAGGGAAAGCCCCAAGCTCCTGATCACTTATGGTTCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTCCGGCAAGGGACAACGGTGAAAA
TCAGACGG (SEQ ID NO: 1187)
- BMS3h-217-2304
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
15 ATTACATTGCCCTCCCTGTTATCTTGGTACCAGGTGAAACAGGGAAAGCCCCAAGCTCCTGATCACTTATGGTTCCTT
GTTGCAGAGTGGGGGCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTCCGGCAAGGGACAACGGTGAAAA
20 TCAAACGG (SEQ ID NO: 1188)
- BMS3h-217-2305
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
25 ATTTTATTGGTAGTCTGTTATCTTGGTACCAGGTGAAACAGGGAAAGCCCCAAGCTCCTGATCACTTGGGCTCCTA
CTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTCCGGCAAGGGACAACGGTGAAAA
TCAAACGG (SEQ ID NO: 1189)
- BMS3h-217-2306
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
30 ATTTTATTGGTAGTCTGTTATCTTGGTACCAGGTGAAACAGGGAAAGCCCCAAGCTCCTGATCACTTGGAGTCCTA
CTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTCCGGCAAGGGACAACGGTGAAAA
35 TCAAACGG (SEQ ID NO: 1190)
- BMS3h-217-2307
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
40 ATTTTATTGGTAGTCTGTTATCTTGGTACCAGGTGAAACAGGGAAAGCCCCAAGCTCCTGATCACTTGGTCGTCTTA
CTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTCCGGCAAGGGACAACGGTGAAAA
TCAAACGG (SEQ ID NO: 1191)
- BMS3h-217-2308
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
45 ATTTTATTGGTAGTCTGTTATCTTGGTACCAGGTGAAACAGGGAAAGCCCCAAGCTCCTGATCACTTGGGGTCTTG
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTCCGGCAAGGGACAACGGTGAAAA
TCAAACGG (SEQ ID NO: 1192)

- BMS3h-217-2309
GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGTCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTGGTAGTCTGTTATCTTGGTACCAGGTGAAACCAGGGAAAGCCCTAAGCTCCTGATCACTTGGGCGTCTG
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
5 CCTGAAGATTTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTTCGGCCAAGGGACAACGGTGGAAT
TCAAACGG (SEQ ID NO: 1193)
- BMS3h-217-2310
GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGTCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTGGTAGTCTGTTATCTTGGTACCAGGTGAAACCAGGGAAAGCCCTAAGCTCCTGATCACTTGGAGCTCCTG
10 GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTTCGGCCAAGGGACAACGGTGGAAT
TCAAACGG (SEQ ID NO: 1194)
- BMS3h-217-2311
GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGTCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTGGATTGCCAGCTGTTATCTTGGTACCAGGTGAAACCAGGGAAAGCCCTAAGCTCCTGATCACTTATGGTTCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
15 CCTGAAGATTTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTTCGGCCAAGGGACAACGGTGGAAT
TCAAACGG (SEQ ID NO: 1195)
- BMS3h-217-2312
GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGTCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTGGTTCGCTCTTACGCTGGTACCAGGTGAAACCAGGGAAAGCCCTAAGCTCCTGATCACTTATGGTTCCTT
25 GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTTCGGCCAAGGGACAACGGTGGAAT
TCAAACGG (SEQ ID NO: 1196)
- BMS3h-217-2313
GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGTCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATCGGATTGCCAGCTGTTATCTTGGTACCAGGTGAAACCAGGGAAAGCCCTAAGCTCCTGATCACTTATGGTTCCTT
30 GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTTCGGCCAAGGGACAACGGTGGAAT
TCAAACGG (SEQ ID NO: 1197)
- BMS3h-217-2314
GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGTCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTACATTGCCCTCCTGTTATCTTGGTACCAGGTGAAACCAGGGAAAGCCCTAAGCTCCTGATCACTTATGGTTCCTT
35 GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTTCGGCCAAGGGACAACGGTGGAAT
40 TCAAACGG (SEQ ID NO: 1198)
- BMS3h-217-2315
GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGTCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTGGTAGTCTGTTATCTTGGTACCAGGTGAAACCAGGGAAAGCCCTAAGCTCCTGATCCGGTTCGGCTCCTT
45 GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTTCGGCCAAGGGACAACGGTGGAAT
TCAAACGG (SEQ ID NO: 1199)

- BMS3h-217-2316
GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGCTCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTGGTAGTCTGTTATCTTGGTACCAGGTGAAACCAGGGAAAGCCCCTAAGCTCCTGATCACTTACAAGTCCTA
CTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
5 CCTGAAGATTTTGTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTTCGGCCAAGGGACAACGGTGAAAA
TCAAACGG (SEQ ID NO: 1200)
- BMS3h-217-2317
GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGCTCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
10 ATTTTATTGGTAGTCTGTTATCTTGGTACCAGGTGAAACCAGGGAAAGCCCCTAAGCTCCTGATCACTTGGGGCTCCTA
CTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTTCGGCCAAGGGACAACGGTGAAAA
TCAAACGG (SEQ ID NO: 1201)
- BMS3h-217-2318
GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGCTCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
15 ATTTTATTGGGGCCCTTATCTTGGTACCAGGTGAAACCAGGGAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTTCGGCCAAGGGACAACGGTGAAAA
20 TCAAACGG (SEQ ID NO: 1202)
- BMS3h-217-2319
GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGCTCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTGGATTGCCACCCCTGTTATCTTGGTACCAGGTGAAACCAGGGAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTT
25 GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTTCGGCCAAGGGACAACGGTGAAAA
TCAAACGG (SEQ ID NO: 1203)
- BMS3h-217-2320
GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGCTCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
30 ATTTTATTGGGGCCCTTATCTTGGTACCAGGTGAAACCAGGGAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTT
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTTCGGCCAAGGGACAACGGTGAAAA
35 TCAAACGG (SEQ ID NO: 1204)
- BMS3h-217-2321
GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGCTCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
ATTTTATTGGTAGCTCTTAACTGGTACCAGGTGAAACCAGGGAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTT
40 GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTTCGGCCAAGGGACAACGGTGAAAA
TCAAACGG (SEQ ID NO: 1205)
- BMS3h-217-2322
GGCATCCAGATGACCCAGTCTCCATCCTCCCTGCTGCTCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTC
45 ATTTTATTGGTAGTCTGTTATCTTGGTACCAGGTGAAACCAGGGAAAGCCCCTAAGCTCCTGATCACTTACGGGTCCTG
GTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGTACGTACTACTGTGGTCAGGGGGTGTGTGGCTGCGACGTTTCGGCCAAGGGACAACGGTGAAAA
TCAAACGG (SEQ ID NO: 1206)

Example 1**Generation of Human Anti-CD40 Variable Domains
BMS3h-1 through BMS3h-225**

The following example describes the generation of a series of anti-human CD40 variable domains, designated BMS3h-1 through BMS3h-225. Following recombinant expression of a repertoire of single immunoglobulin variable domains on the surface of phage, selection is performed by contacting the phage repertoire with immobilized target antigen, washing to remove unbound phage, and propagating the bound phage. This process frequently referred to as "panning." It is applicable to the screening of single immunoglobulin variable domains, as well as other antibody fragments that can be expressed on a display library, e.g., scFv, Fab, and Fab'. Alternatively, phage may be pre-selected for the expression of properly folded member variants by panning against an immobilized generic ligand (e.g., protein A or protein L) that is only bound by folded members. This has the advantage of reducing the proportion of non-functional members, thereby increasing the proportion of members likely to bind a target antigen. Pre-selection with generic ligands is taught in WO 99/20749, for example. The screening of phage antibody libraries is generally described, for example, by Harrison et al., *Meth. Enzymol.* 267: 83-109 (1996).

Screening is commonly performed using purified antigen immobilized on a solid support, for example, plastic tubes or wells, or on a chromatography matrix, for example SepharoseTM (Pharmacia). Screening or selection can also be performed on complex antigens, such as the surface of cells (Marks et al., *BioTechnology* 11: 1145 (1993); de Kruif et al., *Proc. Natl. Acad. Sci. USA* 92: 3938 (1995)). Another alternative involves selection by binding biotinylated antigen in solution, followed by capture on streptavidin-coated beads.

Clones BMS3h-1 to BMS3h-69:

Three rounds of selections using decreasing concentrations of antigen (100 nM at round 1; 10 nM at round 2; 1 nM at round 3) were performed in parallel against both biotinylated human CD40 monomer (supplied by BMS, 1.5 moles biotin / mole CD40) and biotinylated human CD40-Ig (supplied by BMS, 3.3 moles biotin / mole CD40-Ig). Phage from the naïve 4G and 6G Domantis dAb libraries were combined as follows before initiating selections:

- 1) 4G + 6G VH CDR3 lengths between 7 – 9 amino acids.
- 2) 4G + 6G VH CDR3 lengths between 10 – 12 amino acids.
- 3) 4G + 6G VH CDR3 lengths between 13 – 15 amino acids.
- 4) 4G VK
- 5) 6G VK

Each round of selection involved adding the desired concentration of antigen to a mixture of 750 µl of phage from one of the naïve library pools or subsequent selection output phage and 750 µl of PBS+2% Marvel (Phosphate Buffered Saline containing 2% (w/v) Marvel [Premier Foods, UK]) and incubating at room temperature for 1 hour by mixing end-over-end.

10 The biotinylated antigen phage complex was then captured by adding 100 µl of resuspended Dynabeads® M-280 Streptavidin [Invitrogen, UK] and incubated for 5 minutes with mixing end-over-end at room temperature. The Dynabeads® were then recovered using a KingFisher magnetic separator [Thermo Fisher Scientific, UK] and washed 7 x 1 ml PBS + 0.1% Tween

15 20 (PBS containing 0.1% (v/v) polyoxyethylenesorbitan monolaurate [Sigma-Aldrich, UK], PBST) followed by 1 x 1 ml PBS. Bound phage retained on the washed Dynabeads® were eluted by incubation with 500 µl of trypsin-PBS (50 µl of 10 mg/ml trypsin [Sigma-Aldrich, UK] dissolved in 50 mM Tris-HCl pH 7.4, 1 mM CaCl₂ added to 450 µl PBS). The phage-containing solution was recovered and 250 µl used to infect 1.75 ml of logarithmic growth phase *E. coli* TG1 (at an OD₆₀₀ of 0.4) for 30 minutes at 37°C. The *E. coli* TG1 phage infected

20 culture was centrifuged at 11,600 g in a micro centrifuge for 1 minute. The resulting cell pellet was resuspended in 1 ml 2xTY (16 g Tryptone, 10 g Yeast Extract and 5 g NaCl in 1 litre, autoclaved for 15 minutes at 121°C) and plated onto a 9 cm Petri dish containing TY supplemented with 15 µg/ml tetracycline. The plates were incubated overnight at 37°C. Then

25 2 ml of 2xTY supplemented with 15% glycerol was added to each plate, and the cells were loosened with a glass spreader and mixed thoroughly. Fifty microlitres of the scraped bacteria were used to inoculate 50 ml of 2xTY supplemented with 15 µg/ml tetracycline and grown overnight at 37°C with shaking at 250 rpm. The overnight culture was centrifuged at 3,300 g for 15 min to pellet the bacteria. To precipitate phage, 10 ml PEG/NaCl (20% Polyethylene glycol 8000, 2.5 M NaCl) was added to 40 ml supernatant. The phage/PEG solution was

30 mixed and left on ice for 1 h, then spun at 3,300 g for 30 min at 4°C, and the supernatant discarded. The pellet was resuspended in 2 ml PBS and spun at 11,600 g for 10 min in a micro

centrifuge to remove the remaining bacterial debris. The resultant supernatant containing phage was then used for the next round of selection against the appropriate biotinylated CD40 antigen.

- Monoclonal phage ELISAs were carried out following selection rounds 2 and 3. All
- 5 washes were performed using 3 washes of 250 μ l PBST followed by 3 washes of 250 μ l PBS. The plates were coated overnight at 4°C with 50 μ l/well of 1 μ g/ml NeutrAvidin (Thermo Scientific, UK) in 0.2 M carbonate-bicarbonate buffer, pH 9.4. The plates were washed and then blocked with 2% MPBS (2% w/v Marvel skimmed milk powder [Premier Foods] in PBS) for 1 hour at room temperature. The plates were then washed and incubated with 50 μ l/well of
- 10 0.7 μ g/ml biotinylated human CD40 in 2% MPBS. The plates were washed, and phage supernatants were added to an equal volume of 2% MPBS. The plates were then incubated for 1 hour at room temperature. The plates were washed and bound phage detected with anti-M13-HRP conjugate (GE Healthcare, UK) diluted 1:5000 in 2% MPBS and incubated for 1 hour at room temperature. The plates were washed, and the ELISA was developed using
- 15 SureBlue 1-Component TMB MicroWell Peroxidase solution (KPL Inc, USA). Specific phage were identified by comparison to plates coated with NeutrAvidin but without biotinylated CD40. A MidiPrep was used to isolate dAb V-genes from pDOM4 (Domantis) round 2 and round 3 outputs and cloned into pDOM5 (Domantis). pDOM4, disclosed in WO 2007/085815, is a derivative of the F'd phage vector in which the gene III signal peptide sequence is replaced
- 20 with the yeast glycolipid anchored surface protein (GAS) signal peptide (WO 2005/093074). pDOM4 also contains a c-myc tag between the leader sequence and gene III, which puts the gene III back in frame.

- Binding dAbs were identified as follows. Ninety-six individual colonies (in pDOM5) were picked from each output into 200 μ L Terrific Broth containing OnEx Autoinduction
- 25 media (Novagen, UK) overnight at 37° C with shaking at 250 rpm in Costar 96 Well Cell Culture Clusters (Corning Incorporated, USA). The cultures were centrifuged to pellet the cells, and the supernatants were assayed by antigen binding ELISA for CD40 binding dAbs. MaxiSorp 96 well immunoplates (Nunc, USA) were coated overnight at 4°C with 50 μ l/well of 1 μ g/ml NeutrAvidin in 0.2 M carbonate-bicarbonate buffer, pH 9.4. All washes were as
- 30 described for the phage ELISA. The plates were blocked for 1 hour at room temperature with 200 μ l of PBS containing 1% Tween 20. The plate was then washed and incubated with 50

5 μ l/well of 0.7 μ g/ml biotinylated human CD40 in 0.1% PBST. The clarified dAb-containing culture supernatant was added to the ELISA plate with an equal volume of 0.1% PBST. The plates were incubated for 1 hour at room temperature and then washed. Bound dAb was detected using a two step process: firstly 9E10 (anti-myc IgG, Sigma-Aldrich, UK) diluted
 10 1:2000 in 0.1 % PBST was added for 1 hour at room temperature then washed, followed by anti-mouse Fc-HRP (Sigma-Aldrich, UK) diluted 1:2000 in 0.1% PBST for 1 hour at room temperature. The plates were washed, and the ELISA was developed using SureBlue 1-Component TMB MicroWell Peroxidase solution (KPL Inc, USA). The color was allowed to develop, and the colorimetric reaction was stopped by the addition of an equal volume of 1 M
 15 HCl. The ELISA plate was read at 450 nm. Specific phage were identified by comparison to plates coated with NeutrAvidin but without biotinylated CD40.

Clones specific for CD40 were tested in either the bead- or ELISA-based receptor-binding assay (RBA) to assess for inhibition of CD40 ligand binding. Domain antibodies that showed inhibition in the RBA were tested in the B-cell proliferation assay and then in a variety
 15 of other *in vitro* cell assays. These assays are described in greater detail below.

BMS3h-106 to -225:

BMS3h-106 to -225 were isolated from selections against biotinylated CD40 or biotinylated CD40-Fc as described for BMS3h-1 to BMS3h-69, but with the following modifications. Phage from the naïve 4G and 6G libraries were combined as follows before
 20 initiating selections:

- 6) 4G VH CDR3 lengths between 7 – 9 amino acids.
- 7) 4G VH CDR3 lengths between 10 – 12 amino acids.
- 8) 4G VH CDR3 lengths between 13 – 15 amino acids.
- 9) 6G VH CDR3 lengths between 7 – 9 amino acids.
- 25 10) 6G VH CDR3 lengths between 10 – 12 amino acids.
- 11) 6G VH CDR3 lengths between 13 – 15 amino acids.
- 12) 4G VK
- 13) 6G VK

Round one was performed at an antigen concentration of 160 nM for CD40-Fc and 100 nM for
 30 CD40. Output titres were in the range 2.0×10^4 to 9.0×10^7 TU/ml (functional viral titre).

For round two, enriched phage from round one were combined in pairs before using in selections:

- 1) 4G + 6G VH CDR3 lengths between 7 – 9 amino acids (pools 1 + 4 from round 1).
- 2) 4G + 6G VH CDR3 lengths between 10 – 12 amino acids (pools 2 + 5 from round 1).
- 5 3) 4G + 6G VH CDR3 lengths between 13 – 15 amino acids (pools 3+6 from round 1).
- 4) 4G + 6G VK (pools 7+8 from round 1)

Selections were performed at an antigen concentration of 100 nM, and the antigen-phage complexes were captured using M-280 tosyl-activated Dynabeads® (Invitrogen) that had been coupled with NeutrAvidin (Thermo Fisher Scientific, UK). Output titres were in the range
10 6.5×10^7 to 7.5×10^8 TU/ml.

Round three was performed at an antigen concentration of 20 nM and, in the case of the CD40-Fc selections, in the presence of $6.7 \mu\text{M}$ free human Fc tail (BMS). Output titres were in the range 4.3×10^7 to 1.6×10^9 TU/ml.

Round four was performed as described for round two but at an antigen concentration
15 of 2 nM and in the presence and absence of 500-fold excess unlabelled CD40-Fc. The addition of this competitor was made after the initial one hour incubation of the phage with the biotinylated antigen, and the mixture was then incubated overnight, as before. This competition step was included with the aim of enhancing selection of dAbs with a slower off-rate. Output titres were in the range 1.8×10^7 to 4.4×10^7 without competition and 1.8×10^6 to
20 2.3×10^7 TU/ml with competition.

To monitor the progress of the selections, monoclonal phage ELISAs were carried out following rounds 2 and 3. These were performed as described for BMS3h-1 to BMS3h-69. Binding dAbs were identified as described for BMS3h-1 to BMS3h-69 except that, in the case of the VK library screening, protein L was included at a final concentration of $0.8 \mu\text{g/ml}$.

25 Addition of protein L increased the signal strength by cross-linking the dAbs.

BMS3h-70 to -105:

BMS3h-70 to -105 were isolated from selections against antigen that had been passively adsorbed to immunotubes. Phage from the naïve 4G and 6G Domantis dAb libraries were combined as follows before initiating selections:

- 30 1) 4G VH CDR3 lengths between 7 – 9 amino acids.

- 2) 4G VH CDR3 lengths between 10 – 12 amino acids.
- 3) 4G VH CDR3 lengths between 13 – 15 amino acids.
- 4) 6G VH CDR3 lengths between 7 – 9 amino acids.
- 5) 6G VH CDR3 lengths between 10 – 12 amino acids.
- 5 6) 6G VH CDR3 lengths between 13 – 15 amino acids.
- 7) 4G VK
- 8) 6G VK

For the first round of selection, 1 ml of 10 µg/ml human CD40-Fc fusion (BMS) in 0.2 M carbonate-bicarbonate buffer, pH 9.4, was added to a Nunc MaxiSorp immunotube and
 10 then incubated overnight at 4°C with rolling. The tube was then emptied and washed three times with phosphate buffered saline (PBS). The tube was then blocked by filling to the brim with MPBS and incubating for 1 h at room temperature. The tube was then emptied and washed three times with PBS. Library phage in 4 ml MPBS were added to the tube and incubated for 1 hour with rotation end-over-end at room temperature.

15 The tube was emptied and washed 10 times with PBST (PBS with 0.1% (v/v) Tween 20). Bound phage retained on the washed tube were eluted by incubation with 500 µl of trypsin-PBS (50 µl of 10 mg/ml trypsin [Sigma-Aldrich, UK] dissolved in 50 mM Tris-HCl pH 7.4, 1 mM CaCl₂ added to 450 µl PBS) with rotation end-over-end for 10 min at room temperature. The phage-containing solution was recovered, and 250 µl were used to infect
 20 1.75 ml of logarithmic growth phase *E. coli* TG1 (at an OD₆₀₀ of 0.4) for 30 minutes at 37°C. The *E. coli* TG1 phage infected culture was centrifuged at 11,600 g in a microcentrifuge for 1 min, and the resulting cell pellet was re-suspended in 1 ml 2xTY (16 g Tryptone, 10 g Yeast Extract, and 5 g NaCl in 1 litre. The suspension was autoclaved for 15 minutes at 121°C) and plated onto a 9 cm Petri dish containing LB agar supplemented with 15 µg/ml tetracycline.
 25 The plates were incubated overnight at 37°C. Two millilitres of 2xTY supplemented with 15% glycerol was then added to each plate, and the cells were loosened with a glass spreader and mixed thoroughly.

Fifty microlitres of the scraped bacteria were used to inoculate 50 ml of 2xTY supplemented with 15 µg/ml tetracycline and grown overnight at 37°C with shaking at
 30 250 rpm. The overnight culture was centrifuged at 3,300 g for 15 min to pellet the bacteria. To precipitate phage, 10 ml PEG/NaCl (20% Polyethylene glycol 8000, 2.5 M NaCl) was

added to 40 ml supernatant. The phage/PEG solution was mixed and left on ice for 1 h. The solution was then spun at 3,300 g for 30 min at 4°C, and the supernatant was discarded. The pellet was re-suspended in 2 ml PBS and spun at 11,600 g for 10 min in a micro centrifuge to remove the remaining bacterial debris. The resultant supernatant containing phage was then
5 used for the next round of selection against CD40-Fc antigen. Output titres from round one were in the range 7.5×10^4 to 1.5×10^7 TU/ml (transforming units per ml).

A second round of selection was performed using enriched phage recovered from the first round of selection. This was performed exactly as described above and the output titres were in the range 2.5×10^7 to 1.2×10^8 TU/ml.

10 A third round of selection was performed using enriched phage recovered from the second round of selection. These were performed as described above but with an antigen concentration of 1 µg/ml. Output titres were in the range 5.1×10^7 to 7.5×10^8 TU/ml.

To monitor the progress of the selections, monoclonal phage ELISAs were carried out following rounds 2 and 3. A sample of individual colonies were picked into 200 µL 2xTY
15 supplemented with 15 µg/ml tetracycline and incubated overnight at 37°C with shaking at 250 rpm in Costar 96 Well Cell Culture Clusters (Coming Incorporated, USA). The cultures were centrifuged to pellet the cells, and the supernatants were assayed by antigen binding ELISA for CD40-binding phage dAbs. All washes were performed using 3 washes of 250 µl PBST followed by 3 washes of 250 µl PBS. MaxiSorp 96 well immunoplates (Nunc, USA)
20 were coated overnight at 4°C with 50 µl/well of 0.5 µg/ml CD40-Fc (BMS) in 0.2 M carbonate-bicarbonate buffer, pH 9.4. The plates were washed and then blocked with 250 µl of 2% MPBS for 1 hour at room temperature. The plates were washed, and phage supernatants were added to an equal volume of 2% MPBS and incubated for 1 hour at room temperature. The plates were washed, and bound phage were detected with anti-M13-HRP conjugate (GE
25 Healthcare, UK) diluted 1:5000 in 2% MPBS and incubated for 1 hour at room temperature. The plates were washed, and the ELISA was developed using SureBlue 1-Component TMB MicroWell Peroxidase solution (KPL Inc, USA). Specific phage dAbs were identified by comparison to plates coated with free Fc.

The dAb genes from each of the above rounds two and three selection outputs were
30 sub-cloned, as a pool, into soluble expression vector pDOM5 in *E. coli* strain HB2151. This

vector allowed expression of free dAb with a c-myc tag (Roche Diagnostics GmbH) in *E. coli* and secretion to the supernatant.

CD40-binding dAbs from passive selections were identified as follows. Ninety-six individual colonies (in pDOM5) were picked from each output into 200 μ L Terrific Broth containing OnEx Autoinduction media (Novagen, UK) overnight at 37°C with shaking at 250 rpm in Costar 96 Well Cell Culture Clusters (Corning Incorporated, USA). The cultures were centrifuged to pellet the cells, and the supernatants were assayed by antigen binding ELISA for CD40 binding dAbs. MaxiSorp 96 well immunoplates (Nunc, USA) were coated overnight at 4°C with 50 μ L/well of 0.5 μ g/ml CD40-Fc (BMS) in 0.2 M carbonate-bicarbonate buffer, pH 9.4. All washes were as described for the phage ELISA. The plates were blocked for 1 hour at room temperature with 250 μ L of PBS containing 1% Tween 20 (PBST). The clarified dAb-containing culture supernatant was added to the ELISA plate with an equal volume of 0.1% PBST. The plates were incubated for 1 hour at room temperature and then washed. Bound dAb was detected using a two step process: firstly biotinylated 9E10 (anti-myc IgG, Sigma-Aldrich, UK) diluted 1:2000 in 0.1% PBST was added for 1 hour at room temperature then washed, followed by streptavidin-HRP (Bender MedSystems, Austria) diluted 1:5000 in 0.1% PBST for 1 hour at room temperature. The plates were washed and the ELISA developed using SureBlue I-Component TMB. Specific dAbs were identified by comparison to plates coated with free Fc.

Clones specific for CD40 were tested in either the bead- or ELISA-based receptor-binding assay (RBA) to assess for inhibition of CD40 ligand binding. The potency measurements obtained from the RBA are given in Table 5 (Primary Screening effort). Domain antibodies that showed inhibition in the RBA were tested in the B-cell proliferation assay and then in a variety of other *in vitro* cell assays.

25 **BMS3h-210 to -225**

BMS3h-210 to -225 were isolated from selections against whole cells. Phage from the naïve 4G and 6G Domantis dAb libraries were combined as follows before initiating selections:

- 1) 4G + 6G VH CDR3 lengths between 7 – 9 amino acids.
- 2) 4G + 6G VH CDR3 lengths between 10 – 12 amino acids.

3) 4G + 6G VH CDR3 lengths between 13 – 15 amino acids.

4) 4G and 6G VK

For round one a DG44 CHO cell line stably transfected with cell-surface expressed human CD40 (supplied by BMS) was used as antigen. Prior to selection against these cells, the library pools outlined above were incubated with non-transfected CHO cells to deplete them of phage displaying dAbs specific for cell surface antigens other than CD40. Both types of cells were harvested by incubation with Versene (Invitrogen) before assessing for viability. Six million viable non-transfected CHO cells were re-suspended in 4 ml PBS with 2% (w/v) BSA (PBS/BSA) and rotated end-over-end at 4°C for 1 hour to block. All subsequent steps were performed at 4°C unless otherwise noted. The cells were centrifuged at 185 g for 5 min and the supernatant, containing the depleted library phage, transferred to a fresh tube. To this were added 6×10^6 viable CHO-CD40 cells in 1 ml PBS/BSA and the mixture was rotated for 1 hour. The cells were then washed five times by centrifuging at 185 g for 5 min and re-suspending in 10 ml PBS/BSA. After the final wash, the cells were pelleted as previously and were then re-suspended in 0.5 ml of 1 mg/ml trypsin type XIII from bovine pancreas (Sigma Aldrich, UK) in PBS supplemented with 5 mM Tris-HCl pH 7.4, 0.1 mM CaCl_2 and transferred to a microcentrifuge tube. The cells were rotated at room temperature for 10 min before centrifuging at 16000 g for 5 min. Eluted phage in the supernatant were used to infect *E. coli* and the output phage titres were determined to be between 5.1×10^5 and 2.7×10^6 TU/ml (transforming units per ml).

A second round of selection was performed using enriched phage recovered from the first round of selection. These were performed as above but without the initial depletion (de-selection) step and using RAMOS human B cells (ATCC) instead of CHO-CD40. Output titres were in the range 2.3×10^5 to 7.5×10^5 TU/ml.

A third round of selection was performed as for the second round. Output titres were in the range 1.9×10^8 to 3.5×10^8 TU/ml.

The dAb genes from each of the above rounds two and three selection outputs were sub-cloned, as a pool, into soluble expression vector pDOM5 in *E. coli* strain HB2151. This vector allowed expression of free dAb with a c-myc tag in *E. coli* and secretion to the

supernatant.

Clones specific for CD40 were tested in either the CHO cell receptor-binding assay (RBA) to assess for inhibition of CD40 ligand binding. Domain antibodies that showed inhibition in the RBA were tested in the B-cell proliferation assay and then in a variety of other *in vitro* cell assays.

5 *Affinity Maturation by error-prone PCR*

Error-prone phage libraries were constructed for 13 BMS3h dAbs that showed neutralization activity in the B-cell proliferation assay described below in Example 6 (See TABLE 17). This was performed by using Mutazyme II polymerase (part of the GeneMorph II kit from Agilent Technologies) to randomly introduce errors into the dAb gene during
 10 amplification by polymerase chain reaction (PCR). The mutated dAb genes were cloned as a genetic fusion with the fd phage gene III protein under the control of the GAS1 leader sequence in pDOM4 vector, which contained all the fd genes necessary to generate infective phage particles. These libraries were approximately 1×10^8 CFU (colony forming units) in size, with an error-rate of 2-5 amino acids per dAb gene.

15 Phage generated from these libraries were subjected to three rounds of selection against soluble biotinylated human CD40. The first round of phage selection was performed by premixing the phage library with 2% MPBS (phosphate buffered saline supplemented with 2% (w/v) Marvel dried skimmed milk powder) and adding biotinylated human CD40 (BMS) to a final concentration of 20 nM in a final volume of 1 ml. The mixture was incubated for at least
 20 one hour at room temperature with mixing end-over-end. The antigen-phage complexes were then captured using 50 μ l of M-280 streptavidin Dynabeads® (Invitrogen) and washed 7 times with 1 ml PBST followed by a single wash in 1 ml PBS. The washed phage were eluted from the antigen/bead complex by incubating with 0.5 ml of 1 mg/ml trypsin type XIII from bovine pancreas (Sigma Aldrich, UK) in PBS supplemented with 5 mM Tris-HCl pH 7.4, 0.1 mM
 25 CaCl_2 . Eluted phage were used to infect *E. coli* and the output phage titres were determined to be between 2×10^5 and 9×10^7 TU/ml (transforming units per ml).

A second round of selection was performed using enriched phage recovered from the first round of selection, with a final concentration of 2 nM biotinylated CD40 followed by capture using streptavidin beads as described above. Output titres were in the range 3×10^4 to
 30 5×10^6 TU/ml.

A third round of selection using 2 nM biotinylated CD40 followed by capture using streptavidin beads was performed. The eluted phage titres were in the range 8×10^4 to 4×10^6 TU/ml.

BIAcore™ screening

5 The dAb genes from each of the above round three selection outputs were sub-cloned, as a pool, into soluble expression vector pDOM13 (Domantis) in *E. coli* HB2151. The pDOM13 vector is also known as pDOM33 and is disclosed in WO/2008/149143. This vector allowed expression of free dAb in *E. coli* and secretion to the supernatant. Forty-seven individual colonies were picked from each of the outputs and expressed in 200 µl Terrific
10 Broth (TB) containing Novagen Overnight Express Autoinduction media (Merck Chemicals, UK) overnight at 37°C with shaking at 250 rpm in Costar 96 Well Cell Culture Clusters (Corning Incorporated, USA). In the same plate, a single well was inoculated with *E. coli* expressing the appropriate parental (wild-type) dAb. The cultures were centrifuged to pellet the cells and the supernatants screened on a BIAcore™ 3000 instrument (GE Healthcare) for
15 improvements in “off-rate” (i.e. dissociation rate constant, k_d) compared to parental dAb.

Approximately 1600 response units (RU) of biotinylated human CD40 (BMS) were immobilized on one flow-cell of a streptavidin (SA) BIAcore™ chip. A second flow cell without any ligand immobilized served as a reference flow-cell for inline referencing. Each dAb supernatant to be analyzed was diluted 1:3 in HBS-EP buffer (0.01 M HEPES pH 7.4 with
20 0.15 M NaCl, 3 mM EDTA and 0.005% v/v Surfactant P20, GE Healthcare). Ten microlitres of each dAb supernatant were injected, using the instrument’s KINJECT function, across the CD40-immobilized and reference flow-cells in series, with inline subtraction of the signal from the reference cell. The experiment was performed at 25°C and with a flow rate of 10 µl/min of HBS-EP. After each injection had been completed, the dAb was allowed to dissociate from the
25 ligand in buffer for 120 s before regeneration with a 5 µl injection of 10 mM glycine pH 2.0. BIAevaluation 4.1 software (GE Healthcare) was used to subtract the reference flow-cell trace from each analyte trace. The same software was used to perform an approximate fit of a 1:1 (Langmuir) kinetic model to the dissociation phase of the analyte traces. This model yielded approximate dissociation rate constants (“off-rate” or k_d) for each clone and allowed relative
30 comparisons to be made with the wild type dAb.

Clones with improved off-rates were identified for all lineages except BMS3h-129 and -197. Clones with improved off-rates were tested in either the bead- or ELISA-based receptor-binding assay (RBA) to assess for improved potency as described above. The potency measurements obtained from the RBA are given in the Tables labeled "Error-Prone-Matured Clones." Clones that were more potent in the RBA were subsequently tested in a B-cell proliferation assay to assess for enhanced biological potency and these measurements obtained are given in TABLE 17. Domain antibodies that had improved potency in the B-cell proliferation assay were also tested in a variety of other *in vitro* cell assays.

Affinity maturation by triplet scanning diversification

Five improved-potency dAbs isolated from the error-prone maturation, BMS3h-37-2, -38-2, -56-2, -193-25 and -217-23, were chosen to be further affinity matured by triplet scanning diversification. Phage libraries were constructed based on these parents as described above for the error-prone libraries except that, instead of using error-prone PCR, a series of overlapping degenerate triplet oligonucleotides were used to diversify the complementarity determining (CDR) regions of each dAb. For each dAb to be affinity matured, oligonucleotides containing NNS codon triplets (*see* Arkin et al. (1992) *Proc. Nat'l Acad. Sci. USA* 89:7811-7815) were used to make a number of libraries for each CDR by slicing by overlap extension (SOE) PCR. The triplets diversified by the oligonucleotides for a given CDR overlapped by two codons, resulting in two to four libraries per CDR. The amino acid residues diversified in the BMS3h-37-2 libraries were at positions 30, 31, 32, 33, 35, 50, 52, 53, 55, 56, 95, 96, 97, and 98 (Kabat numbering). The residues diversified in the BMS3h-38-2 libraries were as for 37-2, but with the addition of position 100. The residues diversified in the BMS3h-56-2 libraries were as for 37-2, but with the addition of positions 100 and 101. The residues diversified in the BMS3h-193-25 and -217-23 libraries were at positions 27, 28, 30, 31, 32, 34, 49, 50, 51, 53, 89, 91, 92, 93, 94, and 96.

Phage generated from these libraries were pooled by CDR and selections performed as described above, except that, for BMS3h-37-2, -38-2, -56-2 and -193-25, the concentrations of antigen used were 10, 1 and 0.1 nM for rounds one, two and three, respectively. For BMS3h-217-23 the concentrations of antigen used were 20, 2 and 0.2 nM for rounds one, two and three, respectively. For BMS3h-193-25, which is cross-reactive for cynomolgus CD40,

selections were also performed against cyno CD40 in parallel. Additionally, selection rounds two and three were performed in the presence and absence of 100- or 1000-fold excess unlabelled CD40, respectively. The addition of this competitor was made after the initial one hour incubation of the phage with the biotinylated antigen and the mixture was then incubated, as before, for a further hour. This competition step was included with the aim of enhancing selection of dAbs with a slower off-rate. Round one titres were in the range 1.4×10^6 to 1.4×10^9 . Titres in round 2 were 1.3×10^5 to 4.0×10^8 without competition and 8.6×10^4 to 1.3×10^8 with competition. Titres in round 3 were 1.2×10^5 to 1.9×10^8 without competition and 6.0×10^5 to 1.2×10^8 with competition.

These selection outputs were sub-cloned and screened as described for the error-prone affinity maturation. Clones with improved off-rates were identified for all lineages except BMS3h-193-25. Clones with improved off-rates were tested in the ELISA receptor-binding assay (RBA) to assess for improved potency. The potency measurements obtained from the RBA are given in the Tables labeled "Further-Matured Clones." Clones that were more potent in the RBA were subsequently tested in a B-cell proliferation assay to assess for enhanced biological potency and these measurements obtained are given in TABLE 17. Domain antibodies that had improved potency in the B-cell proliferation assay were also tested in a variety of other *in vitro* cell assays.

Example 2

Screening Using Receptor Binding Assays (RBA)

Several *in vitro* receptor binding assays (RBA) were used to determine CD40 affinity of the anti-human CD40 variable domain amino acid sequences generated in Example 1. Three RBA formats were used: (1) a bead RBA, (2) an ELISA RBA, and (3) a CHO cell RBA.

Bead RBA:

Phosphate buffered saline (PBS) washed Sphero streptavidin polystyrene particles (Saxon Europe, UK) were coated with $0.5 \mu\text{g/ml}$ biotinylated human IZ-CD40L (BMS). After coating, biotinylated CD40L particles were washed in PBS and diluted 1:10 in 0.1% (w/v) bovine serum albumin (BSA) (Sigma-Aldrich, UK) in PBS assay buffer. In a 384-well clear

bottom, black walled plate (Applied Biosystems) a dilution range of purified dAb, 0.25 µg/ml human CD40 (BMS, CY24FEB06-01), 1 in 5000 mouse anti-human IgG (Fc) mAb clone GG-7 (Sigma-Aldrich, UK), 0.25 µg/ml goat anti-mouse ALEXA Fluor 647 (Invitrogen, Molecular probes, UK) and the biotinylated CD40L polystyrene particles were combined equally and
 5 allowed to incubate at room temperature for 6 hours in the absence of light. Following incubation, competitive binding of dAb vs. human CD40 to biotinylated CD40L particles was assessed using relative fluorescence with the AB8200 cellular detection mechanism (Applied Biosystems).

ELISA RBA:

10 Clear walled High Bind, 384-well plates (Corning, UK) were coated with 25 µl of 1 µg/ml Neutravidin in 0.2 M carbonate-bicarbonate buffer, pH 9.4 overnight at 4°C. The following day, assay plates were washed with 0.1% (v/v) Tween PBS buffer, blocked with 1% (w/v) BSA in PBS for 1 hour at room temperature and washed again. Following removal of excess washing buffer, 25 µl 1 µg/ml of biotinylated human IZ-CD40L (BMS) was incubated
 15 with the assay plates for 1 hour at room temperature. Simultaneously, a dilution range of purified dAb and 1 µg/ml of human CD40 (BMS, CY24FEB06-01) were complexed in a 1:1 ratio. Following washing of the assay plate, the dAb:human CD40 complex was incubated in the assay plate at room temperature for 2 hours with gentle agitation. Competitive binding of dAb vs. human CD40 to biotinylated CD40L was detected with sequential incubations of 1 in
 20 5000 mouse anti-human IgG (Fc) mAb clone GG-7 (Sigma-Aldrich, UK) followed by 1 in 10,000 horse radish peroxidase (HRP) conjugated goat anti-mouse IgG (Fc) secondary detection antibody (Sigma-Aldrich, UK). Absorbance signal was measured using a SpectraMax M5^e plate reader (Molecular Devices) at 450 nm following neutralization with 1M HCl solution.

25 **Cell assays: CD40 CHO cell RBA:**

Stably transfected human CD40 expressing CHO-DG44 cells or native CHO-DG44 cells (both BMS) were detached from cell culture flasks using Versene (Invitrogen). Forty thousand cells per well were seeded into 96-well High Bind, black walled, clear bottom plates (Corning, UK) in 0.1% (w/v) BSA PBS assay buffer with a dilution range of dAb, 0.25 µg/ml
 30 of biotinylated human IZ-CD40L (BMS), and 0.25 µg/ml of streptavidin Alexa Fluor 647

(Invitrogen, Molecular probes, UK). The mixture was incubated in the absence of light for 6 hours. Following incubation, competitive binding of dAb vs. human CD40 C11O cells to soluble biotinylated IZ-CD40L was assessed using relative fluorescence with the AB8200 cellular detection mechanism (Applied Biosystems).

- 5 TABLES 5-7 respectively show the results from a primary screening effort (“naïve clones”) and subsequent rounds of affinity maturation (“error-prone matured clones” and “further-matured clones”) for the tested anti-human CD40 dAbs.

TABLE 5

Primary Screening Effort:

Naïve Clone	EC ₅₀ Bead RBA (nM)	EC ₅₀ ELISA RBA- (nM)	EC ₅₀ cell RBA (CHO-CD40) (nM)
BMS3h-37	100, 200		
BMS3h-38	600, 650		>10000
BMS3h-41	2000, 1600		>10000
BMS3h-43	100, 50, 50		5000
BMS3h-56	1000, 500		
BMS3h-106	300, 1000, 500, 400		>10000
BMS3h-129	5000		
BMS3h-131	500, >1000		
BMS3h-193	1000		
BMS3h-197	30		
BMS3h-198	80		600
BMS3h-202	3000, 3700		>10000
BMS3h-217	800		1400
BMS3h-231		670, 870	
BMS3h-233		2770	
BMS3h-257		3210, 1340	
BMS3h-242		390, 210	
BMS3h-262		1770, 1160	
BMS3h-263		3130	
BMS3h-271		370, 210	
BMS3h-285		168, 258	
BMS3h-287		>10000, 6758	
BMS3h-289		2390, >10000	

TABLE 6

Error-Prone-Matured Clones:

Clone	EC ₅₀ ELISA RBA (nM)	EC ₅₀ cell RBA (CHO-CD40) (nM)
BMS3h-37-2		32
BMS3h-37-4		45
BMS3h-37-11		27
BMS3h-38-5		1000
BMS3h-38-8		2800
BMS3h-41-3		200
BMS3h-41-10		4300
BMS3h-43-3		320
BMS3h-43-5		90
BMS3h-56-1	7.1	
BMS3h-56-2	17.0	
BMS3h-56-5	4.9, 7.5, 4.7	18, 28
BMS3h-56-7	5.5	
BMS3h-56-8	6.2	
BMS3h-56-9	4.4, 5.5	
BMS3h-56-16	7.0	
BMS3h-56-17	66	
BMS3h-56-18	6.5	
BMS3h-56-19	5.5, 5.1	
BMS3h-56-20	6.8	
BMS3h-56-21	6.5, 6.2	
BMS3h-56-22	6.5	
BMS3h-56-23	24.5	
BMS3h-56-24	11.7	
BMS3h-56-25	5.5	
BMS3h-56-26	5.0	
BMS3h-56-27	16.3	
BMS3h-56-28	8.9	

Clone	EC ₅₀ ELISA RBA (nM)	EC ₅₀ cell RBA (CHO-CD40) (nM)
BMS3h-56-29	9.7	
BMS3h-56-30	24.2	
BMS3h-56-31	61.0	
BMS3h-193-5	>300	
BMS3h-193-7	300	
BMS3h-193-10	200	
BMS3h-193-11	300	
BMS3h-193-12	200	
BMS3h-193-15		300
BMS3h-193-18	100	
BMS3h-193-19	100	
BMS3h-193-25	140	
BMS3h-193-26	100	
BMS3h-193-27	100	
BMS3h-193-29	360, 114	
BMS3h-193-30	290, 116	
BMS3h-198-1	12	70
BMS3h-198-2		115
BMS3h-198-3		330
BMS3h-198-9	20	
BMS3h-198-10	35	
BMS3h-198-11	20	
BMS3h-198-14	9	
BMS3h-198-17	20	
BMS3h-198-19	7.9	
BMS3h-198-22	10	
BMS3h-198-31	6.1	
BMS3h-198-32	24.7	
BMS3h-198-33	8.7	
BMS3h-198-34	32.6	
BMS3h-198-37	15.1	

Clone	EC ₅₀ ELISA RBA (nM)	EC ₅₀ cell RBA (CHO-CD40) (nM)
BMS3h-198-38	7.2	
BMS3h-202-10		7200
BMS3h-202-11		8300
BMS3h-217-1	23	
BMS3h-217-2	78	
BMS3h-217-3	32	
BMS3h-217-4	partial, 15	
BMS3h-217-5	65	
BMS3h-217-6	26	
BMS3h-217-7	39	
BMS3h-217-8	6	
BMS3h-217-9	53	
BMS3h-217-14	8	
BMS3h-217-15	21	
BMS3h-217-16	9	
BMS3h-217-17	60	
BMS3h-217-23	16	

TABLE 7

Further-Matured Clones:

Clone	EC ₅₀ ELISA RBA (nM)	EC ₅₀ ICAM1 cell assay (nM)	EC ₅₀ cell RBA (CHO-CD40) (nM)
BMS3h-37-202	4.1, 35		
BMS3h-37-205	3.1, 4.4		
BMS3h-37-206	3.2, 8.9		
BMS3h-37-207	2.5, 6.6		
BMS3h-37-212	24		
BMS3h-37-213	16		

Clone	EC ₅₀ ELISA RBA (nM)	EC ₅₀ ICAM1 cell assay (nM)	EC ₅₀ cell RBA (CHO- CD40) (nM)
BMS3h-38-201	3.4, inactive		
BMS3h-38-202	4.8		
BMS3h-38-203	5.5		
BMS3h-38-204	4.8		
BMS3h-38-205	4.5, 11.1		
BMS3h-38-209	10.2		
BMS3h-38-211	2.3, 13.8		
BMS3h-38-215	2.3, 3.6		
BMS3h-38-217	1.8, 2.2		
BMS3h-38-218	3.0		
BMS3h-38-219	1.8, 7.1		
BMS3h-38-223	5.7		
BMS3h-38-224	6.3		
BMS3h-38-225	8.8		
BMS3h-38-226	18.1		
BMS3h-38-228	4		
BMS3h-38-231	4.4		
BMS3h-38-235	1.5		
BMS3h-38-237	2		
BMS3h-38-238	5.1		
BMS3h-56-201	3.7, 2.3	10.0	
BMS3h-56-202	3.4, 3.2	80.0	
BMS3h-56-203	5.2, 4.3	70.0	
BMS3h-56-204	4.5		
BMS3h-56-205	9.0		

Clone	EC ₅₀ ELISA RBA (nM)	EC ₅₀ ICAM1 cell assay (nM)	EC ₅₀ cell RBA (CHO- CD40) (nM)
BMS3h-56-206	2.9, 2.3	5.0	
BMS3h-56-207	7.3		
BMS3h-56-215	3.2, 4.6	40.0	
BMS3h-56-217	2.1, 12.6		
BMS3h-56-220	4.2		
BMS3h-56-223	5.0		
BMS3h-56-224	2.1, 4.2		
BMS3h-56-225	2.9		
BMS3h-56-229	4.1		
BMS3h-56-232	2.8, 3.7		
BMS3h-56-239	2.7		
BMS3h-56-243	9.9		
BMS3h-56-244	6.0		
BMS3h-56-246	11.1		
BMS3h-56-248	0.7		
BMS3h-56-253	1.3		
BMS3h-56-258	5.2	23.0	15
BMS3h-56-261	5.7	42.4	17
BMS3h-56-262	4.0	135.0	42
BMS3h-56-265	18.8	289.0	88
BMS3h-56-266	3.8	31.9	27
BMS3h-56-269	3.3	34.2	24
BMS3h-56-270	11.3	93.8	91
BMS3h-193-2501	114		
BMS3h-193-2502	170		
BMS3h-193-2503	3000		

Clone	EC ₅₀ ELISA RBA (nM)	EC ₅₀ ICAM1 cell assay (nM)	EC ₅₀ cell RBA (CHO- CD40) (nM)
BMS3h-193-2504	140		
BMS3h-193-2505	500		
BMS3h-193-2506	180		
BMS3h-193-2507	160		
BMS3h-193-2510	170		
BMS3h-193-2511	270		
BMS3h-193-2512	600		
BMS3h-193-2513	130		
BMS3h-193-2514	525		
BMS3h-193-2515	100		
BMS3h-193-2516	100		

Example 3

CD40 Binding Kinetics

The binding kinetics were determined for anti-human CD40 dAbs identified in the primary screening effort ("naïve clones") and subsequent rounds of affinity maturation ("error-prone matured clones"). The methods used directly measure the affinity of the dAbs for CD40.

A BIAcore™ 3000 instrument (GE Healthcare) was used to analyze the binding kinetics of CD40-specific dAbs to CD40. Approximately 600 response units (RU) of biotinylated human CD40 (BMS) were immobilized on one flow-cell of a streptavidin (SA) BIAcore™ chip. A second flow cell without any ligand immobilized served as a reference flow-cell for inline referencing. An appropriate doubling dilution series of each dAb to be analyzed was prepared in HBS-EP buffer (0.01 M HEPES pH 7.4 with 0.15 M NaCl, 3 mM EDTA and 0.005% v/v Surfactant P20, GE Healthcare). One hundred and eighty microlitres of each dAb were injected in duplicate using the instrument's KINJECT function. Each dAb was injected across the CD40-immobilised and reference flow-cells in series with inline subtraction of the signal from the reference cell. The experiment was performed at 25°C and a flow rate of

30 $\mu\text{l}/\text{min}$ of HBS-EP. After each injection had been completed, the dAb was allowed to dissociate from the ligand in buffer for 300 s before regeneration with a 10 μl injection of 10 mM glycine pH 2.0. A reference injection of HBS-EP buffer blank (containing no analyte) was also injected under the same conditions, to serve as a second reference for subtraction from each analyte trace. BIAevaluation 4.1 software (GE Healthcare) was used to subtract both the reference flow-cell trace and the buffer blank trace from each analyte trace. The same software was used to perform a simultaneous, global fit of a 1:1 (Langmuir) kinetic model to the association and dissociation phases of the analyte dilution series traces. This model yielded association and dissociation rate constants (k_a and k_d , respectively) and the equilibrium dissociation constant (K_D) of the interaction; these are detailed in TABLES 8 and 9.

TABLE 8

Naïve Clones:

Clone	BIACore™ k_a ($\text{M}^{-1}\text{s}^{-1}$)	BIACore™ k_d (s^{-1})	BIACore™ K_D (M)
BMS3h-37	1.9E+04	3.6E-03	1.9E-07
BMS3h-38	2.1E+04	6.2E-03	3.0E-07
BMS3h-41	9.9E+03	8.3E-03	8.4E-07
BMS3h-43	1.4E+03	3.1E-03	2.1E-06
BMS3h-56	2.3E+04	4.0E-03	1.8E-07
BMS3h-106	1.3E+05	4.6E-02	3.5E-07
BMS3h-107	2.0E+05	1.7E-01	8.5E-07
BMS3h-129	4.7E+05	5.1E-01	1.1E-06
BMS3h-131	2.4E+04	2.2E-02	9.3E-07
BMS3h-197	8.1E+04	1.4E-02	1.8E-07
BMS3h-198	1.6E+03	3.8E-04	2.4E-07
BMS3h-202	1.7E+03	3.5E-03	2.0E-06

TABLE 9

Error-Prone Matured Clones:

Clone	BIACore™ k_a ($\text{M}^{-1}\text{s}^{-1}$)	BIACore™ k_d (s^{-1})	BIACore™ K_D (M)
BMS3h-37-2	1.0E+05	4.1E-04	4.0E-09

BMS3h-37-5	3.9E+04	2.2E-04	5.5E-09
BMS3h-37-9	1.5E+04	1.8E-04	1.2E-08
BMS3h-38-1	3.2E+04	1.1E-03	3.3E-08
BMS3h-38-2	6.1E+04	7.5E-04	1.2E-08
BMS3h-38-3	7.5E+04	4.1E-04	5.5E-09
BMS3h-41-1	5.1E+04	5.6E-04	1.1E-08
BMS3h-43-1	4.4E+03	6.3E-04	1.4E-07
BMS3h-43-3	3.1E+04	5.9E-04	1.9E-08
BMS3h-56-1	9.8E+04	5.4E-04	5.5E-09
BMS3h-56-2	1.1E+05	6.0E-04	5.3E-09
BMS3h-56-5	1.1E+05	6.3E-04	5.9E-09
BMS3h-56-7	1.3E+05	4.7E-04	3.5E-09
BMS3h-56-9	1.5E+05	3.9E-04	2.6E-09
BMS3h-131-2	7.9E-04	1.7E-03	2.1E-08
BMS3h-193-25	4.6E-05	3.7E-02	8.1E-08
BMS3h-198-1	1.5E+04	1.8E-04	1.3E-08
BMS3h-202-5	4.4E+03	1.3E-03	3.0E-07

Example 4

Biophysical Characterization

Anti-human CD40 dAbs identified in the primary screening effort ("naïve clones") and subsequent rounds of affinity maturation ("error-prone matured clones" and "further-matured clones") were further characterized by analysis of biophysical parameters. To measure the relative stability of the dAbs, their melting point was determined by differential scanning calorimetry (DSC). dAbs with a higher melting temperature are more stable. To determine whether the dAbs form multimeric aggregates in solution, the dAbs were assayed by size exclusion chromatography/multiangle laser light scattering (SEC-MALLS). The results are shown in TABLES 10-12.

TABLE 10

Naïve clones:

Clone	DSC (T _m /°C)	SEC-MALS solution state
BMS3h-38	59	Monomer and dimer (<5%)
BMS3h-41	59	Monomer and monomer-dimer equilibrium (<5%)
BMS3h-43		Dimer and trimer
BMS3h-56	57	Monomer and dimer (<10%)
BMS3h-106		Monomer
BMS3h-107	63	Monomer
BMS3h-129	59	Monomer
BMS3h-193	56	Monomer
BMS3h-197	62 & 53	Monomer and dimer (<5%)
BMS3h-198	61	Monomer
BMS3h-202	60	Monomer and monomer-dimer equilibrium (<2%)
BMS3h-207		Dimer and tetramer
BMS3h-208		Monomer and dimer
BMS3h-217	57	Dimer
BMS3h-233		Monomer
BMS3h-242		Monomer and monomer-dimer
BMS3h-262		Monomer
BMS3h-265		Dimer
BMS3h-271		Dimer
BMS3h-285		Monomer

TABLE 11

Error-Prone-Matured Clones:

Clone	DSC T _m /°C	SEC-MALS solution state
BMS3h-37-1	57.2	
BMS3h-37-2	56.2	
BMS3h-37-9	59.7	
BMS3h-37-11	60.0	

Clone	DSC T _m /°C	SEC-MALS solution state
BMS3h-56-1	49.6	Monomer
BMS3h-56-2	63.0	Monomer and dimer (<2%)
BMS3h-56-3	64.0	Monomer (>98%)
BMS3h-56-5	51.2	
BMS3h-41-1	56	Monomer (~99%)
BMS3h-41-2	53.4	
BMS3h-41-3	51.8	
BMS3h-41-9	61	Monomer and Monomer/Dimer rapid equilibrium (<2%)
BMS3h-41-12	49.8	Monomer/Dimer
BMS3h-41-13		Monomer/Dimer
BMS3h-43-1	53	Monomer (~99%)
BMS3h-43-3	51.2	
BMS3h-43-5	48.2	Monomer/Dimer
BMS3h-43-10	51.8	
BMS3h-43-11	54.8	
BMS3h-43-12		Dimer (60%) and Monomer (40%)
BMS3h-56-1	59.2	Monomer/Dimer
BMS3h-56-2	60.1	Monomer/Dimer
BMS3h-56-5	57	Monomer (>95%)
BMS3h-56-6	57.5	Monomer/Dimer
BMS3h-56-7	61	Monomer + Monomer/Dimer rapid equilibrium (<5%)
BMS3h-56-8	58	Monomer (>98%)
BMS3h-56-9	61	Monomer + dimer (<5%)
BMS3h-56-14	60.1	Monomer
BMS3h-193-8	60	
BMS3h-193-12	52	
BMS3h-193-16	54.5 & 65.7	Monomer
BMS3h-193-19	56.8	Monomer
BMS3h-193-25	55.8	Monomer

Clone	DSC T _m /°C	SEC-MALS solution state
BMS3h-193-29	60	Monomer
BMS3h-193-30	58	
BMS3h-198-1	52.5	Monomer
BMS3h-198-2		Monomer
BMS3h-198-3	59	
BMS3h-198-5	55.6	
BMS3h-198-19	60.7	
BMS3h-198-24	59.9	Monomer
BMS3h-198-28	60.3	Monomer
BMS3h-202-1	56.8	Monomer
BMS3h-202-5	55.5	Trimer (60%) and Monomer/Dimer (40%)
BMS3h-202-10	58.3	Trimer (60%) and Monomer/Dimer (40%)
BMS3h-217-1		Monomer/Dimer
BMS3h-217-2		Dimer
BMS3h-217-3		Dimer
BMS3h-217-4		Monomer/Dimer
BMS3h-217-5		Dimer
BMS3h-217-6		Dimer
BMS3h-217-8		Dimer
BMS3h-217-14		Monomer/Dimer
BMS3h-217-15		Dimer
BMS3h-217-16		Dimer
BMS3h-217-17		Monomer/Dimer
BMS3h-217-23		Dimer

TABLE 12

Further-Matured Clones:

Clone	DSC T _m /°C	SEC-MALS solution state
BMS3h-37-206		Monomer (73%) and dimer (20%) + HMW
BMS3h-37-212		Dimer
BMS3h-38-201		Monomer (75%) and Dimer (15%)

Clone	DSC Tm/°C	SEC-MALS solution state
BMS3h-38-228		Monomer (90%) and Trimer (10%)
BMS3h-38-231		Monomer (90%) and Dimer (10%)
BMS3h-38-235		Monomer (90%) and Trimer-Dimer
BMS3h-38-237		Monomer (90%) and Tetramer (10%)
BMS3h-38-238		Monomer (95%) and Dimer-Monomer
BMS3h-56-201	57.4 + 61.8	Monomer and Dimer (15%)
BMS3h-56-202		Monomer
BMS3h-56-203		Monomer and Trimer
BMS3h-56-206		Monomer
BMS3h-56-215		Monomer, Dimer (2%) and Trimer (9%)
BMS3h-56-217	52.8 + 54.6	
BMS3h-56-232	51.0 + 56.1	Monomer (95%) and Dimer (5%)
BMS3h-56-239	53.5	Monomer
BMS3h-56-243	51.9	Monomer and Pentamer
BMS3h-56-244		Monomer (90%) and Trimer (10%)
BMS3h-56-248		Monomer (60%), Dimer and Tetramer
BMS3h-56-253		Monomer
BMS3h-56-258	62.5 + 57.5	
BMS3h-56-261	58.6 + 61.5	
BMS3h-56-266	61.3 + 62.3	
BMS3h-56-269	64.5 + 67.2	

Example 5

Competition Analysis

A BIAcore™ 3000 instrument (GE Healthcare) was used to analyze whether CD40-specific dAbs bound the same CD40 epitope. Approximately 600 response units (RU) of biotinylated human CD40 (BMS) were immobilized on one flow-cell of a streptavidin (SA) BIAcore™ chip. A second flow-cell without any ligand immobilized served as a reference flow-cell for inline referencing. An appropriate dilution of each dAb or Fab to be analyzed was prepared in HBS-EP buffer (0.01 M HEPES pH 7.4 with 0.15 M NaCl, 3 mM EDTA and 0.005% v/v Surfactant P20, GE Healthcare). The dilution chosen was one which when injected as described below resulted in >80% of the maximum possible bound RU for the

particular inhibitor, typically 1 - 10 μ M. Next, a mixture of the same dAb or Fab as above (at the same final concentration) was prepared with a second dAb or Fab to be analyzed for competition. The COINJECT function of the instrument was used to inject 60 μ l of the single-inhibitor dilution across the CD40-immobilized and reference flow-cells in series, followed
5 immediately by a 60 μ l injection of the two-inhibitor mixture. Inline subtraction of the signal from the reference cell was performed by the instrument's control software. The experiment was performed at 25°C and a flow rate of 30 μ l/min of HBS-EP. After each co-injection had been completed, the inhibitors were allowed to dissociate from the ligand in buffer for 60 s before regeneration with a 10 μ l injection of 10 mM glycine pH 2.0. The maximum RU
10 obtained for the second injection (the mixture of the two inhibitors) was noted and expressed as a percentage of the RU obtained for the same inhibitor when injected alone.

If the second inhibitor retained at least 100% of the RU usually bound when it was injected alone, then this implied that the two inhibitors bind to discrete epitopes. If less than 100% binding of the second inhibitor was observed, then this was indicative of competition
15 between the two inhibitors for binding to CD40. There are several possible reasons for this competition: the two inhibitors may bind to the same or overlapping epitopes, there may be steric inhibition of binding, or binding of the first inhibitor may induce a conformational change in the antigen that prevents or reduces binding of the second inhibitor.

An example clone from each lineage (except BMS3h-217) was tested for competition
20 with other dAbs in overlapping groups. All the dAbs tested appear to compete with each other for binding to CD40, as shown in TABLES 13 and 14. This data suggests that all antibody polypeptides selected from the group consisting of lineage BMS3h-37, BMS3h-38, BMS3h-41, BMS3h-43, BMS3h-56, BMS3h-131, BMS3h-198, and BMS3h-202 should compete with the binding of a dAb from any of these lineages to human CD40.

TABLE 13

Competition BIAcore™:

First injection	RU first dAb alone	Second Injection (% of single dAb RU)				
		<i>BMS3h-56-5</i>	<i>BMS3h-37-11</i>	<i>BMS3h-131-2</i>	<i>BMS3h-198-1</i>	<i>BMS3h-202-11</i>
<i>BMS3h-56-5</i>	245		-15	17	0.6	7.3
<i>BMS3h-37-11</i>	158	15		25	16	0.3
<i>BMS3h-131-2</i>	220	22	-3.7		23.2	10.3
<i>BMS3h-198-1</i>	176	28	6.4	41		18
<i>BMS3h-202-11</i>	124	50	42	57	39	

TABLE 14

First injection	RU first dAb alone	Second Injection (% of single dAb RU)			
		<i>BMS3h-38-2</i>	<i>BMS3h-41-9</i>	<i>BMS3h-43-1</i>	<i>BMS3h-56-5</i>
<i>BMS3h-38-2</i>	170		11	29	29
<i>BMS3h-41-9</i>	150	27		44	47
<i>BMS3h-43-1</i>	210	20	19		39
<i>BMS3h-56-5</i>	190	4	0	22	

Similarly, various dAbs were tested for competition with Chi220 Fab', as shown in

- 5 TABLES 15 and 16. In this case, all the dAbs do not compete with Chi220 Fab', except BMS3h-217, which shows competition. BMS3h-56-5 and BMS3h-193-12 dAbs bound with at least 100% of single dAb RU in the presence of bound Chi220 or G28-5 Fab', suggesting that the Fab's bind a different epitope(s) than the dAbs. Chi220 Fab' showed a reduction of bound RU in the presence G28-5. The same result was observed in the opposite order of binding.
- 10 This suggests that G28-5 Fab' binds the same epitope as Chi220 Fab'.

TABLE 15

First injection	RU first dAb/Fab alone	Second Injection (% of single dAb/Fab RU)			
		<i>BMS3h-56-5</i>	<i>Chi220 Fab</i>	<i>G28-5 Fab</i>	<i>BMS3h-193-12</i>
<i>BMS3h-56-5</i>	193		98	94	64
<i>Chi220 Fab</i>	1089	105		11	109
<i>G28-5 Fab</i>	730	125	39		116
<i>BMS3h-193-12</i>	282	44	98	93	

TABLE 16

Clone name	μ M dAb or Fab tested	Single dAb RU	% of single dAb RU (Chi220+dAb)
BMS3h-38-2	5	156	121
BMS3h-41-13	5	162	109
BMS3h-43-3	5	300	101
BMS3h-38-2	5	175	114
BMS3h-56-5	5	193	105
BMS3h-106	10	165	111
BMS3h-107	10	35	146
BMS3h-129	10	156	121
BMS3h-193-12	5	282	98
BMS3h-197	1	177	116
BMS3h-217	10	85	25
G28-5 Fab	1	730	11

Example 6

CD40 Activity Assays

Anti-human CD40 dAbs were assayed functionally for their ability to antagonize CD40 activities. The CD40 activities tested were B cell proliferation and cytokine production by hCD40L-driven activation of primary human monocyte-derived dendritic cells (DCs). Unless
 5 otherwise noted, all assays were performed in RPMI media supplemented with 10% fetal calf serum (FCS). The results using the various assays are shown in TABLE 17.

Soluble IZ-hCD40L-driven primary human B cell proliferation:

1×10^5 tonsillar human B cells were incubated with 0.6 $\mu\text{g/ml}$ of IZ-hCD40L along with
 10 varying titrations of antibody polypeptide in a final volume of 200 $\mu\text{l/well}$ in a 96-well round bottom plate. The plates were incubated at 37°C for 72 hours, then thymidine (^3H ; 0.5 $\mu\text{Ci/well}$) was added for 6 hours. B cell proliferation was quantified based on thymidine incorporation.

CHO-hCD40L-driven primary human B cell proliferation:

15 CHO cells were transfected with human CD40L to generate a stable cell line expressing high levels of CD40L on the cell surface. CHO-CD40L cells were irradiated at 10,000 Rads before incubation with human B cells. 1×10^5 tonsillar human B cells were incubated with 1×10^3 CHO-CD40L cells (1:100 ratio of CHO-CD40L: human B cells) along with varying titrations of antibody polypeptide in a final volume of 200 $\mu\text{l/well}$ in a 96-well round bottom
 20 plate. The plates were incubated at 37°C for 72 hours following which ^3H -thymidine (0.5 $\mu\text{Ci/well}$) was added for 6 hours. B cell proliferation was quantified based on thymidine incorporation.

Soluble IZ-hCD40L-driven cyno splenic human B cell proliferation:

1×10^5 cyno splenic B cells were incubated with 0.5 $\mu\text{g/ml}$ of IZ-hCD40L along with
 25 varying titrations of antibody polypeptide in a final volume of 200 $\mu\text{l/well}$ in a 96-well round bottom plate. The plates were incubated at 37°C for 72 hours following which ^3H -thymidine (0.5 $\mu\text{Ci/well}$) was added for 6 hours. B cell proliferation was quantified based on thymidine incorporation.

Primary T cell-driven human B cell proliferation:

T cells were isolated from human peripheral blood mononuclear cells (PBMC) and enriched using sheep red blood cell (SRBC) rosetting. Human tonsillar B cells were isolated by homogenizing tonsil tissue to a single-cell suspension. Leukocytes were obtained by ficoll separation, then B cells were negatively selected using SRBC rosetting and enriched by discarding the rosetted cells.

Enriched human T cells were cultured with PM-LCLs (an EBV-transformed B cell line; irradiated at 10,000 Rads) at a 5:1 ratio (T:LCL) for 6 days at 37°C to generate a population of allogeneic T cells. At day 6, the expanded T cells were isolated and irradiated at 3000 Rads, and then cultured (5×10^4 T cells/well) with primary human tonsillar B cells (1×10^5 B cells/well) at a 1:2 ratio in 96-well flat bottom plates coated with anti-CD3 mAb (OKT3). Varying titrations of antibody polypeptides were added to each well; the final volume in each well was 200 μ l. Test plates were incubated at 37°C for 3 days. Human B cell proliferation was determined via the addition of ^3H -thymidine (0.5 μ ci/well) to the cultures for the last 18 hours.

CHO-hCD40L-driven activation of primary human monocyte-derived dendritic cells (DCs):

Human PBMCs were enriched for monocytes by depleting T cells via SRBC rosetting. The monocyte-enriched PBMCs were cultured with 10ng/ml GM-CSF and 5 ng/ml IL-4 in 6-well plates for 6 days at 37°C. The cultured plates were replenished with fresh media (with GM-CSF and IL-4) on days 2 and 5. The immature dendritic cells (DCs) were used in cell assays on day 6. 8×10^4 immature DCs were cultured with 4×10^3 CHO-hCD40L cells (irradiated at 10,000 Rads) along with varying titrations of antibody polypeptides in a 96-well flat bottom plate. After 24 hours, supernatants were harvested and tested for the presence of various cytokines (IL-12, TNF, IL-23). DC activation was determined by the levels of cytokine production.

TABLE 17

Clone	hIZCD40L- driven Human B Cell Proliferation EC50 (nM)	hIZCD40L- driven Cyno B Cell Proliferation EC50 (nM)	CHO- hCD40L- driven Human B Cell Proliferation EC50 (nM)	T-B cell MLR EC50 (nM)	CHO- hCD40L- driven DC Activation IL-12 EC50 (nM)
3h-5	>7000		>7000		
3h-8	>7000		>7000		
3h-28	>7000		>7000		
3h-33	>7000		>7000		
3h-48	>7000		>7000		
3h-52	>7000		>7000		
3h-57	>7000		>7000		
3h-61	>7000		>7000		
3h-88	>7000				
3h-102	>7000				
3h-106	437.0 ± 214.0	>7000			
3h-107	>7000	>7000			
3h-112	>7000				
3h-129	2100.0 ± 1000.0				
3h-197	360.0 ± 500.0	>7000			
3h-207	>7000				
3h-208	>7000				
3h-37	3400.0 ± 2900.0	>7000			
3h-37-1	250.0 ± 100.0				
3h-37-2	5.0 ± 2.0	>7000		198 ± 35	13.0 ± 7.3
3h-37-202	0.6 ± 0.2			83 ± 18	10.0
3h-37-205	2.0 ± 1.0				6.6
3h-37-206	5.0 ± 0.8				23.0
3h-37-207	4.0 ± 2.0				15.5 ± 8.0
3h-37-212	1.0 ± 0.05				
3h-37-213	0.7 ± 0.2				
3h-37-11	8.0 ± 7.0				

Clone	hIZCD40L- driven Human B Cell Proliferation EC50 (nM)	hIZCD40L- driven Cyno B Cell Proliferation EC50 (nM)	CHO- hCD40L- driven Human B Cell Proliferation EC50 (nM)	T-B cell MLR EC50 (nM)	CHO- hCD40L- driven DC Activation IL-12 EC50 (nM)
3h-38	2800.0 ± 400.0	>7000			
3h-38-1	142.0 ± 86.0				
3h-38-2	10.0 ± 6.0	>7000	723.0 ± 185.0	986 ± 383	289.0 ± 315.0
3h-38-201	>70.0		>7000		>800.0
3h-38-205	4.0 ± 2.0		1100.0 ± 141.0		29.0
3h-38-211	2.0 ± 1.0		82.0 ± 4.0	200 ± 1	18.0 ± 19.0
3h-38-215	1.0 ± 0.0		65.0 ± 1.0	163 ± 14	6.0 ± 4.0
3h-38-217	0.8 ± 0.2		34.0 ± 6.0	74 ± 22	1.7 ± 0.4
3h-38-219	2.0 ± 0.5		93.0 ± 26.0	164 ± 3	9.0 ± 5.0
3h-38-228	0.7 ± 0.05				
3h-38-231	0.66 ± 0.2				
3h-38-235	0.4 ± 0.2				
3h-38-237	0.4 ± 0.2				
3h-38-238	0.7 ± 0.03				
3h-38-3	10.0 ± 7.0				
3h-41	>7000				
3h-41-1	104.0 ± 56.0				
3h-41-2	47.0 ± 67.0				
3h-41-3	12.0 ± 7.0	>7000			
3h-41-9	148.0 ± 98.0				
3h-41-12	104.0 ± 50.0				
3h-41-13	208.0 ± 90.0				
3h-43	83.0 ± 40.0	>7000			
3h-43-1	53.0 ± 20.0				
3h-43-3	87.0 ± 19.0				
3h-43-5	180.0 ± 130.0				
3h-43-10	143.0 ± 131.0				
3h-43-11	30.0 ± 19.0				
3h-43-12	12.0 ± 6.0				
3h-56	713.0 ± 133.0	>7000			

Clone	hIZCD40L- driven Human B Cell Proliferation EC50 (nM)	hIZCD40L- driven Cyno B Cell Proliferation EC50 (nM)	CHO- hCD40L- driven Human B Cell Proliferation EC50 (nM)	T-B cell MLR EC50 (nM)	CHO- hCD40L- driven DC Activation IL-12 EC50 (nM)
3h-56-1	7.0 ± 5.0				
3h-56-2	3.0 ± 1.0		326.0 ± 79.0	276 ± 29	444.0, >2000.0
3h-56-201	0.12 ± 0.04		11.0 ± 6.0	7.25 ± 0.96	0.93 ± 0.7
3h-56-202	0.6 ± 0.2		39.0 ± 16.0	50 ± 9.8	2.9 ± 2.6
3h-56-203	0.45 ± 0.1		51.0 ± 29.0	52 ± 23	3.7 ± 4.0
3h-56-206	0.1 ± 0.01		6.0 ± 2.0	5.25 ± 0.5	0.7 ± 0.4
3h-56-215	0.2 ± 0.03		41.0 ± 15.0	31 ± 7	11.0 ± 12.0
3h-56-217	0.1 ± 0.04		13.0 ± 5.0	16 ± 6.7	9.4 ± 8.0
3h-56-224	0.5 ± 0.2		26.0 ± 5.0	47 ± 11	18.0 ± 22.0
3h-56-232	0.27 ± 0.1		37.0 ± 0.7	42 ± 10	7.3 ± 6.6
3h-56-239	0.11 ± 0.0		18.0 ± 4.0	13.5 ± 4.76	5.8 ± 6.5
3h-56-243	0.15 ± 0.007		13.5 ± 2.0	14.2 ± 4.6	8.8 ± 10.0
3h-56-244	0.17 ± 0.02		26.0 ± 3.0	21 ± 4.1	12.6 ± 16.0
3h-56-246	0.24 ± 0.06		34.0 ± 14.0	23.8 ± 6.2	23.2 ± 22.0
3h-56-248	0.36 ± 0.1				
3h-56-253	0.4 ± 0.2				
3h-56-258	0.079 ± 0.003		11.0 ± 3.0	8.7 ± 1.9	1.52 ± 1.6
3h-56-261	0.17 ± 0.09		25.5 ± 6.0	17 ± 5.4	3.0 ± 1.8
3h-56-262	0.31 ± 0.007				
3h-56-265	0.36 ± 0.06				
3h-56-266	0.19 ± 0.04		19.5 ± 6.0	13.8 ± 2.4	2.8 ± 2.3
3h-56-269	0.14 ± 0.02		15.0 ± 5.0	9.7 ± 1.9	1.8 ± 1.2
3h-56-270	0.31 ± 0.1				
3h-56-5	6.0 ± 4.0	>7000			
3h-56-6	4.0 ± 3.0				
3h-56-7	8.0 ± 6.0				
3h-56-8	5.0 ± 2.0				
3h-56-9	3.0 ± 0.6				
3h-56-15	2.0 ± 0.9				
3h-56-19	3.0 ± 2.0				

Clone	hIZCD40L- driven Human B Cell Proliferation EC50 (nM)	hIZCD40L- driven Cyno B Cell Proliferation EC50 (nM)	CHO- hCD40L- driven Human B Cell Proliferation EC50 (nM)	T-B cell MLR EC50 (nM)	CHO- hCD40L- driven DC Activation IL-12 EC50 (nM)
3h-56-21	2.0 ± 1.0				
3h-131	2700.0 ± 1000.0	>7000			
3h-131-2	55.0 ± 53.0	>7000			
3h-131-6	141.0 ± 37.0				
3h-131-14	24.0 ± 4.0				
3h-193	>7000				
3h-193-12	277.0 ± 167.0				
3h-193-16	387.0 ± 173.0				
3h-193-19	233.0 ± 110.0				
3h-193-25	303.0 ± 214.0	2200.0 ± 1200.0			
3h-193-29	1380.0 ± 721.0				
3h-198	554.0 ± 186.0	>7000			
3h-198-1	64.0 ± 47.0				
3h-198-2	207.0 ± 158.0				
3h-198-5	9.0 ± 6.0				
3h-198-19	19.0 ± 14.0				
3h-198-24	34.0 ± 37.0				
3h-198-28	20.0 ± 9.0				
3h-202	6400.0 ± 1300.0	>7000			
3h-202-1	192.0 ± 77.0	>7000			
3h-202-5	6500.0 ± 1000.0				
3h-202-10	289.0 ± 158.0				
3h-202-11	201.0 ± 103.0				
3h-217	3200.0 ± 2030.0	>7000, 5300, 1690			
3h-217-1	45.0 ± 26.0	35.0 ± 8.0			
3h-217-2	8.0 ± 4.0	7.0			335.0
3h-217-4	61.0 ± 20.0	27.0			

Clone	hIZCD40L- driven Human B Cell Proliferation EC50 (nM)	hIZCD40L- driven Cyno B Cell Proliferation EC50 (nM)	CHO- hCD40L- driven Human B Cell Proliferation EC50 (nM)	T-B cell MLR EC50 (nM)	CHO- hCD40L- driven DC Activation IL-12 EC50 (nM)
3h-217-5	13.0 ± 5.0	15.0			
3h-217-6	11.0 ± 3.0	10.0			
3h-217-7	220.0 ± 20.0				
3h-217-8	33.0 ± 10.0	14.0			
3h-217-9	380.0 ± 170.0				
3h-217-14	26.0 ± 10.0	8.0			
3h-217-15	47.0 ± 21.0	20.0			
3h-217-16	5.0 ± 2.0	7.0			1125.0
3h-217-17	1950.0 ± 110.0				
3h-217-23	16.0 ± 6.0	15.0			
3h-217-2305	11.0 ± 4.0				
3h-217-30	80.0 ± 9.0				>7700
3h-217-31	>700.0				
3h-231	328.0 ± 144.0	>7000			
3h-233	184.0 ± 75.0	>7000			1492.0, >2000
3h-240	>7000	>7000			
3h-242	219.0 ± 53.0	435.0 ± 62.0			2050.0
3h-257	135.0 ± 28.0	>7000			704.0 ± 445.0
3h-262	548.0 ± 121.0	>700			998.0
3h-263	>700.0	>700			
3h-264	1200.0 ± 400.0	>7000			>2000
3h-265	2400.0 ± 1000.0	>7000			>2000
3h-271	295.0 ± 92.0	446.0			>2000
3h-274	1200, >7000	>7000			
3h-275	157.0 ± 11.0	>7000			
3h-285	49.0 ± 0.7	155.0			
3h-287	287.0 ± 156.0	918.0			
3h-289	2300.0 ± 1200.0	4300.0			

Clone	hIZCD40L- driven Human B Cell Proliferation EC50 (nM)	hIZCD40L- driven Cyno B Cell Proliferation EC50 (nM)	CHO- hCD40L- driven Human B Cell Proliferation EC50 (nM)	T-B cell MLR EC50 (nM)	CHO- hCD40L- driven DC Activation IL-12 EC50 (nM)
3h-290	>7000	5650.0			
3h-294	>7000	>7000			
3h-295	>7000	>7000			
3h-296	306.0 $\pm$ 55.0	>7000			
3h-309	648.0 $\pm$ 268.0	838.0			
3h-312	1100.0 $\pm$ 346.0	>7000			

Example 7**Dual Specific dAbs Binding CD40 and Serum Albumin**

Dual specific dAbs that specifically bind CD40 and human serum albumin (HSA) or cynomolgus serum albumin (CSA) were constructed and tested for activity in cell-based assays. The albumin-specific dAbs are called "AlbudAbs." In this example, AlbudAb fusions comprise a BMS3h dAb that binds CD40 and another domain antibody, DOM7h, that recognizes HSA. The two dAbs are fused in frame to the amino and carboxyl termini of an amino acid linker to form an inline fusion (ILF) polypeptide. The ILF polypeptide is expressed recombinantly as a single fusion protein. RBAs demonstrating activity of the AlbudAb ILFs are described below, and the results are shown in TABLE 18. TABLE 19 summarizes the linker sequences used in the tested AlbudAb ILFs. Kinetic binding data determined by a BIAcoreTM assay are shown in TABLE 20.

Human CD40 CHO cell ELISA for the detection of dAbs in a supernatant:

Stably transfected human CD40 expressing CHO-DG44 cells or native CHO-DG44 cells (both BMS) were detached from cell culture flasks using 0.25% trypsin EDTA, and 100,000 cells per well were seeded in growth media into 96 well tissue culture treated plates (NUNC). The cells were allowed to adhere overnight in a humidified atmosphere at 37°C, 5% CO₂. On the day of assay, the cell sheet was washed with PBS prior to being fixed with 2% paraformaldehyde (Sigma-Aldrich) for 20 minutes. Following fixing, the cell sheet was washed again in PBS prior to a 1 hr blocking step with 15% fetal bovine serum (FBS, PAA) in

PBS. Plates were washed once more prior to addition of 100 μ l/well of dAb supernatant and incubated for 2 h at room temperature. Following incubation of dAb supernatants with cells, the plates were washed and dAb binding was detected with incubation of horse radish peroxidase (HRP) conjugate anti-protein A or L, depending on whether dAbs are V_H or V_L domains. Absorbance signal was measured using a SpectraMax M5^e plate reader (Molecular Devices) at 450 nm following neutralization with 1 M HCl.

ICAM-1 up-regulation cell assay:

Stably transfected human CD40L expressing COS cells were detached from cell culture flasks using Versene (Invitrogen). 20,000 cells per well were seeded into 96 well Highbind, black walled, clear bottom plates (Corning, UK) in assay buffer (RPMI 1640 without phenol red (Sigma-Aldrich, UK) + 1% penicillin/streptomycin + 10% FBS Gold (both PAA Laboratories, UK). The cells were left to adhere overnight in a humidified atmosphere at 37°C with 5% CO₂. The following day, exhausted assay buffer containing non attached cells was replenished with 100 μ l of fresh assay buffer. To this, 20,000 RAMOS cells/well were added in assay buffer in addition to a dilution range of dAb. The assay plate was returned to a humidified atmosphere at 37°C with 5% CO₂ for a further 24 hours. For negative control wells, no RAMOS cells were added. The ability of dAb to inhibit the up-regulation of ICAM-1 on the cell surface of RAMOS cells in response to exposure to CD40L on the cell surface of COS cells was assessed by addition of 0.5 μ g/ml mouse anti human ICAM-1 antibody (R&D systems) and 0.2 μ g/ml goat anti mouse ALEXA flour 647 (Invitrogen, Molecular probes, UK). Following a 3hour incubation period in the absence of light, relative fluorescence was detected as measured by the AB8200 cellular detection platform (Applied Biosystems).

Analysis of inline fusion (ILF) kinetics of binding to serum albumin:

A BIAcoreTM 3000 instrument (GE Healthcare) was used to analyze the binding kinetics of anti-CD40-AlbudAb ILFs to human and cynomolgus serum albumin. Approximately 400 response units (RU) of human serum albumin (HSA) or cynomolgus serum albumin (CSA) were immobilized on a flow-cell of a CM5 BIAcoreTM chip using an Amine Coupling Kit (GE Healthcare). A second flow cell without any ligand immobilized served as a reference flow-cell for inline referencing. An appropriate doubling dilution series of each dAb to be analyzed was prepared in HBS-EP buffer (0.01 M HEPES pH 7.4 with 0.15 M NaCl,

3 mM EDTA and 0.005% v/v Surfactant P20, GE Healthcare). Two hundred microlitres of each ILF were injected in duplicate using the instrument's KINJECT function. The injections were made across the serum albumin-immobilized and reference flow-cells in series, with inline subtraction of the signal from the reference cell. The experiment was performed at 25°C

5 and a flow rate of 40 μ l/min of HBS-EP. After each injection had been completed, the dAb was allowed to dissociate from the ligand in buffer for 120 s before regeneration with a 10 μ l injection of 10 mM glycine pH 2.0. A reference injection of HBS-EP buffer blank (containing no analyte) was also injected under the same conditions to serve as a second reference for subtraction from each analyte trace. BIAevaluation 4.1 software (GE Healthcare) was used to

10 subtract both the reference flow-cell trace and the buffer blank trace from each analyte trace. The same software was used to perform a simultaneous, global fit of a 1:1 (Langmuir) kinetic model to the association and dissociation phases of the analyte dilution series traces. This model yielded association and dissociation rate constants (k_a and k_d , respectively) and the equilibrium dissociation constant (K_D) of the interaction. The parameter values are shown in

15 TABLE 20.

TABLE 18

Activity Assays

DMS No.	N-term. dAb	Linker	C-term. dAb	CHO-CD40 Cell RBA			ICAM-1 Cell Assay		
				EC ₅₀ (nM)			EC ₅₀ (nM)		
				0.1% BSA	50 μ M HSA		10% bovine serum	10% human serum	
DMS0654	BMS3h-56-201	AST	DOM7h-11-3	15	8.6				
DMS0655	BMS3h-56-201	AST	DOM7h-11-87	6.3	2.7				
DMS0656	BMS3h-56-258	AST	DOM7h-11-3	11.8	26.8				
DMS0657	BMS3h-56-258	AST	DOM7h-11-87	6.8	16.6				
DMS0658	DOM7h-11-3	TVAAPS	BMS3h-56-201	12.2	9.1				
DMS0659	DOM7h-11-87	TVAAPS	BMS3h-56-201	7.2	3.3				
DMS0660	DOM7h-11-3	TVAAPS	BMS3h-56-258	21.8	13.1				
DMS0661	DOM7h-11-87	TVAAPS	BMS3h-56-258	4.1	5.7				
DMS0662	DOM7h-11-90	TVAAPS	BMS3h-56-201				33.5	>1000	
DMS0663	DOM7h-11-86	TVAAPS	BMS3h-56-201				21.4	>1000	
DMS0664	DOM7h-11-69	TVAAPS	BMS3h-56-201				16.5	>1000	
DMS0677	DOM7h-11-90	TVA	BMS3h-56-258				21.7	20.35	
DMS0679	DOM7h-11-90	G ₄ S	BMS3h-56-258				21.7	39.2	

DMS No.	N-term. dAb	Linker	C-term. dAb	CHO-CD40 Cell RBA		ICAM-1 Cell Assay	
				EC ₅₀ (nM)	50 μ M HSA	10% bovine serum	10% human serum
DMS0680	DOM7h-11-90	(G ₄ S) ₃	BMS3h-56-258			39.3	74.2
DMS0681	DOM7h-11-90	(G ₄ S) ₃	BMS3h-56-258			43.6	53.3
DMS0682	BMS3h-56-258	TV _A	DOM7h-11-90			10.2	94.8
DMS0683	BMS3h-56-258	ASTSGPS	DOM7h-11-90			32.4	50.9
DMS0684	BMS3h-56-258	G ₄ S	DOM7h-11-90			37.9	74.3
DMS0685	BMS3h-56-258	(G ₄ S) ₃	DOM7h-11-90			31.9	62.4
DMS0686	BMS3h-56-258	(G ₄ S) ₃	DOM7h-11-90			48.3	66.6

TABLE 19

Representative Linker Sequences

AST	SEQ ID NO: 5
TVAAAPS	SEQ ID NO: 6
TV _A	SEQ ID NO: 7
GGGS	SEQ ID NO: 1207
(GGGS) ₃	SEQ ID NO: 1208

(GGGGS) ₅	SEQ ID NO: 1209
ASTSGPS	SEQ ID NO: 8

TABLE 20
BIAcore™ Analysis

DMS No.	N-Term dAb	Linker ("TVAAAPS" disclosed as SEQ ID NO: 6)	C-Term dAb	Human Serum Albumin		Cyno Serum Albumin			
				k_a (1/Ms) $\times 10^{-6}$	k_d (1/s) $\times 10^3$	K_D (nM)	k_a (1/Ms) $\times 10^{-6}$	k_d (1/s) $\times 10^3$	K_D (nM)
DMS0659	DOM7h-11-87	TVAAAPS	BMS3h-56-201	0.85, 2.85, 2.6	1.17, 1.69, 1.2	1.37, 0.60, 0.45	0.85, 2.79, 2.9	2.37, 3.37, 2.4	2.79, 1.21, 0.83
DMS0662	DOM7h-11-90	TVAAAPS	BMS3h-56-201	1.1, 1.19	1.33, 1.47	1.21, 1.23	1.01, 1.10	2.52, 2.66	2.5, 2.42
DMS0663	DOM7h-11-86	TVAAAPS	BMS3h-56-201	1.25, 1.32	1.40, 1.60	1.12, 1.21	1.18, 1.18	2.81, 2.96	2.38, 2.52
DMS0664	DOM7h-11-69	TVAAAPS	BMS3h-56-201	2.5, 0.93	1.42, 1.49	0.57, 1.59	2.51, 0.92	2.73, 2.72	1.09, 2.97

TABLE 21 lists amino acid sequences of representative AlbuAb ILFs that can specifically bind CD40 and HSA or CSA. The designation of each ILF identifies the particular linker sequence: "GxS" means the linker has "x" residues of glycine followed by serine, and "(GxS)y" means the linker has y repeating units of GxS. TABLE 22
 5 discloses representative nucleic acids that encode the ILF sequences listed in TABLE 21. As is known in the art, multiple codons can encode the same amino acid. Nucleic acids encoding a protein sequence thus include nucleic acids having codon degeneracy.

TABLE 21

Dual Specificity dAb Amino Acid Sequences

10 (Table 21 discloses "AST," "TVAAPS," "TVA," "G4S," "(G4S)3," "(G4S)5," and "ASTSGPS" disclosed as SEQ ID NOS 5-7, 1207-1209 and 8, respectively)

DMS0654 BMS3h-56-201-AST-DOM7h-11-3
 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWVVRQAPGKGLERVSAINPQGTRTY
 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKLPFYFQEWGQGTLLVTVSSAS
 15 TDIQMTQSPSSLSASVGDRTITCRASRPISGTLTSLWYQQKPKAPKLLILWNSRLQSGV
 PSRFGSGSGTDFTLTISSLQPEDFATYYCAQAGTHPTTFGQGTKVEIKR (SEQ ID
 NO: 1210)

DMS0655 BMS3h-56-201-AST-DOM7h-11-87
 20 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWVVRQAPGKGLERVSAINPQGTRTY
 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKLPFYFQEWGQGTLLVTVSSAS
 TDIQMTQSPSSLSASVGDRTITCRASRPISGTLTSLWYQQKPKAPKLLILAFSRLQSGV
 PSRFGSGSGTDFTLTISSLQPEDFATYYCAQAGTHHTTFGQGTKVEIKR (SEQ ID
 NO: 1211)

25 DMS0656 BMS3h-56-258-AST-DOM7h-11-3
 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWVVRQAPGKGLERVSAINPQGTRTY
 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGTLLVTVSSAS
 TDIQMTQSPSSLSASVGDRTITCRASRPISGTLTSLWYQQKPKAPKLLILWNSRLQSGV
 30 PSRFGSGSGTDFTLTISSLQPEDFATYYCAQAGTHPTTFGQGTKVEIKR (SEQ ID
 NO: 1212)

DMS0657 BMS3h-56-258-AST-DOM7h-11-87
 35 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWVVRQAPGKGLERVSAINPQGTRTY
 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGTLLVTVSSAS
 TDIQMTQSPSSLSASVGDRTITCRASRPISGTLTSLWYQQKPKAPKLLILAFSRLQSGV

- PSRFGSGSGTDFTLTISSLPEDFATYYCAQAGTHHTTFGQGTKVEIKR (SEQ ID NO: 1213)
- 5 DMS0658 DOM7h-11-3-TVAAPS-BMS3h-56-201
 DIQMTQSPSSLSASVGDRVITICRASRPITGLSWYQQKPGKAPKLLILAFSRLQSGVP
 SRFGSGSGTDFTLTISSLPEDFATYYCAQAGTHHTTFGQGTKVEIKRTVAAPSEVQL
 LESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADS
 VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFQEWGQGLVTVSS (SEQ ID NO: 1214)
- 10 DMS0659 DOM7h-11-87-TVAAPS-BMS3h-56-201
 DIQMTQSPSSLSASVGDRVITICRASRPITGLSWYQQKPGKAPKLLILAFSRLQSGVP
 SRFGSGSGTDFTLTISSLPEDFATYYCAQAGTHHTTFGQGTKVEIKRTVAAPSEVQL
 LESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADS
 15 VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFQEWGQGLVTVSS (SEQ ID NO: 1215)
- DMS0660 DOM7h-11-3-TVAAPS-BMS3h-56-258
 20 DIQMTQSPSSLSASVGDRVITICRASRPITGLSWYQQKPGKAPKLLILAFSRLQSGVP
 SRFGSGSGTDFTLTISSLPEDFATYYCAQAGTHHTTFGQGTKVEIKRTVAAPSEVQL
 LESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADS
 VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGLVTVSS (SEQ ID NO: 1216)
- 25 DMS0661 DOM7h-11-87-TVAAPS-BMS3h-56-258
 DIQMTQSPSSLSASVGDRVITICRASRPITGLSWYQQKPGKAPKLLILAFSRLQSGVP
 SRFGSGSGTDFTLTISSLPEDFATYYCAQAGTHHTTFGQGTKVEIKRTVAAPSEVQL
 LESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADS
 30 VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGLVTVSS (SEQ ID NO: 1217)
- DMS0662 DOM7h-11-90-TVAAPS-BMS3h-56-201
 DIQMTQSPSSLSASVGDRVITICRASRPITGLSWYQQKPGKAPKLLILAFSRLQSGVP
 SRFGSGSGTDFTLTISSLPEDFATYYCAQAGTHHTTFGQGTKVEIKRTVAAPSEVQL
 35 LESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADS
 VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFQEWGQGLVTVSS (SEQ ID NO: 1218)
- DMS0663 DOM7h-11-86-TVAAPS-BMS3h-56-201
 40 DIQMTQSPSSLSASVGDRVITICRASRPITGLSWYQQKPGKAPKLLILAFSRLQSGVP
 SRFGSGSGTDFTLTISSLPEDFATYYCAQAGTHHTTFGQGTKVEIKRTVAAPSEVQL
 LESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADS
 VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFQEWGQGLVTVSS (SEQ ID NO: 1219)
- 45 DMS0664 DOM7h-11-69-TVAAPS-BMS3h-56-201

DIQMTQSPSSLSASVGDRTITCRASRPITGLSWYQQKPGKAPKLLILAFSRLQSGVP
 SRFSGSGSGTDFTLTISLQPEDFATYYCAQAGVHPTTFGQGTKVEIKRTVAAPSEVQL
 LESGGGLVQPGGSLRLSCAASGFTFRDYEMWVRQAPGKGLERVSAINPQGRTRYADS
 VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKLPFYQEWGQGTTLTVSS (SEQ
 5 ID NO: 1220)

DMS0667 DOM7h-11-3-TVAAPS-BMS3h-38-240
 DIQMTQSPSSLSASVGDRTITCRASRPITGLSWYQQKPGKAPKLLILWNSRLQSGVP
 SRFSGSGSGTDFTLTISLQPEDFATYYCAQAGTHPTTFGQGTKVEIKRTVAAPSEVQL
 10 LESGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWVSAISRNGYSTYYADS
 VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCGKEPFYDYWGQGTTLTVSS (SEQ
 ID NO: 1221)

DMS0668 BMS3h-38-240-AST-DOM7h-11-3
 15 EVQLLES GGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWVSAISRNGYSTY
 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCGKEPFYDYWGQGTTLTVSSAS
 TDIQMTQSPSSLSASVGDRTITCRASRPITGLSWYQQKPGKAPKLLILWNSRLQSGV
 PSRFSGSGSGTDFTLTISLQPEDFATYYCAQAGTHPTTFGQGTKVEIKR (SEQ ID
 NO: 1222)

20 DMS0669 DOM7h-14-10-TVAAPS-BMS3h-38-240
 DIQMTQSPSSLSASVGDRTITCRASQWIGSQLSWYQQKPGKAPKLLIMWRSSLQSGVP
 SRFSGSGSGTDFTLTISLQPEDFATYYCAQGLRHPKTFGQGTKVEIKRTVAAPSEVQL
 LESGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWVSAISRNGYSTYYADS
 25 VKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCGKEPFYDYWGQGTTLTVSS (SEQ
 ID NO: 1223)

DMS0670 BMS3h-38-240-AST-DOM7h-14-10
 EVQLLES GGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWVSAISRNGYSTY
 30 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCGKEPFYDYWGQGTTLTVSSAS
 TDIQMTQSPSSLSASVGDRTITCRASQWIGSQLSWYQQKPGKAPKLLIMWRSSLQSGV
 PSRFSGSGSGTDFTLTISLQPEDFATYYCAQGLRHPKTFGQGTKVEIKR (SEQ ID
 NO: 1224)

35 DMS0671 BMS3h-38-235-AST-DOM7h-11-3
 EVQLLAS GGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWVSAISRNGYSTY
 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCGKEPFYDYWGQGTTLTVSSAS
 TDIQMTQSPSSLSASVGDRTITCRASRPITGLSWYQQKPGKAPKLLILWNSRLQSGV
 PSRFSGSGSGTDFTLTISLQPEDFATYYCAQAGTHPTTFGQGTKVEIKR (SEQ ID
 40 NO: 1225)

DMS0672 BMS3h-38-235-AST-DOM7h-11-90
 EVQLLAS GGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWVSAISRNGYSTY
 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCGKEPFYDYWGQGTTLTVSSAS
 45 TDIQMTQSPSSLSASVGDRTITCRASRPITGLSWYQQKPGKAPKLLILAFSRLQSGV
 PSRFSGSGSGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKR (SEQ ID
 NO: 1226)

- DMS0674 DOM7h-11-3-TVAAPS-BMS3h-38-235
 DIQMTQSPSSLSASVGDRVITTCRASRPITGMLSWYQQKPGKAPKLLILAFSRLQSGVP
 SRFGSGSGGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKRTVAAPSEVQL
 5 LASGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWVSAISRNGYSTYYADS
 VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCCKEPFRYDYGQGT LVTVSS (SEQ
 ID NO: 1227)
- DMS0675 DOM7h-11-90-TVAAPS-BMS3h-38-235
 10 DIQMTQSPSSLSASVGDRVITTCRASRPITGMLSWYQQKPGKAPKLLILAFSRLQSGVP
 SRFGSGSGGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKRTVAAPSEVQL
 LASGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWVSAISRNGYSTYYADS
 VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCCKEPFRYDYGQGT LVTVSS (SEQ
 ID NO: 1228)
- 15 DMS0677 DOM7h-11-90-TVA-BMS3h-56-258
 DIQMTQSPSSLSASVGDRVITTCRASRPITGMLSWYQQKPGKAPKLLILAFSRLQSGVP
 SRFGSGSGGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKRTVAEVQLLES
 GGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGT RTYYADSVK
 20 RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGT LVTVSS (SEQ
 ID NO: 1229)
- DMS0678 DOM7h-11-90-ASTSGPS-BMS3h-56-258
 25 DIQMTQSPSSLSASVGDRVITTCRASRPITGMLSWYQQKPGKAPKLLILAFSRLQSGVP
 SRFGSGSGGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKRASTSGPSEVQ
 LLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGT RTYYAD
 SVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGT LVTVSS (SEQ
 ID NO: 1230)
- 30 DMS0679 DOM7h-11-90-G4S-BMS3h-56-258
 DIQMTQSPSSLSASVGDRVITTCRASRPITGMLSWYQQKPGKAPKLLILAFSRLQSGVP
 SRFGSGSGGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKRGGGSGEVQLL
 ESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGT RTYYADSV
 35 KGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGT LVTVSS (SEQ
 ID NO: 1231)
- DMS0680 DOM7h-11-90-(G4S)3-BMS3h-56-258
 DIQMTQSPSSLSASVGDRVITTCRASRPITGMLSWYQQKPGKAPKLLILAFSRLQSGVP
 SRFGSGSGGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKRGGGSGGGGS
 40 GGGGSEVQLLES GGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQ
 GT RTYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGT LVT
 VSS (SEQ ID NO: 1232)
- DMS0681 DOM7h-11-90-(G4S)5-BMS3h-56-258
 45 DIQMTQSPSSLSASVGDRVITTCRASRPITGMLSWYQQKPGKAPKLLILAFSRLQSGVP
 SRFGSGSGGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKRGGGSGGGGS
 GGGGSGGGSGGGGSEVQLLES GGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGK

LERVSAINPQGTRTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYF
HEWGQGLVTVSS (SEQ ID NO: 1233)

DMS0682 BMS3h-56-258-TVA-DOM7h-11-90
5 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTY
YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGLVTVSSSTV
ADIQMTQSPSSLSASVGDRVTITCRASRPITGMLSWYQQKPGKAPKLLILAFSRLQSGV
PSRFSGSGSGTDFTLTISNLPEDFATYYCAQAGTHPTTFGQGTKVEIKR (SEQ ID
NO: 1234)

10 DMS0683 BMS3h-56-258-ASTSGPS-DOM7h-11-90
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTY
YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGLVTVSSAS
TSGPDIQMTQSPSSLSASVGDRVTITCRASRPITGMLSWYQQKPGKAPKLLILAFSRL
15 QSGVPSRFSGSGSGTDFTLTISNLPEDFATYYCAQAGTHPTTFGQGTKVEIKR (SEQ
ID NO: 1235)

DMS0684 BMS3h-56-258-G4S-DOM7h-11-90
20 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTY
YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGLVTVSSGG
GGSDIQMTQSPSSLSASVGDRVTITCRASRPITGMLSWYQQKPGKAPKLLILAFSRLQS
GVPSRFSGSGSGTDFTLTISNLPEDFATYYCAQAGTHPTTFGQGTKVEIKR (SEQ
ID NO: 1236)

25 DMS0685 BMS3h-56-258-(G4S)3-DOM7h-11-90
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTY
YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGLVTVSSGG
CGSGGGGGGGSDIQMTQSPSSLSASVGDRVTITCRASRPITGMLSWYQQKPGKAPKL
LILAFSRLQSGVPSRFSGSGSGTDFTLTISNLPEDFATYYCAQAGTHPTTFGQGTKVE
30 IKR (SEQ ID NO: 1237)

DMS0686 BMS3h-56-258-(G4S)5-DOM7h-11-90
EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTY
YADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGLVTVSSGG
35 GGSGGGGGGGGGGGGGSDIQMTQSPSSLSASVGDRVTITCRASRPITGMLSWY
QQKPGKAPKLLILAFSRLQSGVPSRFSGSGSGTDFTLTISNLPEDFATYYCAQAGTHP
TTFGQGTKVEIKR (SEQ ID NO: 1238)

DMS0688 DOM7h-11-90-TVAAPS-BMS3h-56-258
40 DIQMTQSPSSLSASVGDRVTITCRASRPITGMLSWYQQKPGKAPKLLILAFSRLQSGVP
SRFSGSGSGTDFTLTISNLPEDFATYYCAQAGTHPTTFGQGTKVEIKRTVAAPSEVQL
LES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADS
VKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGLVTVSS (SEQ
ID NO: 1239)

TABLE 22

Polynucleotides Encoding Dual Specificity dAbs

(Table 22 discloses "AST," "TVAAPS," "TVA," "G4S," "(G4S)3," "(G4S)5," and "ASTSGPS" disclosed as SEQ ID NOS 5-7, 1207-1209 and 8, respectively)

5 DMS0654 BMS3h-56-201-AST-DOM7h-11-3
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTCCGGGATTATGAGATGTGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTGTAT
 10 CTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAACTTCCG
 TTTTACTTTTCAGGAGTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGCGCTAGCACCGAC
 ATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATC
 ACTTGCCGGGCAAGTCCGATTCGGACACGTTAAGTTGGTACCAGCAGAAACAGGG
 AAAGCCCCTAAGCTCCTGATCCTTTGGAATTCCTGTTGCAAAGTGGGGTCCCATCAGCT
 15 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAA
 GATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCCTACGACGTTCCGCCAAGGG
 ACCAAGGTGAAATCAAACGG (SEQ ID NO: 1240)

20 DMS0655 BMS3h-56-201-AST-DOM7h-11-87
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTCCGGGATTATGAGATGTGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTGTAT
 25 CTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAACTTCCG
 TTTTACTTTTCAGGAGTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGCGCTAGCACCGAC
 ATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATC
 ACTTGCCGGGCAAGTCCGATTCGGACGATGTTAAGTTGGTACCAGCAGAAACAGGG
 AAAGCCCCTAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCAGCT
 30 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAA
 GATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCCTACGACGTTCCGCCAAGGG
 ACCAAGGTGAAATCAAACGG (SEQ ID NO: 1241)

35 DMS0656 BMS3h-56-258-AST-DOM7h-11-3
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTCCGGGATTATGAGATGTGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGGACAATTCCAAGAACACGCTGTAT
 40 CTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGGGTATATTACTGTGCGAACTTCCG
 TTTTACTTTTCAGGAGTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGCGCTAGCACCGAC
 ATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATC
 ACTTGCCGGGCAAGTCCGATTCGGACGATGTTAAGTTGGTACCAGCAGAAACAGGG
 AAAGCCCCTAAGCTCCTGATCCTTTGGAATTCCTGTTGCAAAGTGGGGTCCCATCAGCT
 45 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAA
 GATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCCTACGACGTTCCGCCAAGGG
 ACCAAGGTGAAATCAAACGG (SEQ ID NO: 1242)

DMS0657 BMS3h-56-258-AST-DOM7h-11-87
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCT
 CCAGGGAAGGCTCTAGAGCGGCTCTCAGCTATTAATCCGAGGGTACGCGTACATACTAC
 5 GCAGACTCCGTGAAGGGCCGTTACCATCTCCCGCGACAATCCAAGAACACGCTGTAT
 CTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCG
 TTTTACTTTACAGAGTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGCGCTAGCACCGAC
 ATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACCATC
 ACTTGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACAGGG
 10 AAAGCCCCTAAGTCTCTGATCCTTGCTTTTCCCGTTGCAAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTCTACTCTCACCATCAGCAGTCTGCAACCTGAA
 GATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCATACGAGCTTCGGCCAAAGGG
 ACCAAGGTGGAATCAACCG (SEQ ID NO: 1243)

DMS0658 DOM7h-11-3-TVAAPS-BMS3h-56-201
 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
 ATCACTTGCCGGGCAAGTCGTCCGATTGGGACGACGTTAAGTTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGTCTCTGATCCTTTGGAAATTCCTGTTTGGCAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 20 GAAGATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCTACGAGCTTCGGCCAA
 GGGACCAAGGTGGAATCAACGCTACCGTGGCTGCACCATCTGAGGTGCAGCTGTGGAG
 TCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCTGTGCAAGCTCCGGA
 TTCACCTTTCCGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAG
 CCGGTCTCAGCTATTAAATCCGAGGCTACCGGTACATACTACGAGACTCCGTGAAGGGC
 25 CGGTTCAACCATCTCCGCGACAATTCCAAGAACAGCTGTATCTGCAAAATGAACAGCCTG
 CGTGCCGAGGACACCGCGGTATATTACTCTGCCAAACTTCCGTTTTACTTTCACGAGTGG
 GTTCAGGGAACCTGGTCACCGTCTCCAGC (SEQ ID NO: 1244)

DMS0659 DOM7h-11-87-TVAAPS-BMS3h-56-201
 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
 30 ATCACTTGCCGGGCAAGTCGTCCGATTGGGACGACGTTAAGTTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGTCTCTGATCCTTTGCTTTTCCCGTTTGGCAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCTACGAGCTTCGGCCAA
 35 GGGACCAAGGTGGAATCAACGCTACCGTGGCTGCACCATCTGAGGTGCAGCTGTGGAG
 TCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCTGTGCAAGCTCCGGA
 TTCACCTTTCCGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAG
 CCGGTCTCAGCTATTAAATCCGAGGCTACCGGTACATACTACGAGACTCCGTGAAGGGC
 CGGTTCAACCATCTCCGCGACAATTCCAAGAACAGCTGTATCTGCAAAATGAACAGCCTG
 40 CGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTACTTTCAGGAGTGG
 GTTCAGGGAACCTGGTCACCGTCTCCAGC (SEQ ID NO: 1245)

DMS0660 DOM7h-11-3-TVAAPS-BMS3h-56-258
 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
 45 ATCACTTGCCGGGCAAGTCGTCCGATTGGGACGACGTTAAGTTGGTACCAGCAGAAACCA
 GGGAAAGCCCCTAAGTCTCTGATCCTTTGGAATTCCTGTTTGGCAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
 GAAGATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCTACGAGCTTCGGCCAA
 50 GGGACCAAGGTGGAATCAACGCTACCGTGGCTGCACCATCTGAGGTGCAGCTGTGGAG
 TCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCTGTGCAAGCTCCGGA
 TTCACCTTTCCGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAG
 CCGGTCTCAGCTATTAAATCCGAGGCTACCGGTACATACTACGAGACTCCGTGAAGGGC
 CGGTTCAACCATCTCCGCGACAATTCCAAGAACAGCTGTATCTGCAAAATGAACAGCCTG
 CGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTACTTTCAGGAGTGG

GGTCAGGGAACCCCTGGTCACCGTCTCCAGC (SEQ ID NO: 1246)

DMS0661 DOM7h-11-87-TVAAPS-BMS3h-56-258

5 GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCTGGGCAAGTCCTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCCTAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCAGCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCATACGACGTTCCGGCCAA
GGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCACCATCTGAGGTGCAGCTGTTGGAG
10 TCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGA
TTCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAG
CGGGTCTCAGCTATTAAATCCGACGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGC
CGGTTCAACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAAATGAACAGCCTG
CGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTCACGAGTGG
15 GGTCAGGGAACCCCTGGTCACCGTCTCCAGC (SEQ ID NO: 1247)

DMS0662 DOM7h-11-90-TVAAPS-BMS3h-56-201

20 GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCTGGGCAAGTCCTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCCTAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCAGCATCAGCAATCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCCTACGACGTTCCGGCCAA
GGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCACCATCTGAGGTGCAGCTGTTGGAG
25 TCCGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGA
TTCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAG
CGGGTCTCAGCTATTAAATCCGACGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGC
CGGTTCAACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAAATGAACAGCCTG
CGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTCAGGAGTGG
30 GGTCAGGGAACCCCTGGTCACCGTCTCCAGC (SEQ ID NO: 1248)

DMS0663 DOM7h-11-86-TVAAPS-BMS3h-56-201

35 GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCTGGGCAAGTCCTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCCTAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCAGCATCAGCAGTCTGCAACCT
GAAGATGTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCCTACGACGTTCCGGCCAA
CGGACCAAGGTGCAAAATCAAACGTACGCTGGCTGCACCATCTCAGCTCCAGCTGTTCCAG
TCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGA
40 TTCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAG
CGGGTCTCAGCTATTAAATCCGACGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGC
CGGTTCAACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAAATGAACAGCCTG
CGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTTCAGGAGTGG
35 GGTCAGGGAACCCCTGGTCACCGTCTCCAGC (SEQ ID NO: 1249)

DMS0664 DOM7h-11-69-TVAAPS-BMS3h-56-201

45 GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCTGGGCAAGTCCTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCCTAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCAGCATCAGCAGTCTGCAACCT
50 GAAGATTTTGCTACGTACTACTGTGCGCAGGCTGGGGTGCATCCTACGACGTTCCGGCCAA
GGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCACCATCTGAGGTGCAGCTGTTGGAG
TCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGA
TTCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAG

- CGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGC
CGGTTACCATCTCCCGCGACAATCCAAGAACACGCTGTATCTGCAATGAACAGCCTG
CGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCGCTTTTACTTTACAGGAGTGG
GGTCAGGGAACCTGGTCACCGTCTCCAGC (SEQ ID NO: 1250)
- 5 DMS0667 DOM7h-11-3-TVAAPS-BMS3h-38-240
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCGTCCGATTGGGACGACGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCTAAGCTCCTGATCCTTTGGAATTCCCGTTTGCAAGTGGGGTCCCATCA
10 CGTTTCAGTGGCAGTGGATCTGGGACAGATTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCCTACGACGTTCCGCCAA
GGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCACCATCTGAGGTGCAGCTGTTGGAG
TCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGA
TTCACTTTGAGGAGGAGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAG
15 TGGGTCTCAGCTATTAGTAGGAACGGTTACAGCACATACTACGCAGACTCCGTGAAGGGC
CGGTTACCATCTCCCGCGACAATCCAAGAACACGCTGTATCTGCAATGAACAGCCTG
CGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACTGG
GGTCAGGGAACCTGGTCAACCGTCTCCAGC (SEQ ID NO: 1251)
- 20 DMS0668 BMS3h-38-240-AST-DOM7h-11-3
GAGGTGCAGCTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAGGAACGGTTACAGCACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTGTAT
25 CTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCG
TTTCGTTATGACTACTTGGGGTCAAGGAACCTTGGTCAACGCTCTCGAGCGCTAGCACCGCA
ATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACCATC
ACTTCCCGGCAAGTCTGCGATTGGGACGACGTTAAGTTGGTACCAGCAGAAACAGGG
AAAGCCCTAAGCTCCTGATCCTTTGGAATTCGCTTTGCAAGTGGGGTCCCATCACGT
30 TTCACTGGCAGTGGATCTGGGACAGATTCACTCTCACCATCAGCAGTCTGCAACCTGAA
GATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCCTACGACGTTCCGGCAAGGG
ACCAAGGTGGAATCAAACGG (SEQ ID NO: 1252)
- DMS0669 DOM7h-14-10-TVAAPS-BMS3h-38-240
35 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCAGTGGATTGGGTCTCAGTTATCTTGGTACCAGCAGAAACCA
GGGAAAGCCCTAAGCTCCTGATCATGTGGCTTCTCGTTGCAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCTCAGGGTTTGAGGCATCCTAAGACGTTCCGCCAA
40 GGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCACCATCTGAGGTGCAGCTGTTGGAG
TCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGA
TTCACTTTGAGGAGGAGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAG
TGGGTCTCAGCTATTAGTAGGAACGGTTACAGCACATACTACGCAGACTCCGTGAAGGGC
CGGTTACCATCTCCCGCGACAATCCAAGAACACGCTGTATCTGCAATGAACAGCCTG
45 CGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACTGG
GGTCAGGGAACCTGGTCAACCGTCTCCAGC (SEQ ID NO: 1253)
- DMS0670 BMS3h-38-240-AST-DOM7h-14-10
50 GAGGTGCAGCTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAGGAACGGTTACAGCACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGGACAATTCCAAGAACACGCTGTAT
CTGCAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCG

TTTCGTTATGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGCGCTAGCACCGAC
ATCCAGATGACCCAGTCTCCATCCTCCCTGTCGTCATCTGTAGGAGACCGTGTACCATC
ACTTGCCGGGCAAGTCAGTGGATTGGGTCTCAGTTATCTTGGTACCAGCAGAAACCAAGG
5 AAAGCCCCTAAGCTCCTGATCATGTGGCGTTCCCTCGTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTCACTCTCACCATCAGCAGTCTGCAACCTGAA
GATTTTGCCTACGTACTACTGTGCTCAGGGTTTGAGGCATCCTAAGACGTTCCGCCAAGGG
ACCAAGGTGGAAATCAAACGG (SEQ ID NO: 1254)

DMS0671 BMS3h-38-235-AST-DOM7h-11-3
10 GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGCGCAGCTCCGGATTACCTTTGAGGAGGAGGAGATGATTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAGGAACGGTTACAGCACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACCGCTGTAT
CTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCG
15 TTTCGTTATGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGCGCTTCAACCGAC
ATCCAGATGACCCAGTCTCCATCCTCCCTGTCGTCATCTGTAGGAGACCGTGTCAACATC
ACTTGCCGGGCAAGTCTGTCGATTGGGACGAGCTTAAGTTGGTACCAGCAGAAACCAAGG
AAAGCCCCTAAGCTCCTGATCCTTTGGAAATCCCGTTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTCACTCTCACCATCAGCAGTCTGCAACCTGAA
20 GATTTTGCCTACGTACTACTGTGCGCAGGCTGGGACGCAATCCTACGACGTTCCGCCAAGGG
ACCAAGGTGGAAATCAAACGG (SEQ ID NO: 1255)

DMS0672 BMS3h-38-235-AST-DOM7h-11-90
25 GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGCGCAGCTCCGGATTACCTTTGAGGAGGAGGAGATGATTGGGTCCGCCAGGCC
CCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAGGAACGGTTACAGCACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACCGCTGTAT
CTGCAAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCG
30 TTTCGTTATGACTACTGGGGTCAGGGAACCTGGTCACCGTCTCGAGCGCTTCAACCGAC
ATCCAGATGACCCAGTCTCCATCCTCCCTGTCGTCATCTGTAGGAGACCGTGTCAACATC
ACTTGCCGGGCAAGTCTGTCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCAAGG
AAAGCCCCTAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTCACTCTCACCATCAGCAATCTGCAACCTGAA
GATTTTGCCTACGTACTACTGTGCGCAGGCTGGGACGCAATCCTACGACGTTCCGCCAAGGG
35 ACCAAGGTGGAAATCAAACGG (SEQ ID NO: 1256)

DMS0674 DOM7h-11-3-TVAAPS-BMS3h-38-235
40 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCGTCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCTGTCGATTGGGACGACGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCCTTTGGAATTCCTCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCCTACGTACTACTGTGCGCAGGCTGGGACGCAATCCTACGACGTTCCGCCAA
GGACCAACCTGCAAAATCAAACGACCGTGGCCGCCCGAGTGAGGTGCAGCTGTTGGCG
45 TCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGA
TTCACCTTTGAGGAGGAGGAGATGATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAG
TGGGTCTCAGCTATTAGTAGGAACGGTTACAGCACATACTACGACAGCTCCGTGAAGGCC
CGGTTCAACATCTCCCGGACAATCCAAGAACACGCTGTATCTGCAAAATGAACAGCCTG
CGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACTGG
50 GGTACAGGGAACCTGGTACCGCTCTCCAGC (SEQ ID NO: 1257)

DMS0675 DOM7h-11-90-TVAAPS-BMS3h-38-235
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCGTCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCTGTCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA

GGGAAAGCCCCCTAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACCTCTCACCATCAGCAATCTGCAACCT
GAAGATTTTGCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTCCGCCAA
GGGACCAAGGTGGAAATCAAACGGACCGTGGCGGCGCCGAGTGAGGTGCAACTGTTGGCG
5 TCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGA
TTCACCTTTGAGGAGGAGGAGATGATTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAG
TGGGTCTCAGCTATTAGTAGGAACGGTTACAGCACATACTACGCAGACTCCGTGAAGGGC
CGGTTCCACATCTCCCGCAGCAATTCCAAGAACACGCTGTATCTGCAAAATGAACAGCCTG
CGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACTGG
10 GGTACAGGAACCTGGTCACCGTCTCCAGC (SEQ ID NO: 1258)

DMS0677 DOM7h-11-90-TVA-BMS3h-56-258
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGGTGTCAAC
ATCACTTGGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
15 GGGAAAGCCCCCTAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACCTCTCACCATCAGCAATCTGCAACCT
GAAGATTTTGCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTCCGCCAA
GGGACCAAGGTGGAAATCAAACGTACGGTGGCGGAGGTGCAGCTGTTGGAGTCTGGGGGA
GGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGATTACCTTT
20 CGGATTTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCA
GCTATTAATCCGCAGGCTACGGGTACATACACTACGCAGACTCCGTGAAGGGCCGGTTCACC
ATCTCCCGCAGCAATTCCAAGAACACGCTGTATCTGCAAAATGAACAGCCTGCGTCCCGAG
GACACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTCAGAGTGGGGTCCAGGA
ACCTTGGTCACCGTCTCCAGC (SEQ ID NO: 1259)

25 DMS0678 DOM7h-11-90-ASTSGPS-BMS3h-56-258
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGGTGTCAAC
ATCACTTGGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCCTAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
30 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACCTCTCACCATCAGCAATCTGCAACCT
GAAGATTTTGCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTCCGCCAA
GGGACCAAGGTGGAAATCAAACGGGCTAGCACCTCAGGTCCATCGGAGGTGCAGCTGTTG
GAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCC
GGATTACCTTTCCGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTA
35 GAGCGGGTCTCAGCTATTAATCCGCAGGCTACGCTACATACTACGCAGACTCCGTGAAG
GGCCGGTTTACCATCTCCCGCAGCAATTCCAAGAACACGCTGTATCTGCAAAATGAACAGC
CTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTCACGAG
TGGGGTCCAGGAACCTGGTCACCGTCTCCAGC (SEQ ID NO: 1260)

40 DMS0679 DOM7h-11-90-G4S-BMS3h-56-258
GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGGTGTCAAC
ATCACTTGGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCCTAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACCTCTCACCATCAGCAATCTGCAACCT
45 GAAGATTTTGCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTCCGCCAA
GGGACCAAGGTGGAAATCAAACGGGCTGAGGTTGGCTCTGAGGTGCAGCTGTTGGAGTCT
GGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGATT
ACCTTCCGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGG
GTCTCAGCTATTAATCCGCAGGCTACGCTACATACTACGCAGACTCCGTGAAGGGCCGG
50 TTCACCATCTCCCGCAGCAATTCCAAGAACACGCTGTATCTGCAAAATGAACAGCCTGCGT
GCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTACTTTCAGAGTGGGGT
CAGGGAACCTGGTCACCGTCTCCAGC (SEQ ID NO: 1261)

DMS0680 DOM7h-11-90-(G4S) 3-BMS3h-56-258
 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGC CGGGCAAGTCGTCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
 5 GGGAAAGCCCCTAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
 GAAGATTTTGCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGGGGTGGAGGTGGCTCTGGAGGTGGCGGTAGCGCGGGA
 GGCGGTTACAGAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTGGTACAGCCTGGGGGTC
 10 CTGCGCTCTCTCTGTGACGCTCCGGATTCACTTTTCGGGATTATGAGATCTGGTGGGTC
 CGCCAGGCTCCAGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGAGGGTACGCGT
 ACATACTACGCAGACTCCGTGAAGGGCCGTTTCACTCTCCCGCGACAATTCGAAGAAC
 ACGCTGATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGGTTATATTAATGTGCG
 AAACITCCGTTTACTTTACGAGTGGGGTCAGGAACCTCCTACCGTCTCCAGC (SEQ ID
 NO: 1262)
 15
 DMS0681 DOM7h-11-90-(G4S) 5-BMS3h-56-258
 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
 ATCACTTGC CGGGCAAGTCGTCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
 20 GGGAAAGCCCCTAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
 GAAGATTTTGCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGGGGTGGAGGTGGCTCTGGAGGTGGCGGTAGCGCGGGA
 GGCGGTTACAGTGGCGGAGGTTCTGGAGGCGGTGGATCTGAGGTGCAGCTGTTGGAGTCT
 25 GGGGAGGCTTGGTACAGCCTGGGGGTCCTGCGTCTCTCTGTGACGCTCCGGATTCT
 ACCTTTCCGGATTATGAGATGTGGTGGGTCCGCGAGGCTCCAGGGAAGGGTCTAGAGCGG
 GTCTCAGCTATTAATCCGAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGG
 TTCACCATCTCCCGCGACAATTCGAAGAACACGCTGTAATCTGCAAATGAACAGCCTGCGT
 GCGGAGGACACCCCGCTATATTAATGTGCGAACTTCCGTTTACTTTACGAGTGGGGT
 CAGGGAACCTTGGTACCGTCTCCAGC (SEQ ID NO: 1263)
 30
 DMS0682 BMS3h-56-258-TVA-DOM7h-11-90
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTTGGCTCTC
 TCCTGTGCAGCCTCCGGATTCACTTTTCGGGATTATGAGATGTGGTGGGTCCGCGAGGCT
 35 CCAGGGAAGGCTCTAGAGCGGGTCTCAGCTATTAATCCGAGGGTACGCGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTGTAT
 CTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTAATGTGCGAAACTTCCG
 TTTTACTTTACAGTGGGGTCAGGGAACCTGGTACCCTTTCGAGCACGGTGGCGGAC
 ATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATC
 40 ACTTTCGCGGGCAAGTCGTCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACAGGG
 AAAGCCCTTAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCAGGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCTGAA
 GATTTTGTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTTCGGCCAAGGG
 ACCAAGGTGAAATCAAACCG (SEQ ID NO: 1264)
 45
 DMS0683 BMS3h-56-258-ASTSGPS-DOM7h-11-90
 GAGGTGCAGCTGTTGGACTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCTTGGCTCTC
 TCCTGTGCAGCCTCCGGATTCACTTTTCGGGATTATGAGATGTGGTGGGTCCGCGAGGCT
 50 CCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGAGGGTACGCGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCGAAGAACACGCTGTAT
 CTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTAATGTGCGAAACTTCCG
 TTTTACTTTACAGTGGGGTCAGGGAACCTGGTACCCTTTCGAGCGCTAGCACCTCA
 GGTCCATCCGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGAC
 CGTGTACCATCACTTCCCGGCAACTCTCCGATTGGGACGATGTTAAGTTGGTACCAG
 CAGAAACAGGGGAAGCCCTAAGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGG

- GTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAAT
CTGCAACCTGAAGATTTTGTCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACG
TCGGCCAAAGGACCAAGGTGAAATCAAACGG (SEQ ID NO: 1265)
- 5 DMS0684 BMS3h-56-258-(G4S)-DOM7h-11-90
GAGGTGCAGCTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCCTCTC
TCCTGTGCAGCCTCCGGATTACCTTTCCGGATTATGAGATGTGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAAATCCGAGGGTACGCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCAGACAATTCGAAGAACACGCTGTAT
10 CTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCG
TTTTACTTTACAGAGTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGCGGTGGAGGCGGC
TCTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCT
ACCATCACTTGCCTGGCAAGTCCGTCGATTTGGGACGATGTTAAGTTGGTACCAGCAGAAA
CCAGGGAAGCCCTAAGCTCTGATCCTTGTCTTTTCCCGTTTGCAGAAAGTGGGGTCCCA
15 TCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAA
CCTGAAGATTTTGTCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTTCGGC
CAAGGACCAAGGTGAAATCAAACGG (SEQ ID NO: 1266)
- DMS0685 BMS3h-56-258-(G4S)3-DOM7h-11-90
20 GAGGTGCAGCTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCCTCTC
TCCTGTGCAGCCTCCGGATTACCTTTCCGGATTATGAGATGTGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAAATCCGAGGGTACGCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCAGACAATTCGAAGAACACGCTGTAT
CTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCG
25 TTTTACTTTACAGAGTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGCGGTGGAGGTGGC
TCTGGAGGTGGCGGTAGCGCGGTGGCGGTTCCAGACATCCAGATGACCCAGTCTCCATCTC
TCCTCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCTGGGCAAGTCCGTCGATTT
GGACCATGTTAAGTTGGTACCAGCAGAAACCAAGGAAAGCCCTAAGCTCTCTGATCCTT
GCTTTTCCCGTTTGCAGAAAGTGGGGTCCCATCACGTTTTCAGTGGCAGTGGATCTGGGACA
30 GATTTCACTCTCACCATCAGCAATCTGCAACCTGAAGATTTTGTCTACGTACTACTGCGCG
CAGGCTGGGACGCATCCTACGACGTTTCGGCCAAAGGACCAAGGTGAAATCAAACGG (SEQ ID
NO: 1267)
- DMS0686 BMS3h-56-258-(G4S)5-DOM7h-11-90
35 GAGGTGCAGCTGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCCTCTC
TCCTGTGCAGCCTCCGGATTACCTTTCCGGATTATGAGATGTGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAAATCCGAGGGTACGCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCAGACAATTCGAAGAACACGCTGTAT
CTGCAAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCG
40 TTTTACTTTACAGAGTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGCGGTGGAGGTGGC
TCTGGAGGTGGCGGTAGCGCGGTGGCGGTTCCAGTGGCGGAGGTTCTGGAGGCGGTGGA
TCTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCT
ACCATCACTTGCCTGGCAAGTCCGTCGATTTGGGACGATGTTAAGTTGGTACCAGCAGAAA
CCAGGGAAGCCCTAAGCTCTGATCCTTGTCTTTTCCCGTTTGCAGAAAGTGGGGTCCCA
45 TCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAA
CCTGAAGATTTTGTCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTTCGGC
CAAGGACCAAGGTGAAATCAAACGG (SEQ ID NO: 1268)
- DMS0688 DOM7h-11-90-TVAAPS-BMS3h-56-258
50 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCC
ATCACTTGCCTGGGCAAGTCCGTCGATTTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCTAAGCTCTGATCCTTGTCTTTTCCCGTTTGCAGAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT

GAAGATTTTGTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGGACCGTAGCGGCGCCGACTGAGGTGCAGCTGTTGGAG
 TCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCTGTGCAGCCTCCGGA
 TTTACCTTTTCGGGATTATGAGATGTGGTGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAG
 5 CGGGTCTCAGCTATTATCCGCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGC
 CGGTTACCATCTCCCGGACAAATTCGAAGAACACGCTGTATCTGCAATGAACAGCCTG
 CGTGCCGAGGACACCGCGGTATATTACTGTGCGAACTTCCGTTTTCACGAGTGG
 GGTACGGGAACCTGGTCACCGTCTCCAGC (SEQ ID NO: 1269)

Example 8

10 Anti-Cynomolgus CD40 dAbs

The methods disclosed herein to generate antibody polypeptides that specifically bind human CD40 may be used to generate antibody polypeptides that specifically bind CD40 of other species. For example, anti-cynomolgus (anti-cyno) CD40 antibody polypeptides can be produced using the presently disclosed methods. The anti-
 15 cynoCD40 antibody polypeptides can be generated using the same scheme of initial/primary screening and affinity maturation as anti-human CD40 dAbs, for example. Methods for obtaining anti-cynoCD40 dAbs are disclosed, and representative examples of anti-cynoCD40 dAbs are provided in TABLE 23 below.

ELISA RBA:

20 Clear walled Highbind, 384 well plates (Corning, UK) were coated with 25µl of 1 µg/ml neutravidin in carbonate buffer overnight at 4°C. The following day, assay plates were washed with 0.1% Tween PBS buffer, blocked with 1% BSA in PBS for 1 hour at room temperature, and washed again. Following removal of excess washing buffer, 25 µl of 1 µg/ml of biotinylated human IZ-CD40L (BMS, 1.2 mg/ml stock
 25 concentration) was incubated with the assay plates for 1 hour at room temperature. Simultaneously, a dilution range of purified dAb and 1 µg/ml of cynoCD40 (BMS) were complexed in a 1:1 ratio. Following washing of the assay plate, the dAb:cyno CD40 complex was incubated in the assay plate at room temperature for 2 hours with gentle agitation. Competitive binding of dAb vs. cynoCD40 to biotinylated CD40L was
 30 detected with horse radish peroxidase (HRP) conjugated anti human (Fc) secondary antibody (Sigma-Aldrich, UK). Absorbance signal was measured using a Spectromax M5e plate reader (Molecular Devices) at 450 nm following neutralization with 1M HCl.

cynoCD40 CHO cell RBA using AB8200 F/MAT:

Stably transfected cynoCD40-expressing CHO-DG44 cells or native CHO-DG44 cells (BMS) were detached from cell culture flasks using Versene (Invitrogen). 40,000 cells per well were seeded into 96 well Highbind, black walled, clear bottom plates (Corning, UK) in 0.1% BSA PBS assay buffer with a dilution range of dAb, 0.25 µg/ml of biotinylated human IZ-CD40L (BMS, 1.2 mg/ml stock concentration), and 0.25 µg/ml of streptavidin Alexa Fluor 647 (Invitrogen, Molecular probes, UK). The mixture was incubated in the absence of light for 6 hours. Following incubation, competitive binding of dAb vs. cynoCD40 CHO cells to soluble biotinylated IZ-CD40L was assessed using relative fluorescence as measured by the AB8200 cellular detection platform (Applied Biosystems).

CHO-hCD40L-driven primary human B cell proliferation:

CHO cells (ATCC) were transfected with human CD40L to generate a stable cell line expressing high levels of CD40L on the cell surface. CHO-CD40L cells were irradiated at 10,000 Rads before incubation with human B cells. 1×10^5 tonsillar human B cells were incubated with 1×10^3 CHO-CD40L cells (1:100 ratio of CHO-CD40L: human B cells) along with varying titration of dAb or monoclonal antibody in a final volume of 200 µl/well in a 96-well round bottom plate. The plates were incubated at 37°C for 72 hours, following which thymidine (^3H ; 0.5 µCi/well) was added for 6 hours. B cell proliferation was quantified based on thymidine incorporation. All assays, unless otherwise noted, were performed in RPMI media supplemented with 10% fetal calf serum (FCS).

Soluble IZ-hCD40L-driven cyno splenic B cell proliferation:

1×10^5 B cells isolated from cynomolgous monkey spleens were incubated with 0.5 µg/ml of IZ-hCD40L along with varying titration of dAb or mAb in a final volume of 200 µl/well in a 96-well round bottom plate. The plates were incubated at 37°C for 72 hours, following which ^3H -thymidine (µCi/well) was added for 6 hours. B cell proliferation was quantified based on thymidine incorporation. All assays, unless

otherwise noted, were performed in RPMI media supplemented with 10% fetal calf serum (FCS).

TABLE 23

Clone	ELISA RBA (nM)	Cell RBA (nM)	B cell proliferation assay (EC50 nM)	
			Human	Cyno
BMS5c8				8,10,12,8,8
BMS3c-85	370		>7000, >7000	747, 2700, 7000, 7000
BMS3c-85-1	52, 8	12	2600, 1100	18, 39, 47
BMS3c-85-2	12, 4	4, 17	1800, 800	2, 5, 6, 1
BMS3c-85-3	7	23	>7000, >7000	33, 31, 21, 31
BMS3c-85-8	22	17.2	>7000, >7000	33, 33, 25
BMS3c-85-9	10		>7000, >7000	>70, >70, 104
BMS3c-85-21	11	18		24
BMS3c-85-24	8	13, 14		
BMS3c-85-25	62			
BMS3c-85-26	3		3300, 3900	>70, >70, 385
BMS3c-85-27	13	23		39
BMS3c-85-31	13	11, 9		
BMS3c-85-32	21	56		111
BMS3c-85-33	15	10, 21.3		17
BMS3c-85-34	48			
BMS3c-85-35	-	19, 1.5	>700	2
BMS3c-85-36	-	28		
BMS3c-85-37	-	71		
BMS3c-85-38	-	17		
BMS3c-85-47	-	2.9	>700	<2, 0.5
BMS3c-85-49	-	10	>700	3, 3
BMS3c-85-51	-	2.5	>700	3
BMS3c-85-52	-	8.5		
BMS3c-85-55	-	13.3, 6.7	>700	3, 3
BMS3c-85-56	-	no convergence		
BMS3c-85-57	-	13.8, 5.3	>700	2, 4
BMS3c-85-62	-	9.9, 2.7, 2.0	>700	<2, 0.63
BMS3c-85-63	-	80.9		
BMS3c-85-64	-	16.1		
BMS3c-85-65	-	13.9, 7.4	>700	3, 2

Clone	ELISA RBA (nM)	Cell RBA (nM)	B cell proliferation assay (EC50 nM)	
			Human	Cyno
BMS3c-85-67	-	1.5		0.17
BMS3c-85-69	-	1.8		0.33
BMS3c-85-72	-	2		0.16
BMS3c-85-73	-	2.3		
BMS3c-85-77	-	2.3		0.2
BMS3c-85-84	-	1.3		0.21
BMS3c-85-88	-	3		0.25
BMS3c-85-91	-	1.3		0.26

Example 9

Anti-Human CD40 dAbs Do Not Bind CynoCD40

CynoCD40 has a Leu109 residue instead of a Trp109, as in human CD40. The amino acid sequence of *Macaca fascicularis* CD40 is reproduced below:

```

5  1  MVRLEPLQCVL WGCLLTAVYP EPPTACREKQ YLINSQCCSL CQPGQKLVS
51 CTEFTETECL PCGESEFLDT WNRETRCHQH KYCDPNLGLR VQKGTSETD
101 TICTCEEGLH CTSESCESC VPHRSCLPGFG VKQIATGVSD TICEPCPVGF
151 FSNVSSAFEK CRPWTSCETK DLVVQQAGTN KTDVVCGPQD RQRALVVIPI
201 CLGILFVILL LVLVFIKKVA KKPNDKVPHP KQEPQEINFP DDLPGSNPAA
10 251 PVQETLHGCQ PVTQEDGKES RISVQERQ (SEQ ID NO: 2)

```

Anti-human CD40 dAbs were tested for cross reactivity to B cells in cynomolgus monkey, rhesus macaque and chimpanzee blood, and lymphocytes from marmoset blood using flow cytometric methods. The procedures detailed below summarize methods used for CD40 dAb detection over multiple experiments. The results, shown in TABLE 24, suggest that anti-human CD40 dAbs do not bind cynoCD40. This is consistent with the evidence disclosed above (see FIG. 1 and 2) that Trp109 in human CD40 (which is absent in cynoCD40) is important for complex formation between the dAbs and human CD40.

Methods:

PEGylated anti-human CD40 dAbs (BMS3h-56-5C-40L and BMS3h38-2C-P40Br) or a biotin-conjugated dAb (BMS3h38-2-biotin) were incubated with human and

primate blood samples on a rotator for 1 hour at 37°C. 100 µl from each blood sample was aliquoted to 12 x 75mm tubes and washed 3 times with FACS buffer (0.5% FBS/PBS/0.1% sodium azide). Tubes were centrifuged for 5 minutes at 1500 rpm, and supernatants were decanted between washes. Following the washes, tubes were placed
5 on ice and incubated with human IgG for 5 minutes to block non-specific binding via Fc receptors.

For PEGylated dAb detection, anti-PEG antibodies (clone CH-2074, Silver Lake Research or clone 2-2, Open Biosystems) were added to tubes and incubated for 30 minutes. Samples were washed once in FACS buffer, then incubated with an APC-
10 labeled CD20 antibody (clone 2H7, BD Biosciences) and PE labeled-anti-mouse IgG (Fcγ1 specific; Calbiochem) for an additional 30 minutes on ice.

For biotin-conjugated dAb detection, PE-labeled streptavidin (Invitrogen) and APC-labeled CD20 antibody (clone 2H7, BD Biosciences) were added to tubes and incubated 30 minutes at room temperature.

15 Additionally, to measure CD40 levels on human and primate blood, an aliquot of each blood sample was incubated with an APC-labeled CD20 antibody (clone 2H7, BD Biosciences) and a PE-labeled anti-human CD40 antibody that cross reacts with primate species (clone 5C3, BD Biosciences) for 30 minutes at room temperature.

To lyse red blood cells and fix white blood cells following detection antibody
20 incubation, FACS Lysing Solution (BD Biosciences) was added to all tubes, and samples were incubated for 15 minutes at room temperature. Samples were centrifuged and resuspended in FACS Lysing Solution, and analyzed by flow cytometry on a BD FACSCanto™, gating on CD20+ B cells for analysis. For marmoset samples, the CD20 antibody was not cross reactive; therefore analysis was performed on all lymphocytes as
25 identified by forward and side scatter properties (size).

Results:

Binding of PEGylated and biotinylated anti-human CD40 dAbs was tested in human and primate blood samples according to the method above. Anti-human CD40 dAb binding to CD20+ B cells in human blood samples was detected. In contrast, the

binding of PEGylated and biotinylated CD40 dAbs was not detected on CD20+ B cells in cynomolgus, rhesus, or chimp blood samples or on lymphocytes in marmoset blood samples. Results for BMS3h-38-2C-P40Br dAb are shown in FIG. 3, Panels A and B. Similar results were obtained for the other dAbs. Comparable levels of CD40 on the B cells of human and primate species were confirmed using an anti-human CD40 antibody that cross reacts with primate CD40. These data indicate that human CD40 dAbs from the BMS3h-56 and BMS3h-38 lineages are unable to bind CD40 in primate species. The data are consistent with the importance of the Trp109 residue in forming a complex between CD40 and the anti-CD40 dAbs, as shown in FIGS. 1 and 2.

10 **Example 10**

X-Ray Crystallography of a Complex Between CD40 and dAb BMS3h-56-5

Data collection and processing:

Two different crystal forms were analyzed during the structure determination of the human CD40 (SEQ ID NO: 1)/BMS3h-56-5 (SEQ ID NO: 321) complex. Data were collected from a crystal of the CD40/BMS3h56-5 complex, flash-cooled to and maintained at 100 K, and mounted on a Rigaku AFC-9 goniometer. The X-ray source was a Rigaku FR-E using a copper target with MicroMax™ confocal optics and a Saturn 92 detector. Data were collected at extremely high redundancy to enhance the sulfur anomalous diffraction signal in the hopes of using that signal to phase the data. Data were processed with HKL2000 (HKL Research; Otwinowski et al., In *Methods Enzymol. Macromolecular Crystallography* part A, Carter et al., eds., vol. 276, p. 307-326, Academic Press, Inc., New York, NY (1997)). Data collection statistics for this crystal are summarized below and in Table 24:

Space Group: I222;
Unit Cell: a = 156.6 Å; b = 158.3 Å; c = 200.7 Å;
Mosaicity 0.59-0.84; Rejected observations: 1028; 0.06%.

TABLE 24

s09-167	Resolution, Å	Measured	Unique	Redun.	%Complete	R value	I/ σ_1
Overall	50.00-3.30	1603547	37772	42.5	99.8	0.137	33.7
First Shell	50.00-8.94	≥ 38193	1971	40.1	97.1	0.049	58.7
Last Shell	3.36-3.30	≥ 37054	1861	43.6	99.8	0.439	12.5

5 A second crystal form was collected from a crystal flash-cooled to 100 K and mounted on a Rayonix MX-225 detector at the Canadian Light Source beamline CMCF1 (08-ID-1) and the wavelength was 0.9793 Å. These data were collected by Shamrock Structures (R. Walter and G. Ranieri) and were processed with HKL2000. Data collection statistics for this crystal are summarized below and in Table 25:

10 Space Group: C2;
Unit Cell: a = 199.3 Å; b = 48.7 Å; c = 138.8 Å; β = 118.2°;
Mosaicity 0.62-0.71; Rejected observations: 70; 0.08%.

TABLE 25

x09-275	Resolution, Å	Measured	Unique	Redun.	%Complete	R value	I/ σ_1
Overall	50.00-2.80	92545	29303	3.2	98.6	0.091	14.6
First Shell	50.00-6.03	9265	3060	3.0	98.5	0.052	18.0
Last Shell	2.90-2.80	8857	2882	3.1	98.0	0.421	3.4

Molecular Replacement Models:

15 The model of the dAb, BMS3h-56-5, was derived from PDB ID 2VYR chain E residues 1-124 with sequential residues corresponding to CDRs 31-35, 50-57, and 99-111

removed by SPLIT_PDB (which corresponds to Kabat numbering 31-35, 50-56, and 95-100G) and then run through MUTATE and finally renumbered by RENUMBER. MUTATE changes non-identical residues to the minimum identical, i.e., normally Ala or Gly, but, for example Tyr→Phe and Phe→Tyr would result in Phe. It does not build any atoms, although for Thr→Val, Val→Thr, Cys→Ser, and Ser→Cys, it will substitute the appropriate atom name, but not change the position. RENUMBER changed the numbering to Kabat numbering (Kabat et al., *Sequences of Immunological Interest*, 5th ed., U.S. Dept. Health & Human Services, Washington, D.C. (1991)), which is a standard numbering system for antibodies that makes description of CDRs and framework residues straight-forward.

A CD40 model was constructed from PDB IDs 1JMA (chain B), 1NCF (chain A), 1TNR (chain R), 2HEV (chain R), 2HEY (chains R, T), and 2UWI (chains A, B) using phenix.ensemble (University of Cambridge, UK) to create an ensemble of structures. The N-termini (residues 24-78) plus a six residue segment (residues 95-100) of these molecules were superimposable with an acceptable root mean square distance for Cα atoms, and that was used as a model for the N-terminal region of CD40.

Molecular Replacement Methods:

The program PHASER (McCoy et al., *J. Appl. Crystallogr.* 40: 658-674 (2007)) was used for molecular replacement. The translation function Z-score (TFZ) and the increase in the log-likelihood gain were monitored to decide whether real solutions had been found. TFZ scores of 8 and above generally represent a solution. Lesser TFZ scores accompanied by substantial increases (>50) in the log-likelihood gain also are acceptable indicators.

Model building, Density Modification, and Crystallographic Refinement Methods:

Model-building tools for molecular graphics included the COOT program (Emsley et al., *Acta Crystallogr Sect. D* 60: 2126-2132 (2004); Emsley et al., "Features and Development of Coot," *Acta Crystallogr Sect. D* 66: 486-501 (2010)). Density modification using non-crystallographic symmetry map averaging was performed using known density modification programs and other programs to calculate the Eulerian

angles and translations between molecules. Refinement was run using autoBUSTER (GlobalPhasing, Ltd.; Bricogne et al., *Acta Crystallogr. Sect. D* 60: 2210–2221 (2004); Tronrud et al., *Acta Crystallogr. Sect. A* 43: 489–501 (1987)).

Domain Antibody numbering system:

5 The residue numbering system for the domain antibody follows that of Kabat. The Kabat numbering is compared to straight sequential numbering below for BMS3h-56-5:

```

-2-1
  ||
BMS-3h-56-5 ST

                                CDR1
Kabat          10          20          30          40
50
- | - | - | - |
Sequential      10          20          30          40
50
- | - | - | - |

BMS-3h-56-5
FVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSA

                                CDR2
Kabat          60          70          80          90
A - | - | - | ABC - |
Sequential      60          70          80          90
100
- | - | - | - |

BMS-3h-56-5
INPQGTRTYADSVMGRTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLP

                                CDR3
Kabat          99101      110      116
|| - | -|
Sequential      110      119
- | - |
BMS-3h-56-5 FTFDDWGQGLTVTVSSAAA (SEQ ID NO: 3)

```

In Kabat numbering BMS3h-56-5 has insertion residues 52A, 82A, 82B, 82C and is missing residue 100. In both numbering systems the Ser and Thr at the N-terminus that are part of the expression construct are given negative numbers.

Determination of the structure of CD40/BMS3h-56-5 complex:

5 PHASER was able to locate four BMS3h-56-5 dAb molecules in the I222 crystal form and three BMS3h-56-5 dAb molecules in the C2 crystal form. In the I222 crystal form the TFZ scores ranged from 7.6 to 41.0, and the increase in the log-likelihood gain ranged from 77 to 446. These solutions for the BMS3h-56-5 dAb molecules formed helical columns of dAb molecules through the I222 crystal that were separated from other
10 columns by large channels. In the C2 crystal the TFZ scores ranged from 7.7 to 16.5, and the increase in the log-likelihood gain ranged from 110 to 150. The packing of the dAbs in this crystal form was not repetitive or symmetric.

Using the ensemble model for the CD40 N-terminal domain, four molecules of the N-terminal domain of CD40 could be placed in the I222 crystal form with TFZ scores
15 ranging from 5.7 to 8.5, and the increase in the log-likelihood gain ranged from 83 to 389. The four N-terminal domains of CD40 in the I222 crystal form formed a clump equally centered between four columns of dAb molecules. However, they did not touch the BMS3h-56-5 dAb molecules. In the C2 crystal form three molecules of the N-terminal domain of CD40 could be placed with TFZ scores ranging from 5.8 to 12.1, and
20 the increase in the log-likelihood gain ranged from 100 to 198. In this crystal form, the N-terminal domains also did not contact the BMS3h-56-5 dAb molecules.

In the I222 crystal form, the N-terminal domain of the CD40 from the CD40/Chi220 Fab complex and the N-terminal domain from 2UW1 were superimposed on the CD40 N-terminal domain. The ability to associate the N-terminal with a particular
25 BMS3h-56-5 dAb allowed the use of non-crystallographic symmetry (NCS) map averaging. The starting correlation coefficients for NCS averaging gave off-diagonal values of 0.71-0.81. The final off-diagonal values were 0.88-0.92. The electron density close to the N-terminal region was clear, and a path could be traced for CDR3 of the BMS3h-56-5 dAb. Residues 82-94 and 101-121 from the CD40/Chi220 Fab' complex
30 were superimposed on the corresponding residues on 2UW1 and then COOT was used to

improve the fit manually. This position for the second domain (residues 82-94 and 101-121) of CD40 was then transformed onto the other three N-terminal domains.

A cycle of refinement was run with R-free decreasing from 0.437 to 0.380 and R-work from 0.447 to 0.381 with improvement in root mean square bond and angle
 5 deviations from ideal. The resulting electron density map showed that residue 109 had a side chain that was consistent with Trp and that density existed for at least some residues in the C-terminal 70 residues of CD40.

Since CD40 has little secondary structure, fitting the C-terminal ~70 residues to the electron proved difficult, so the Research Collaboratory for Structural Bioinformatics
 10 Protein Data Base was searched for a suitable model to help guide chain tracing. The top two hits with 16 out of 44 identities and 24 out of 44 matches were 2AW2 and 1JMA, which have the same sequence:

```

15          125  130      140      150      160
           |    |      |      |      |
CD40      CSPGFGVKQIATGVSDTICEPCPVGFFSNVSSAFEKCHPWTSCE
2AW2      CSPGYRVKEACGELTGTVCEPCPPGTYYIAHLNGLSKCLQCQMCD
Cor.sensus CSPG* VK*   ** T CEGCP G *   *   KC   C*
20      | .   |   .   |   .   |   .   |   .
          23   30   40   50   60   66
           |   .   |   .   |   .   |
1JMA     19   30   40   50   62
        (SEQ ID NOS 1270-1271)

```

25 Identical residues are noted with the appropriate single letter code on the consensus line and similar residues are noted on the consensus line as asterisks. This was the same stretch of residues as for residues 41-84 of the N-terminal domain of CD40:

```

30          41      50      60      70      80
           |      |      |      |      |
CD40      CQPGQKLVSDCTEFTETECPCGESEFLDTWNRETHCHQHXYCD
CD40      CSPGFGVKQIATGVSDTICEPCPVGFFSNVSSAFEKCHPWTSCE
35 Consensus C PG *   T   **T C PC   F *   *   *CH   C*
           |       |       |       |
          125  130   -   140      150   -   160   -
        (SEQ ID NOS 1272 and 1270)

```

Identical residues are noted with the appropriate single letter code on the consensus line and similar residues are noted on the consensus line as asterisks.

5 Matching disulfide bonds:

Comparison of Disulfide linkages in residues 41-84 and 125-168 of CD40

Residues 41-84	Residues 125-168
C41-C59	C125-C143
[C38]-C51	
C62-C77	C146-C161
C83[-C103]	C167[-C186]

Residues in brackets fall outside of the residue ranges in the sequence repeat.

- 10 With the 1JMA/2AW2 model as a guide, the COOT program was used to fit one of the CD40 chains. This fitted model was then superimposed on one of the other three CD40 chains. However, it appeared that the position of this new stretch of residues was differently oriented in the other two CD40 chains, and they were not fitted at this time. A cycle of refinement was run with R-free decreasing from 0.393 to 0.366 and R-work from 0.400 to 0.349 with considerable improvement in root mean square bond and angle deviations from ideal.

The BMS3h-56-5 dAb from one of the molecules in the I222 crystal form was superimposed on each of the three dAbs in the C2 crystal form. That transformation matrix was used to orient the second and C-terminal domains of the I222 crystal form.

- 20 The model was rebuilt using the COOT program. A cycle of refinement was run with R-free decreasing from 0.361 to 0.334 and R-work from 0.375 to 0.306 with improved root mean square bond and angle deviations from ideal. The resulting electron density map provided guidance for placing many more CD40 residues. Another cycle of refinement was run with R-free decreasing from 0.302 to 0.287 and R-work from 0.299 to 0.270 with improved root mean square bond and angle deviations from ideal

Conventional model building and refinement then were used to complete the structure determination. Several more rounds of optimization led to a final refinement with the following statistics: R-free 0.260, R-work 0.228, root mean square bonds 0.010

Å, root mean square angles 1.4°. The real space correlation coefficients are 0.92 for main-chain atoms and 0.80 for side-chain atoms. The final model had 13 water molecules.

Using the model of the C-terminal domain from the C2 crystal form as a guide,
 5 the CD40 models in I222 crystal form were further refined. Several more cycles of model building using the COOT program and refinement with the autoBUSTER program led to the following statistics: R-free 0.323, R-work 0.292, root mean square bonds 0.011 Å, root mean square angles 1.5°. The real space correlation coefficients are 0.91 for main-chain atoms and 0.80 for side-chain atoms. The model contained no water
 10 molecules.

Overall Structure of the CD40/BMS3h-56-5 complex:

One BMS3h-56-5 dAb binds to one CD40 molecule. As shown in FIG. 1, BMS3h-56-5 binds to an epitope that is distinct from that of the antibody Chi220, which binds in the N-terminal region. CD40 residues (SEQ ID NO: 1) are shown in green,
 15 except for epitope residues. CD40 epitope residues for Chi220 are shown in blue; BMS3h-56-5 dAb epitope residues are shown in cyan. Chi220 Fab and BMS3h-56-5 β-strands are shown in red, CDR residues are shown in magenta, and other loops are shown in orange. Disulfide bonds are shown for the CD40, Chi220, and BMS3h-56-5 molecules with the sulfur atoms in yellow.

20 The I222 crystal form contains four crystallographically independent CD40/BMS3h-56-5 complexes, and the C2 crystal form contains three crystallographically independent CD40/BMS3h-56-5 complexes. The CD40 molecule has a certain amount of flexibility, and the domains are arrayed differently in the seven unique versions of the complex, but the overall nature of the interaction is retained in all cases.

BMS3h-56-5 dAb epitope residues:

The minimal CD40 epitope for BMS3h-56-5 is defined as CD40 residues containing at least one atom in van der Waals or hydrogen-bond contact with a BMS3h-56-5 atom. The minimal epitope in all the complexes contains the following CD40 residues with reference to SEQ ID NO: 1: Trp109, Leu121, His122, Ser124, Ser156,

Ala157, Phe158, Glu159, and His162. The following additional residues are in van der Waals or hydrogen-bond contact in some complexes: Pro85, Asn86, Leu87, Gly88, Glu106, Glu107, Gly108, His110, Thr112, Cys119, Val120, Gln133, Ile134, Ala135, Thr136, Ser155, Lys160.

5 A maximal CD40 epitope is defined as residues containing atoms that are buried by a 1.7 Å probe sphere. These residues include all the residues above, plus Val 154 in all complexes. In some complexes, additional buried residues are: Ser118, Arg123, Thr141, Phe151, Asp153, Cys161, and Pro163.

A depiction of the surface of BMS3h-56-5 with contacting residues is shown in
 10 FIG. 2. Contacting BMS3h-56-5 residues are shown. Buried residues are also shown. CD40 is represented as a cartoon with orange representing non-repetitive secondary structure and magenta representing the epitope residues. Also shown as sticks (carbon atoms in cyan) are CD40 residues Trp109, Ala115, Leu121, Ser126, and His162, which are five of the seven residues that differ between human and cynomolgus monkey
 15 (*Macaca fascicularis*). Ala115 and Ser126 are on the opposite side of CD40 from the BMS3h-56-5 binding site. Trp109 and Leu121 bind in a cleft of BMS-h-56-5 that lies between CDR-3 and FR-2 (BMS-3h-56-5 residues Leu45 and Arg47). His162 of CD40 interacts with Arg56 of CDR-2 of the BMS3h-56-5 dAb. Mutation of Trp109 considerably reduces or ablates BMS3h-56-5 activity.

20 Depending on the crystallographically independent complex, 660-740 Å² of CD40 surface area is buried with between 16-21 contacting residues represented at a finer level with contacting 46-67 atoms. For BMS3h-56-5, 660-780 Å² of surface area is buried with contacting 14-17 residues represented at a finer level with contacting 48-62 atoms. These contacts yield 3-7 hydrogen bonds and 111-142 van der Waals interactions,
 25 depending on the crystallographically independent complex.

Example 11

Identifying dAb Binding Epitopes on CD40

To identify dAb binding epitopes on CD40, dAb binding was tested against seven CD40-Fc fusion proteins containing specific amino acid residue substitutions at residues

76, 109, or 121. These CD40-Fc fusion proteins include wild type human CD40 (wt-hCD40), wild type cynomolgus monkey CD40 (wt-cCD40), and five mutant human CD40 proteins (M1-M5) with specific amino acid residues mutated to the corresponding residue from the sequence of cynomolgus monkey CD40 (M1, M2, M4, M5) or chimpanzee CD40 (M3). The amino acid substitutions are listed in Table 26.

The sequence of the wild type human CD40 extracellular domain (1-193) is from REFSEQ:accession NM_001250.3. Cynomolgous and mutant constructs were generated using site-directed mutagenesis of the wild type sequence at the positions shown in Table 26. The extracellular domains were fused with a thrombin-cleavable linker DPGGGGGRLVPRGFGTGDP (SEQ ID NO: 1273), which was fused with human IgG1 Fc. The proteins were expressed in HEK-293-6E cells transfected with TIG-pYD7-GATE Durocher expression vectors. The supernatants were harvested after five days. Each CD40 protein was purified from conditioned media using protein A fast flow chromatography. The column was washed with PBS (20 mM sodium phosphate, 0.15 M NaCl, pH 7.2) and then eluted using 80 mM sodium acetate, pH 3, into 1/5th volume of 1 M Tris-HCl, pH 8. The eluate was run on a Superdex-200 column in PBS.

TABLE 26

Name	Short name	Residue 76	Residue 109	Residue 121
wild type human CD40 Fc fusion	wt-hCD40	H	W	L
human CD40 (H76R) Fc fusion	hCD40-M1	R	W	L
human CD40 (W109L) Fc fusion	hCD40-M2	H	L	L
human CD40 (W109R) Fc fusion (Chimpanzee CD40)	hCD40-M3	H	R	L
human CD40 (W109L, L121P) Fc fusion	hCD40-M4	H	L	P
human CD40 (H76R, W109L, L121P) Fc fusion	hCD40-M5	R	L	P
wild type cynomolgus monkey CD40 Fc fusion	wt-cyno-CD40	R	L	P

Representative dAb's from the 3h217, 3h37, 3h38, and 3h56 lineages were assayed for their binding to CD40-Fc fusion proteins listed in Table 26. Assays were performed on a BioRad ProteOn XPR36 SPR instrument. The SPR surfaces were prepared by immobilizing 8 $\mu\text{g/ml}$ anti-human IgG(Fc) antibody (Biacore/GE Healthcare) in 10 mM sodium acetate pH 4.5 on a BioRad GLC sensor chip using standard ethyl(dimethylaminopropyl) carbodiimide (EDC) / N-hydroxysuccinimide (NHS) chemistry, with ethanolamine blocking. The running buffer for immobilization and kinetic binding analysis was 10 mM sodium phosphate, 130 mM sodium chloride, 0.05% tween 20, pH 7.1. CD40-Fc fusion proteins at concentrations of 20 $\mu\text{g/ml}$ were captured in the vertical orientation on these surfaces via the Fc tail, and reference surfaces lacking CD40-Fc proteins were used for reference subtraction. Kinetic experiments were performed by flowing 405, 135, 45, 15, and 5nM dAb analytes in the horizontal orientation over the captured CD40-Fc surfaces at 25°C, using a 240 s association time, and a 420 s dissociation time, at a flow rate of 30 $\mu\text{l/min}$. The surfaces were regenerated in both horizontal and vertical orientations with 30 s pulses of 3 M MgCl_2 followed by running buffer at 60 $\mu\text{l/min}$. Sensogram data was double-referenced and then fitted to a 1:1 Langmuir model using BioRad ProteOn Manager V.2.1.0.38 software, to determine the association rate constant (k_a), the dissociation rate constant (k_d), and the equilibrium dissociation constant (K_D).

All dAbs of the 3h-37, 3h-38, and 3h-56 lineages were found to bind with high affinity ($K_D < 10^{-8}$ M) to CD40-Fc fusion proteins containing the human CD40 residues W109 and L121, but binding was significantly reduced or undetectable to CD40-Fc fusion proteins with the corresponding residues from cynomolgus monkey CD40 (L109, P121) or chimpanzee CD40 (R109). This indicates that dAbs from each of the 3h37, 3h38-, and 3h56- lineages bind specifically to an epitope that includes residues 109 and 121 of human CD40. In contrast, all tested members of the 3h-217 lineage bound with similar affinity to all CD40-Fc fusion proteins tested, indicating that the members of the 3h-217 lineage bind to a site on CD40 which does not include residues 76, 109, or 121. Therefore, the 3h-217 lineage binds to a different epitope than the 3h-37, 3h-38, and 3h-56 lineages. Table 27 summarizes K_D values determined for dAb binding to CD40-Fc

fusion proteins using SPR on a ProteOn XPR36 instrument. An "X" in Table 27 means that no evidence for binding was found under these conditions.

TABLE 27

	wt- hCD40	hCD40- M1 (H76R)	hCD40- M2 (W109L)	hCD40- M3 (W109R)	hCD40- M4 (W109L, L121P)	hCD40- M5 (H76R, W109L, L121P)	cyno CD40
3h-217-5	0.47, 0.48	0.94	0.99	0.72	0.93	1.0	0.9
3h-217-16	0.22, 0.26	0.35	0.41	0.27	0.35	0.5	0.4
3h-217-23	0.78, 1.5	1.6	2.0	1.2	1.6	2.2	1.9
3h-37-2	2.0, 2.0	2.6	>1000	X	X	X	X
3h-37-11	1.9, 2.3	2.4	>1000	X	X	X	X
3h-38-2	5.1, 8.0	7.2	X	X	X	X	X
3h-38-211	3.3, 6.1	4.0	>1000	X	X	X	X
3h-38-215	2.1, 6.0	3.0	>1000	X	X	X	X
3h-38-217	2.3, 2.4	3.4	>1000	X	X	X	X
3h-56-1	3.0, 5.4	4.2	29	>1000	X	X	X
3h-56-2	3.8, 3.2	6.1	44	>1000	X	X	X
3h-56-5	5.3, 4.7	7.2	65	>1000	X	X	X
3h-56-202	2.3, 1.3	3.3	160	X	X	X	X
3h-56-206	0.60, 1.4	1.0	55	X	X	X	X
3h-56-217	1.0, 1.9	1.4	2.5	23	X	X	X

5 Table 28 shows the association rate constant (k_a), dissociation rate constant (k_d), and equilibrium dissociation constant (K_D) determined for dAb binding to CD40-Fc fusion proteins using SPR on a ProteOn XPR36 instrument. An "X" in Table 28 means that no evidence for binding was found under these conditions.

TABLE 28

Ligand	dAb	k_a (1/Ms)	k_d (1/s)	K_d (nM)
wt-hCD40	3h-217-5	2.71×10^6	1.27×10^{-3}	0.47
wt-hCD40 (repeat)	3h-217-5	2.03×10^6	9.81×10^{-4}	0.48
hCD40 M1 (H76R)	3h-217-5	3.17×10^6	2.99×10^{-3}	0.94
hCD40 M2 (W109L)	3h-217-5	2.55×10^6	2.51×10^{-3}	0.99
hCD40 M3 (W109R)	3h-217-5	2.73×10^6	1.96×10^{-3}	0.72
hCD40 M4 (W109L, L121P)	3h-217-5	2.78×10^6	2.59×10^{-3}	0.93
hCD40-M5 (H76R, W109L, L121P)	3h-217-5	2.44×10^6	2.42×10^{-3}	0.99
wt-cCD40	3h-217-5	2.46×10^6	2.12×10^{-3}	0.86
wt-hCD40	3h-217-16	4.47×10^6	9.91×10^{-4}	0.22
wt-hCD40 (repeat)	3h-217-16	3.30×10^6	8.47×10^{-4}	0.26
hCD40 M1 (H76R)	3h-217-16	4.83×10^6	1.68×10^{-3}	0.35
hCD40 M2 (W109L)	3h-217-16	4.06×10^6	1.67×10^{-3}	0.41
hCD40 M3 (W109R)	3h-217-16	3.78×10^6	1.04×10^{-3}	0.27
hCD40 M4 (W109L, L121P)	3h-217-16	4.39×10^6	1.52×10^{-3}	0.35
hCD40-M5 (H76R, W109L, L121P)	3h-217-16	3.65×10^6	1.70×10^{-3}	0.47
wt-cCD40	3h-217-16	3.44×10^6	1.47×10^{-3}	0.43
wt-hCD40	3h-217-23	1.64×10^6	1.27×10^{-3}	0.78
wt-hCD40 (repeat)	3h-217-23	1.07×10^6	1.63×10^{-3}	1.52
hCD40 M1 (H76R)	3h-217-23	1.64×10^6	2.62×10^{-3}	1.59
hCD40 M2 (W109L)	3h-217-23	1.49×10^6	2.91×10^{-3}	1.95
hCD40 M3 (W109R)	3h-217-23	1.53×10^6	1.86×10^{-3}	1.22
hCD40 M4 (W109L, L121P)	3h-217-23	1.67×10^6	2.68×10^{-3}	1.61
hCD40-M5 (H76R, W109L, L121P)	3h-217-23	1.30×10^6	2.87×10^{-3}	2.21
wt-cCD40	3h-217-23	1.24×10^6	2.35×10^{-3}	1.90

wt-hCD40	3h-37-2	2.12×10^5	4.17×10^{-4}	1.96
wt-hCD40 (repeat)	3h-37-2	2.13×10^5	4.26×10^{-4}	2.00
hCD40 M1 (H76R)	3h-37-2	2.17×10^5	5.62×10^{-4}	2.58
hCD40 M2 (W109L)	3h-37-2			>1000
hCD40 M3 (W109R)	3h-37-2			X
hCD40 M4 (W109L, L121P)	3h-37-2			X
hCD40-M5 (H76R, W109L, L121P)	3h-37-2			X
wt-cCD40	3h-37-2			X
wt-hCD40	3h-37-11	2.91×10^5	5.60×10^{-4}	1.92
wt-hCD40 (repeat)	3h-37-11	2.81×10^5	6.40×10^{-4}	2.28
hCD40 M1 (H76R)	3h-37-11	3.00×10^5	7.17×10^{-4}	2.39
hCD40 M2 (W109L)	3h-37-11			>1000
hCD40 M3 (W109R)	3h-37-11			X
hCD40 M4 (W109L, L121P)	3h-37-11			X
hCD40-M5 (H76R, W109L, L121P)	3h-37-11			X
wt-cCD40	3h-37-11			X
wt-hCD40	3h-38-2	1.20×10^5	6.08×10^{-4}	5.07
wt-hCD40 (repeat)	3h-38-2	1.42×10^5	1.14×10^{-3}	8.04
hCD40 M1 (H76R)	3h-38-2	1.40×10^5	1.00×10^{-3}	7.15
hCD40 M2 (W109L)	3h-38-2			X
hCD40 M3 (W109R)	3h-38-2			X
hCD40 M4 (W109L, L121P)	3h-38-2			X
hCD40-M5 (H76R, W109L, L121P)	3h-38-2			X
wt-cCD40	3h-38-2			X
wt-hCD40	3h-38-211	1.11×10^5	3.62×10^{-4}	3.26
wt-hCD40 (repeat)	3h-38-211	1.20×10^5	7.28×10^{-4}	6.08
hCD40 M1 (H76R)	3h-38-211	1.28×10^5	5.10×10^{-4}	3.98

hCD40 M2 (W109L)	3h-38-211			>1000
hCD40 M3 (W109R)	3h-38-211			X
hCD40 M4 (W109L, L121P)	3h-38-211			X
hCD40-M5 (H76R, W109L, L121P)	3h-38-211			X
wt-cCD40	3h-38-211			X
wt-hCD40	3h-38-215	1.37×10^5	2.88×10^{-4}	2.10
wt-hCD40 (repeat)	3h-38-215	1.36×10^5	8.20×10^{-4}	6.02
hCD40 M1 (H76R)	3h-38-215	1.75×10^5	5.30×10^{-4}	3.03
hCD40 M2 (W109L)	3h-38-215			>1000
hCD40 M3 (W109R)	3h-38-215			X
hCD40 M4 (W109L, L121P)	3h-38-215			X
hCD40-M5 (H76R, W109L, L121P)	3h-38-215			X
wt-cCD40	3h-38-215			X
wt-hCD40	3h-38-217	1.27×10^5	2.96×10^{-4}	2.34
wt-hCD40 (repeat)	3h-38-217	1.44×10^5	3.40×10^{-4}	2.37
hCD40 M1 (H76R)	3h-38-217	1.41×10^5	4.81×10^{-4}	3.41
hCD40 M2 (W109L)	3h-38-217			>1000
hCD40 M3 (W109R)	3h-38-217			X
hCD40 M4 (W109L, L121P)	3h-38-217			X
hCD40-M5 (H76R, W109L, L121P)	3h-38-217			X
wt-cCD40	3h-38-217			X
wt-hCD40	3h-56-1	2.52×10^5	7.50×10^{-4}	2.97
wt-hCD40 (repeat)	3h-56-1	1.93×10^5	1.03×10^{-3}	5.35
hCD40 M1 (H76R)	3h-56-1	2.31×10^5	9.67×10^{-4}	4.18
hCD40 M2 (W109L)	3h-56-1	1.92×10^5	5.57×10^{-3}	29.10
hCD40 M3 (W109R)	3h-56-1			>1000
hCD40 M4 (W109L, L121P)	3h-56-1			X

hCD40-M5 (H76R, W109L, L121P)	3h-56-1			X
wt-cCD40	3h-56-1			X
wt-hCD40	3h-56-2	2.46×10^5	9.27×10^{-4}	3.77
wt-hCD40 (repeat)	3h-56-2	1.97×10^5	6.24×10^{-4}	3.17
hCD40 M1 (H76R)	3h-56-2	2.20×10^5	1.33×10^{-3}	6.05
hCD40 M2 (W109L)	3h-56-2	1.89×10^5	8.30×10^{-3}	43.90
hCD40 M3 (W109R)	3h-56-2			>1000
hCD40 M4 (W109L, L121P)	3h-56-2			X
hCD40-M5 (H76R, W109L, L121P)	3h-56-2			X
wt-cCD40	3h-56-2			X
wt-hCD40	3h-56-5	1.78×10^5	9.38×10^{-4}	5.26
wt-hCD40 (repeat)	3h-56-5	1.53×10^5	7.19×10^{-4}	4.69
hCD40 M1 (H76R)	3h-56-5	1.69×10^5	1.21×10^{-3}	7.18
hCD40 M2 (W109L)	3h-56-5	1.38×10^5	8.89×10^{-3}	64.60
hCD40 M3 (W109R)	3h-56-5			>1000
hCD40 M4 (W109L, L121P)	3h-56-5			X
hCD40-M5 (H76R, W109L, L121P)	3h-56-5			X
wt-cCD40	3h-56-5			X
wt-hCD40	3h-56-202	1.82×10^5	4.15×10^{-4}	2.27
wt-hCD40 (repeat)	3h-56-202	1.77×10^5	2.21×10^{-4}	1.25
hCD40 M1 (H76R)	3h-56-202	1.76×10^5	5.79×10^{-4}	3.29
hCD40 M2 (W109L)	3h-56-202	1.35×10^5	2.00×10^{-2}	155.00
hCD40 M3 (W109R)	3h-56-202			X
hCD40 M4 (W109L, L121P)	3h-56-202			X
hCD40-M5 (H76R, W109L, L121P)	3h-56-202			X
wt-cCD40	3h-56-202			X
wt-hCD40	3h-56-206	6.48×10^5	3.89×10^{-4}	0.60

wt-hCD40 (repeat)	3h-56-206	3.27E+05	4.72x10 ⁻⁴	1.44
hCD40 M1 (H76R)	3h-56-206	5.65E+05	5.45x10 ⁻⁴	0.96
hCD40 M2 (W109L)	3h-56-206	3.38E+05	2.00x10 ⁻²	54.70
hCD40 M3 (W109R)	3h-56-206			X
hCD40 M4 (W109L, L121P)	3h-56-206			X
hCD40-M5 (H76R, W109L, L121P)	3h-56-206			X
wt-cCD40	3h-56-206			X
wt-hCD40	3h-56-217	4.71E+05	4.70x10 ⁻⁴	1.00
wt-hCD40 (repeat)	3h-56-217	2.91E+05	5.46x10 ⁻⁴	1.87
hCD40 M1 (H76R)	3h-56-217	4.45E+05	6.35x10 ⁻⁴	1.43
hCD40 M2 (W109L)	3h-56-217	4.25E+05	1.05x10 ⁻³	2.48
hCD40 M3 (W109R)	3h-56-217	2.91E+05	6.70x10 ⁻³	23.00
hCD40 M4 (W109L, L121P)	3h-56-217			X
hCD40-M5 (H76R, W109L, L121P)	3h-56-217			X
wt-cCD40	3h-56-217			X

Example 12

Construction of Fc Fusion Polypeptides

Antibody polypeptides comprising dAbs can be constructed in various configurations, as disclosed herein. In this example, various dAbs were fused with a Fc domain to generate Fc fusion polypeptides of anti-human CD40 variable domain constructs such as 3h37-202, 3h37-235, 3h37-258, and 3h37-202.

In one representative example, the dAb BMS3h-56-269 (SEQ ID NO: 417) was fused with a modified IgG1 (IgG1*) Fc domain (SEQ ID NO: 1284). In the dAb-IgG1* Fc domain fusion polypeptide, the C-terminus of dAb BMS3h-56-269 was fused to a linker tripeptide having the sequence Ala-Ser-Thr, which in turn was fused with the IgG1* Fc domain (SEQ ID NO: 1284). The IgG1* Fc domain contained the modification C5S, referring to the numbering of positions in SEQ ID NO: 1284. C5 of the IgG1 Fc

domain normally forms a disulfide bond with a Cys residue in the light chain of an IgG molecule. The IgG1* Fc domain also contained C11S and C14S mutations to eliminate interchain disulfide bonds in the IgG1 hinge region. Finally, the IgG1* Fc domain contained a P23S mutation to lower Fc domain effector function. The dAb-IgG1* Fc fusion polypeptide has the following sequence, where the Ala-Ser-Thr linker is in bold font and the modifications to the Fc domain are in bold italics:

1 EVQLLES~~GGG~~ LVQPGGSLRL SCAASGFTFR DYEMWWVRQA PGKGLERVSA
51 INPQGTRITYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLP
101 FRFSDRGQGT LVTVSS**ASTE** PKS**SD**KTHT**S** PF**SP**APPELLG G**SS**VFLFPPK
10 151 PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY
201 NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP
251 QVYTLPPSRD ELTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTTTP
301 VLDSGGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG
351 K (SEQ ID NO: 1286)

15 The dAb-IgG1* Fc fusion polypeptide depicted in SEQ ID NO: 1286 is a monomer having a calculated molecular weight of 39,127 Da. It can form a dimer having a calculated molecular weight of 78,254 Da.

dAb BMS3h-56-269 (SEQ ID NO: 417) alternatively was fused with a human IgG₄ Fc domain (SEQ ID NO: 1285). The C-terminus of dAb BMS3h-56-269 was again fused to the Ala-Ser-Thr linker, which was fused with the IgG₄ Fc domain (SEQ ID NO: 1285). The IgG₄ Fc domain contained the modification S10P, referring to the numbering of positions in SEQ ID NO: 1285. The BMS3h-56-269-IgG₄ Fc fusion polypeptide has the following sequence, where the Ala-Ser-Thr linker is in bold font and the S10P modification is in bold italics:

25 1 EVQLLES~~GGG~~ LVQPGGSLRL SCAASGFTFR DYEMWWVRQA PGKGLERVSA
51 INPQGTRITYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLP
101 FRFSDRGQGT LVTVSS**ASTE** SKYGPPCP**PC** PAPEFLGGPS VFLFPPKPKD
151 TLMISRTPEV TCVVVDVSQ**E** DPEVQFNWYV DGVEVHNAKT KPREEQFNST
201 YRVVSVLTVL HQDWLNGKEY KCKVSNKGLP SSIEKTISKA KGQPREPQVY
30 251 TLPPSQEEMT KNQVSLTCLV KGFYPSDIAV EWESNGQ**PEN** NYKTTTPVLD
301 SDGSFFLYSR LTVDKSRWQ**E** GNVFSCSVMH EALHNHYTQK SLSLSLGK
(SEQ ID NO: 1287)

The BMS3h-56-269-IgG₄ Fc fusion polypeptide depicted in SEQ ID NO: 1287 is a monomer having a calculated molecular weight of 38,867 Da. It can form a dimer having a calculated molecular weight of 77,734 Da.

The sequences of BMS3h-56-269 (SEQ ID NO: 417), BMS3h-56-269-IgG1* Fc fusion polypeptide (SEQ ID NO: 1286), and BMS3h-56-269-IgG₄ Fc fusion polypeptide (SEQ ID NO: 1287) are aligned below, where the start of the Fc domain is marked by an arrow:

```

5  BMS3h56-269 (SEQ ID NO:417)      (1)
   EYQDLESQGGIVQKGGTIFSSIASTHTFEDYENWYFOARCKGLERYSA
   BMS3h56-269-CTL2 (SEQ ID NO:1286) (1)
   EYQDLESQGGIVQKGGTIFSSIASTHTFEDYENWYFOARCKGLERYSA
   BMS3h56-269-Ig4 (SEQ ID NO:1287) (1)
10  EYQDLESQGGIVQKGGTIFSSIASTHTFEDYENWYFOARCKGLERYSA

   BMS3h56-269 (SEQ ID NO:417)      (34)
   ENPOETHYADPWKQGLISRNISKWIVYQNTKAFDPAYFOAKIT
   BMS3h56-269-CTL2 (SEQ ID NO:1286) (51)
   ENPOETHYADPWKQGLISRNISKWIVYQNTKAFDPAYFOAKIT
15  BMS3h56-269-Ig4 (SEQ ID NO:1287) (51)
   ENPOETHYADPWKQGLISRNISKWIVYQNTKAFDPAYFOAKIT

   BMS3h56-269 (SEQ ID NO:417)      (84)
20  ERFDRSGGVIAAS-----
   BMS3h56-269-CTL2 (SEQ ID NO:1286) (101)
   ERFDRSGGVIAASASTIPSSDKTHTSSSSSLSSVHTPPA
   BMS3h56-269-Ig4 (SEQ ID NO:1287) (101)
   ERFDRSGGVIAASASTISKYGV---PPCPCYAFSSP
25  ERFDRSGGVIAASASTISKYGV---PPCPCYAFSSP

           ↑
           Start of Fc

   BMS3h56-269 (SEQ ID NO:417)      (117)
30  -----
   BMS3h56-269-CTL2 (SEQ ID NO:1286) (151)
   EFDIMSKIPRYHGVVLYQHDFYQENWYSGEWHNAKTRKMF
   BMS3h56-269-Ig4 (SEQ ID NO:1287) (148)
   EFDIMSKIPRYHGVVLYQHDFYQENWYSGEWHNAKTRKMF

35  BMS3h56-269 (SEQ ID NO:417)      (117)
   -----
   BMS3h56-269-CTL2 (SEQ ID NO:1286) (201)
   NSYRWVSVTVTHQWVNGKPKKGVNKAALHAPKPKTSKAGQPRNF
40  BMS3h56-269-Ig4 (SEQ ID NO:1287) (198)
   NSYRWVSVTVTHQWVNGKPKKGVNKAALHAPKPKTSKAGQPRNF

   BMS3h56-269 (SEQ ID NO:417)      (117) -----
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BMS3h56-269-CTL2 (SEQ ID NO:1286) (251)
 QVYILPPSRDELTKNQMSITCLVKGFPESDAVEWESNGOPENNYKTTDP
 BMS3h56-269-Ig4 (SEQ ID NO:1287) (248)
 QVYILPPSQEPMKKNQMSITCLVKGFPESDAVEWESNGOPENNYKTTDP
 5 BMS3h56-269 (SEQ ID NO:417) (117)

 BMS3h56-269-CTL2 (SEQ ID NO:1286) (301)
 VTLDGSEFFHAKTINVDKSRVQORVDSVWVHAAHNEFQPSLSLSPG
 10 BMS3h56-269-Ig4 (SEQ ID NO:1287) (298)
 VTLDGSEFFHAKSRINVDKSRVQDENVDSVWVHAAHNEFQPSLSLSPG
 BMS3h56-269 (SEQ ID NO:417) (117) -
 BMS3h56-269-CTL2 (SEQ ID NO:1286) (351)
 15 BMS3h56-269-Ig4 (SEQ ID NO:1287) (348)

The Fc fusion polypeptides were expressed using the cell culture methods disclosed in Example 11. The column was washed with PBS (20 mM sodium phosphate, 0.15 M NaCl, pH 7.2) and then eluted using 80 mM sodium acetate, pH 3, into 1/5th volume of 1 M Tris-HCl, pH 8. The eluate was run on a Superdex-200 column in PBS.
 20

Example 13

CD40 Fc Fusion Polypeptide Activity Assays

25 Anti-human CD40 Fc Fusion Polypeptides were assayed functionally for their ability to antagonize CD40 activities. The CD40 activities tested were B cell proliferation and cytokine production by hCD40L-driven activation of primary human monocyte-derived dendritic cells (DCs). B cell proliferation and cytokine production were measured using the assays disclosed in Example 6. Unless otherwise noted, all
 30 assays were performed in RPMI media supplemented with 10% fetal calf serum (FCS). The dAb-Fc domain fusion polypeptides exhibited potent inhibition (i.e., antagonism) of CD40-dependent activation. There were no agonistic properties noted among any of the humanCD40-specific dAb-Fc domain fusion polypeptides. The results using the various assays are shown in TABLE 29. 3h56-269-IgG4 was assayed for its binding to
 35 immobilized human-CD40 using the assays disclosed in Example 11. For 3h56-269-

IgG4, the apparent avidity influenced Kd value for binding immobilized human-CD40 is measured at 30 pM at 25C and 40 pM at 37C.

TABLE 29

dAb-Fc	hIZCD40L-driven Human B Cell Proliferation EC50 (nM)	CHO-hCD40L-driven Human B Cell Proliferation EC50 (nM)	T-B cell MLR EC50 (nM)	CHO-hCD40L-driven DC Activation TNF EC50 (nM)	CHO-hCD40L-driven DC Activation IL-6 EC50 (nM)	CHO-hCD40L-driven DC Activation IL-12 EC50 (nM)
3h37-202-IgG4	0.16 ± 0.08	5.0, 3.0	5.0, 6.0			0.53 ± 0.1
3h37-202-IgG1*	0.27, 0.22	3.0, 7.0				0.74 ± 0.2
3h38-235-IgG4	0.20, 0.15	6.0, 10.0	16.7 ± 5.7			0.67 ± 0.3
3h38-235-IgG1*	0.25 ± 0.1	4.0 ± 1.0				0.88 ± 0.3
3h56-258-IgG4	0.16 ± 0.05	1.0 ± 0.8	2.4 ± 0.99	0.22 ± 0.08	0.11 ± 0.05	0.3 ± 0.2
3h56-258-IgG1*	0.063 ± 0.03	0.6 ± 0.4	2.0 ± 0.63			0.31 ± 0.1

3h56- 269- IgG4	0.028 ± 0.01	0.27 ± 0.08	0.52 ± 0.07	0.16 ± 0.03	0.09 ± 0.02	0.092 ± 0.03
3h56- 269- IgG1*	0.025 ± 0.01	0.25 ± 0.04	0.53 ± 0.1	0.27 ± 0.06	0.15 ± 0.05	0.14 ± 0.06

Although the present embodiments have been described in detail with reference to examples above, it is understood that various modifications can be made without departing from the spirit of these embodiments, and would be readily known to the

5 skilled artisan.

What is Claimed Is:

1. An antibody polypeptide comprising a first variable domain, wherein said antibody polypeptide specifically binds an epitope of human CD40, wherein the antibody polypeptide competes with the binding of domain antibody (dAb) BMS3h-56-269 (SEQ ID NO: 417) to CD40, wherein CD40 comprises the amino acid sequence of SEQ ID NO: 1, and wherein the epitope comprises at least one CD40 amino acid residue selected from the group consisting of Trp109, Leu121, His122, Ser124, Ser156, Ala157, Phe158, Glu159, and His162.

2. The antibody polypeptide of claim 1, wherein the first variable domain comprises the amino acid sequence of one of the antibody polypeptides selected from the lineage group consisting of BMS3h-37, BMS3h-38, BMS3h-56, and BMS3h-198, and wherein the first variable domain has an apparent binding constant of 1 pM to 100 nM.

3. The antibody polypeptide of any of claims 1-2, wherein the first variable domain comprises the amino acid sequence of one of the antibody polypeptides selected from the lineage group consisting of BMS3h-37, BMS3h-38, and BMS3h-56, and wherein the first variable domain has a hIZCD40L-driven Human B Cell Proliferation EC50 of 0.01nM to 100.0 nM.

4. The antibody polypeptide of claim 1, wherein the amino acid sequence of the first variable domain comprises

(a) a CDR1 region which differs from the CDR1 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids,

(b) a CDR2 region which differs from the CDR2 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids,

(c) a CDR3 region which differs from the CDR3 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids,

(d) a FR1 region which differs from the FR1 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids,

(e) a FR2 region which differs from the FR2 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids,

(f) a FR3 region which differs from the FR3 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids, and

(g) a FR4 region which differs from the FR4 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids.

5. The antibody polypeptide of claim 1, wherein the amino acid sequence of the first variable domain comprises

(a) a CDR1 region which differs from the CDR1 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids,

(b) a CDR2 region which differs from the CDR2 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids,

(c) a CDR3 region which differs from the CDR3 region of BMS3h-56-269 (SEQ ID NO: 417) by up to two amino acids.

6. The antibody polypeptide of claim 1, wherein the amino acid sequence of the first variable domain differs from the amino acid sequence of BMS3h-56-258 (SEQ ID NO: 10) or BMS3h-56-269 (SEQ ID NO: 417) by up to 10 amino acids.

7. The antibody polypeptide of claim 6, wherein the amino acid sequence of the first variable domain differs from the amino acid sequence of BMS3h-56-258 (SEQ ID NO: 10) or BMS3h-56-269 (SEQ ID NO: 417) by up to 5 amino acids.

8. The antibody polypeptide of claim 7, wherein the amino acid sequence of the first variable domain differs from the amino acid sequence of BMS3h-56-258 (SEQ ID NO: 10) or BMS3h-56-269 (SEQ ID NO: 417) by two amino acids.

9. The antibody polypeptide of claim 8, wherein the amino acid sequence of the first variable domain differs from the amino acid sequence of BMS3h-56-258 (SEQ ID NO: 10) or BMS3h-56-269 (SEQ ID NO: 417) by one amino acid.

10. The antibody polypeptide of any of claims 2-3, wherein the antibody polypeptide is selected from the lineage group of BMS3h-56, and wherein the amino acid sequence of the first variable domain further comprises:

- (a) a CDR1 region having a sequence X_1 -Tyr-Glu- Y_1 -Trp (SEQ ID NO: 1274), wherein X_1 is Asp or Gly, and Y_1 is Met or Leu;
- (b) a CDR2 region having a sequence Ala-Ile-Asn-Pro- X_2 -Gly- Y_2 - Z_2 -Thr-Tyr-Tyr-Ala-Asp-Ser-Val- A_2 -Gly (SEQ ID NO: 1275), wherein X_2 is Gln, Tyr, Pro, Trp, or Ala, Y_2 is Thr, Ser, Asn, Gly, Met, or Gln, Z_2 is Arg, Leu, Tyr, His, or Phe, and A_2 is Lys or Met; and
- (c) a CDR3 region having a sequence X_3 -Pro- Y_3 - Z_3 -Phe- A_3 - B_3 (SEQ ID NO: 1276), wherein X_3 is Leu or Pro, Y_3 is Phe, Gln, Thr, or Met, Z_3 is Tyr, Pro, Leu, Thr, Ile, Phe, or Met, A_3 is Gln, His, Asp, Ser, Lys, Glu, or Gly, and B_3 is Glu, Asp, or Tyr.

11. The antibody polypeptide of claim 10, wherein the amino acid sequence of the first variable domain comprises:

- (a) a FR1 region having a sequence Glu-Val-Gln-Leu-Leu-Glu-Ser-Gly-Gly-Gly-Leu-Val-Gln-Pro-Gly-Gly-Ser- X_1 -Arg-Leu-Ser-Cys-Ala-Ala-Ser-Gly-Phe-Thr-Phe- Y_1 (SEQ ID NO: 1277), wherein X_1 is Leu or Arg, and Y_1 is Arg or Ala;
- (b) a FR2 region having a sequence Trp-Val-Arg- X_2 -Ala-Pro-Gly- Y_2 - Z_2 -Leu-Glu-Arg-Val-Ser (SEQ ID NO: 1278), wherein X_2 is Gln or Arg, Y_2 is Lys or Arg, and Z_2 is Gly or Val;
- (c) a FR3 region having a sequence Arg-Phe-Thr-Ile-Ser-Arg-Asp-Asn-Ser-Lys-Asn- X_3 -Lys-Tyr-Leu-Gln-Met-Asn-Ser-Leu-Arg-Ala- Y_3 -Asp-Thr- Z_3 -Val-Tyr- A_3 -Cys- B_3 -Lys (SEQ ID NO: 1279), wherein X_3 is Thr or Met, Y_3 is Glu or Asp, Z_3 is Ala or Ser, A_3 is Tyr or His, and B_3 is Ala or Thr; and

- (d) a FR4 region having a sequence X₄-Gly-Y₄-Gly-Thr-Leu-Val-Thr-Val-Ser-Z₄ (SEQ ID NO: 1280), wherein X₄ is Trp or Arg, Y₄ is Gln or Pro, and Z₄ is Ser or Asn.

12. The antibody polypeptide of any of claims 2-3, wherein the first variable domain comprises the amino acid sequence of BMS3h-56-258 (SEQ ID NO: 10) or BMS3h-56-269 (SEQ ID NO:417).

13. The antibody polypeptide of any of claims 2-3, wherein the antibody polypeptide is selected from the lineage group of BMS3h-37, wherein the first variable domain comprises the sequence Glu-Val-Gln-Leu-Leu-Glu-Ser-Gly-Gly-Gly-Leu-Val-X₁-Pro-Gly-Gly-Ser-Leu-Arg-Leu-Ser-Cys-Ala-Ala-Ser-Gly-Phe-Thr-Phe-Glu-Trp-Tyr-Glu-Met-Gln-Trp-Val-Arg-Arg-Ala-Pro-Gly-Lys-Gly-Leu-Glu-Trp-Val-Ser-Ala-Ile-Ser-Gly-Asp-Gly-Tyr-Arg-Thr-Tyr-Tyr-Ala-Asp-Ser-Val-Lys-Gly-Arg-Phe-Thr-Ile-Ser-Arg-Asp-Asn-Ser-Lys-Asn-Thr-Leu-Tyr-Leu-Gln-Met-Asn-Ser-Leu-Arg-Ala-Glu-Asp-Thr-Ala-Val-Tyr-Tyr-Cys-Ala-Lys-Y₁-Leu-Z₁-A₁-Phe-Asp-Tyr-B₁-Gly-Arg-Gly-Thr-Leu-Val-Thr-Val-Ser-Ser (SEQ ID NO: 1281); and

wherein X₁ is Gln or Arg; Y₁ is Glu or Gly; Z₁ is Ala, Leu, or Glu; A₁ is Phe or Tyr; and B₁ is Trp or Arg.

14. The antibody polypeptide of any of claims 2-3, wherein the antibody polypeptide is selected from the lineage group of BMS3h-38, wherein the first variable domain comprises the sequence Glu-Val-Gln-Leu-Leu-Ala-Ser-Gly-Gly-Gly-Leu-Val-Gln-Pro-Gly-Gly-Ser-Leu-Arg-Leu-Ser-Cys-Ala-Ala-Ser-Gly-Phe-X₁-Phe-Glu-Glu-Glu-Glu-Met-Ile-Trp-Val-Arg-Gln-Ala-Pro-Gly-Lys-Gly-Leu-Glu-Trp-Val-Ser-Y₁-Ile-Ser-Z₁-A₁-Gly- B₁-C₁-Thr-Tyr-Tyr-Ala-Asp-Ser-Val-Lys-Gly-Arg-Phe-Thr-Ile-Ser-Arg-Asp-Asn-Ser-Lys-Asn-Thr-Leu-Tyr-Leu-Gln-Met-Asn-Ser-Leu-Arg-Ala-Glu-Asp-Thr-Ala-Val-Tyr-Tyr-Cys-Gly-Lys-Glu-Pro-Phe-D₁-Tyr-Asp-Tyr-Trp-Gly-Gln-Gly-Thr-Leu-Val-Thr-Val-Ser-Ser (SEQ ID NO: 1282); and

wherein X₁ is Thr or Pro; Y₁ is Ala or Ser; Z₁ is Arg or Gly; A₁ is Arg, Ser, Asn, Gln, Gly, His, or Leu; B₁ is Tyr, Phe, Trp, or Gly; C₁ is Ser or Gly; and D₁ is Arg, Met, or Pro.

15. The antibody polypeptide of any of claims 2-3, wherein the antibody polypeptide is selected from the lineage group of BMS3h-198, wherein the first variable domain comprises the sequence Glu-Val-Gln-Leu-Leu-Glu-Ser-Gly-Gly-Gly-Leu-Val-Gln-Pro-Gly-Gly-Ser-Leu-Arg-Leu-Ser-Cys-Ala-Ala-Ser-Gly-Phe-Thr-Phe-Ala-Gly-Try-Glu-X₁-Trp-Trp-Y₁-Arg-Gln-Ala-Pro-Gly-Lys-Gly-Leu-Glu-Arg-Val-Ser-Ala-Ile-Ser-Gly-Ser-Gly-Gly-Ser-Thr-Tyr-Tyr-Ala-Asp-Ser-Val-Lys-Gly-Arg-Phe-Thr-Ile-Ser-Arg-Asp-Z₁-A₁-Lys-Asn-Thr-Leu-Tyr-Leu-Gln-Met-Asn-Ser-Leu-Arg-Ala-Glu-Asp-Thr-Ala-Val-Tyr-B₁-Cys-Ala-C₁-D₁-Pro-Tyr-Ser-E₁-Asp-Tyr-F₁-G₁-H₁-Gly-Thr-Leu-Val-Thr-Val-Ser-Ser (SEQ ID NO: 1283); and

wherein X₁ is Met or Leu; Y₁ is Val or Phe; Z₁ is Asp or Asn; A₁ is Ser or Thr; B₁ is Tyr or His; C₁ is Lys or Arg; D₁ is Asp or Glu; E₁ is Tyr or Phe; F₁ is Trp or Arg; G₁ is Gly or Arg; and H₁ is Gln or His.

16. The antibody polypeptide of any of claims 1-15, wherein the antibody polypeptide is a domain antibody (dAb).

17. The antibody polypeptide of any of claims 1-16, wherein the antibody polypeptide is a fusion polypeptide comprising the first variable domain and an Fc domain.

18. The fusion polypeptide of claim 17, wherein the fusion polypeptide comprises an IgG4 Fc domain.

19. The fusion polypeptide of claim 18, wherein the fusion polypeptide comprises an IgG1 Fc domain.

20. The fusion polypeptide of any of claims 17-19, where the fusion polypeptide comprises the amino acid sequence of one of the antibody polypeptides selected from the lineage group consisting of BMS3h-37, BMS3h-38, and BMS3h-56, and wherein the fusion polypeptide has a hIZCD40L-driven Human B Cell Proliferation EC₅₀ of 0.001nM to 100.0 nM.

21. The antibody polypeptide of any of claims 1-20, wherein the antibody polypeptide further comprises a second variable domain that specifically binds a second antigen, wherein the second antigen is an antigen other than human CD40.

22. The antibody polypeptide of claim 21, wherein the second antigen is a cluster of differentiation (CD) molecule or a Major Histocompatibility Complex (MHC) Class II molecule.

23. The antibody polypeptide of claim 21, wherein the second antigen is serum albumin (SA).

24. A nucleic acid encoding the antibody polypeptide of any one of claims 1-23.

25. A vector comprising the nucleic acid of claim 24.

26. An isolated host cell comprising the vector of claim 25.

27. A pharmaceutical composition comprising a therapeutically-effective amount of the antibody polypeptide of claim 1 and a pharmaceutically acceptable carrier.

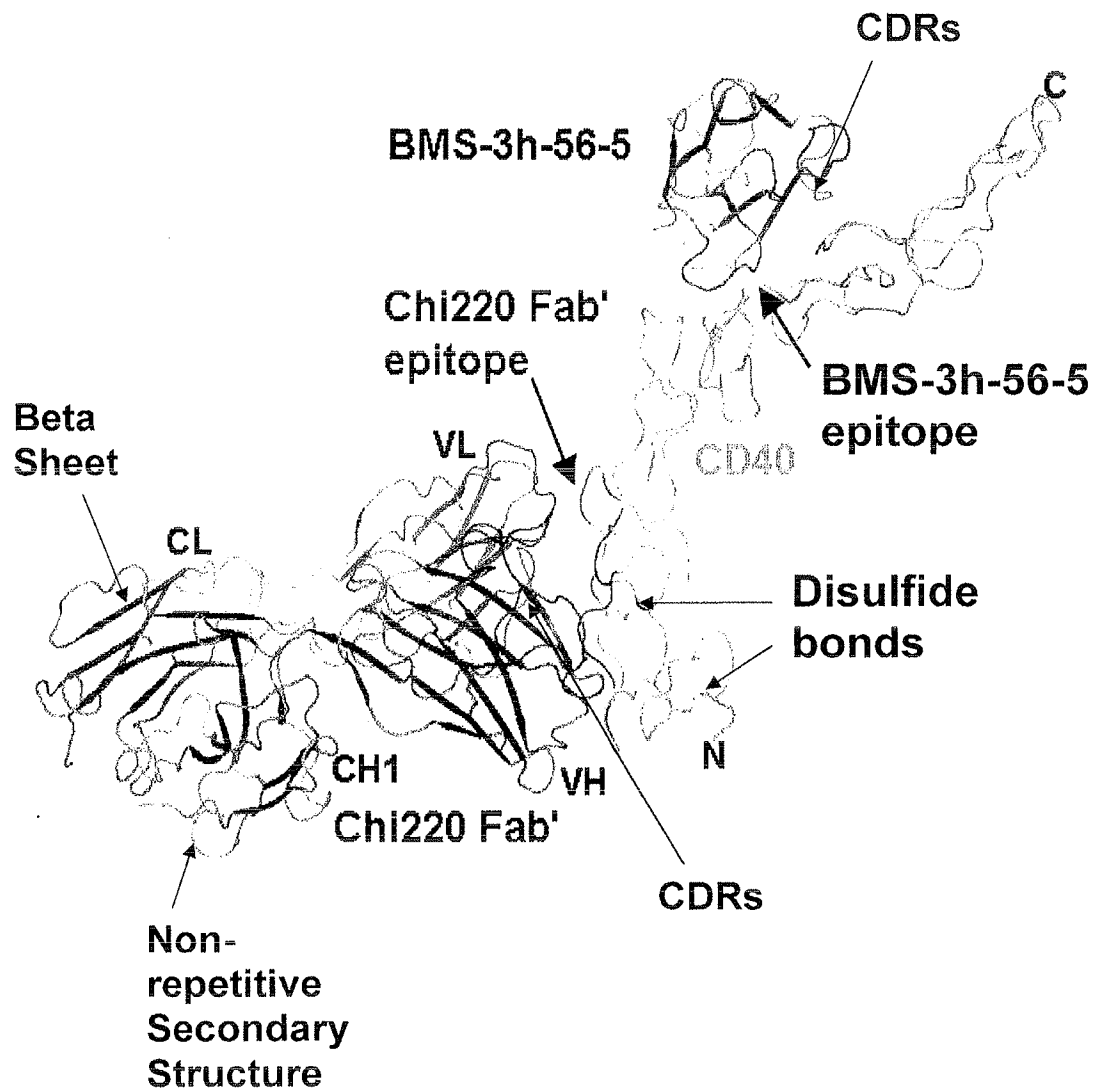
28. The pharmaceutical composition of claim 27, further comprising an immunosuppressive/immunomodulatory and/or anti-inflammatory agent.

29. A method of treating an immune disease in a patient in need of such treatment, comprising administering to the patient a therapeutically effective amount of the pharmaceutical composition of claim 27.

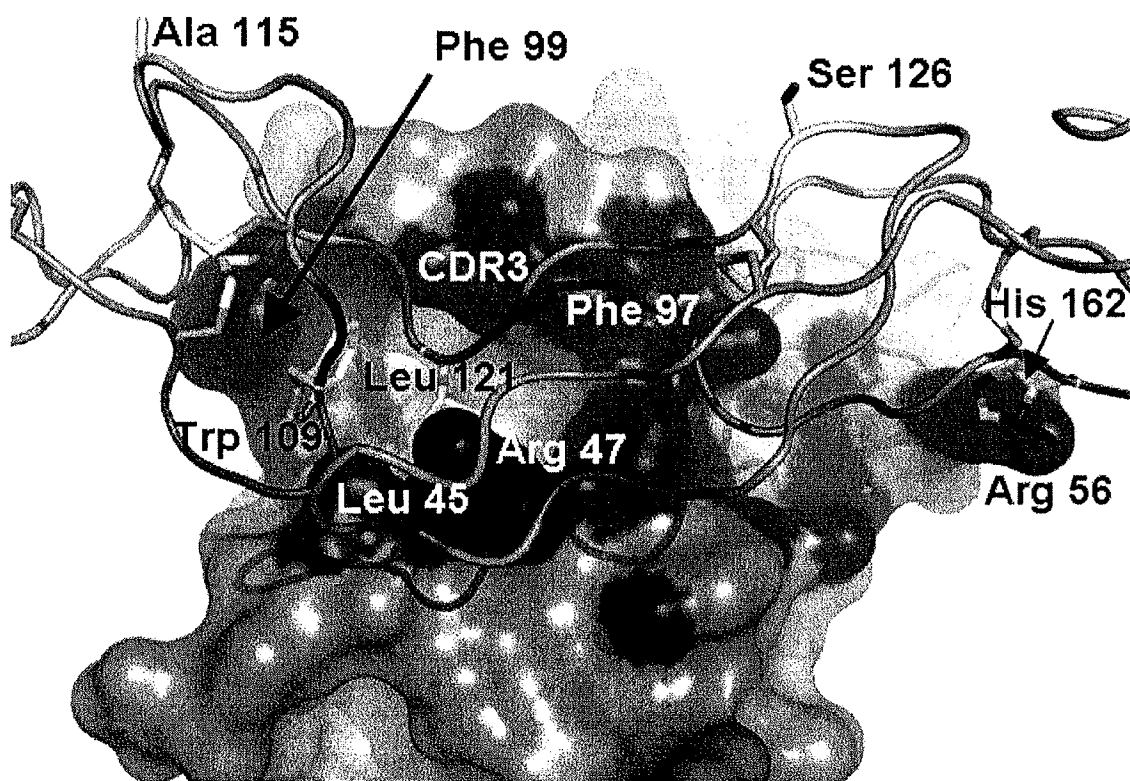
30. The method of claim 29, wherein the pharmaceutical composition is administered in combination with an immunosuppressive/immunomodulatory and/or anti-inflammatory agent.

31. The method of claim 29, wherein the immune disease is an autoimmune disease or a graft-related disease.

32. The method of claim 29, wherein the immune disease is selected from the group consisting of selected from the group consisting of Addison's disease, allergies, ankylosing spondylitis, asthma, atherosclerosis, autoimmune diseases of the ear, autoimmune diseases of the eye, autoimmune hepatitis, autoimmune parotitis, colitis, coronary heart disease, Crohn's disease, diabetes, including Type 1 and/or Type 2 diabetes, epididymitis, glomerulonephritis, Graves' disease, Guillain-Barre syndrome, Hashimoto's disease, hemolytic anemia, idiopathic thrombocytopenic purpura, inflammatory bowel disease, immune response to recombinant drug products, systemic lupus erythematosus, male infertility, multiple sclerosis, myasthenia gravis, pemphigus, psoriasis, rheumatic fever, rheumatoid arthritis, sarcoidosis, scleroderma, Sjogren's syndrome, spondyloarthropathies, thyroiditis, transplant rejection, vasculitis, AIDS, atopic allergy, bronchial asthma, eczema, leprosy, schizophrenia, inherited depression, transplantation of tissues and organs, chronic fatigue syndrome, Alzheimer's disease, Parkinson's disease, myocardial infarction, stroke, autism, epilepsy, Arthus's phenomenon, anaphylaxis, alcohol addiction, and drug addiction.

FIG. 1

2/7
FIG. 2



3/7

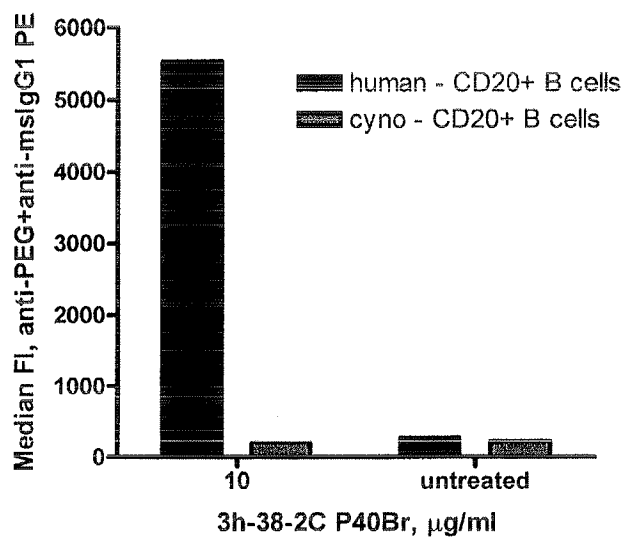
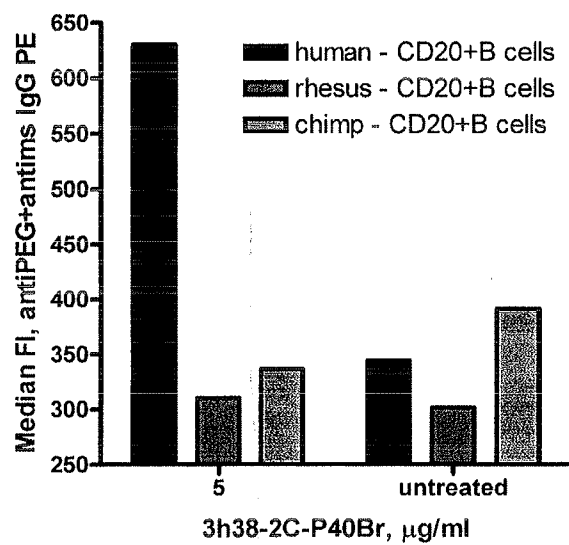
**FIG. 3A****FIG. 3B**

FIG. 4

[illegible]

Fig. 5

[illegible]

FIG. 6

BMS3h-38-217	CDR1	EVQLIASGGGLVQPGGSLRLSCAASGFTFEEDMIWVROAPGKGLEWVSAISRSGYSTYY	CDR2	60
BMS3h-38-238		EVQLIASGGGLVQPGGSLRLSCAASGFTFEEDMIWVROAPGKGLEWVSAISRSGYSTYY		60
BMS3h-38-228		EVQLIASGGGLVQPGGSLRLSCAASGFTFEEDMIWVROAPGKGLEWVSAISRNGFSTYY		60
BMS3h-38-235		EVQLIASGGGLVQPGGSLRLSCAASGFTFEEDMIWVROAPGKGLEWVSAISRNGFSTYY		60
BMS3h-38-231		EVQLIASGGGLVQPGGSLRLSCAASGFTFEEDMIWVROAPGKGLEWVSAISRNGFSTYY		60
BMS3h-38-237		EVQLIASGGGLVQPGGSLRLSCAASGFTFEEDMIWVROAPGKGLEWVSAISRNGFSTYY		60
BMS3h-38-218		EVQLIASGGGLVQPGGSLRLSCAASGFTFEEDMIWVROAPGKGLEWVSAISRNGFSTYY		60
BMS3h-38-215		EVQLIASGGGLVQPGGSLRLSCAASGFTFEEDMIWVROAPGKGLEWVSAISRNGFSTYY		60
BMS3h-38-223		EVQLIASGGGLVQPGGSLRLSCAASGFTFEEDMIWVROAPGKGLEWVSAISRNGFSTYY		60
BMS3h-38-224		EVQLIASGGGLVQPGGSLRLSCAASGFTFEEDMIWVROAPGKGLEWVSAISRNGFSTYY		60
BMS3h-38-225		EVQLIASGGGLVQPGGSLRLSCAASGFTFEEDMIWVROAPGKGLEWVSAISRNGFSTYY		60
BMS3h-38-219		EVQLIASGGGLVQPGGSLRLSCAASGFTFEEDMIWVROAPGKGLEWVSAISRNGFSTYY		60
		*****	*****	***
		*****	*****	*
		*****	*****	***
BMS3h-38-217	CDR2	ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYCGKEPRFYDYGQGTTLTVSS	CDR3	116 (SEQ ID NO: 264)
BMS3h-38-238		ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYCGKEPRFYDYGQGTTLTVSS		116 (SEQ ID NO: 285)
BMS3h-38-228		ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYCGKEPRFYDYGQGTTLTVSS		116 (SEQ ID NO: 275)
BMS3h-38-235		ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYCGKEPRFYDYGQGTTLTVSS		116 (SEQ ID NO: 282)
BMS3h-38-231		ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYCGKEPRFYDYGQGTTLTVSS		116 (SEQ ID NO: 278)
BMS3h-38-237		ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYCGKEPRFYDYGQGTTLTVSS		116 (SEQ ID NO: 284)
BMS3h-38-218		ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYCGKEPRFYDYGQGTTLTVSS		116 (SEQ ID NO: 265)
BMS3h-38-215		ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYCGKEPRFYDYGQGTTLTVSS		116 (SEQ ID NO: 262)
BMS3h-38-223		ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYCGKEPRFYDYGQGTTLTVSS		116 (SEQ ID NO: 270)
BMS3h-38-224		ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYCGKEPRFYDYGQGTTLTVSS		116 (SEQ ID NO: 271)
BMS3h-38-225		ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYCGKEPRFYDYGQGTTLTVSS		116 (SEQ ID NO: 272)
BMS3h-38-219		ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYCGKEPRFYDYGQGTTLTVSS		116 (SEQ ID NO: 266)
		*****	*****	*****

FIG. 7

BMS3h-198-22	CDR1	CDR2	
BMS3h-198-31	EVQLLESGGGLVQPGGSLRLS	CAASGFTFAGYEMWVRQAPGKGLERVS	AISSGSGSTYY 60
BMS3h-198-33	EVQLLESGGGLVQPGGSLRLS	CAASGFTFAGYEMWVRQAPGKGLERVS	AISSGSGSTYY 60
BMS3h-198-19	EVQLLESGGGLVQPGGSLRLS	CAASGFTFAGYEMWVRQAPGKGLERVS	AISSGSGSTYY 60
BMS3h-198-38	EVQLLESGGGLVQPGGSLRLS	CAASGFTFAGYELWVRQAPGKGLERVS	AISSGSGSTYY 60
BMS3h-198-14	EVQLLESGGGLVQPGGSLRLS	CAASGFTFAGYEMWVRQAPGKGLERVS	AISSGSGSTYY 60
	*****	*****	*****
	CDR2	CDR3	
BMS3h-198-22	ADSVKGRFTISRDDSKNTLYLQ	MNSLRAEDTAVYCAKEPYS	SDYWGHTLVTVSS 116 (SEQ ID NO: 523)
BMS3h-198-31	ADSVKGRFTISRDNKNTLYLQ	MNSLRAEDTAVYHCAKEPYS	DYWGQGLTVTVSS 116 (SEQ ID NO: 532)
BMS3h-198-33	ADSVKGRFTISRDDSKNTLYLQ	MNSLRAEDTAVYCAKEPYS	DYWGQGLTVTVSS 116 (SEQ ID NO: 534)
BMS3h-198-19	ADSVKGRFTISRDDSKNTLYLQ	MNSLRAEDTAVYCARDPYS	FYRGQGLTVTVSS 116 (SEQ ID NO: 520)
BMS3h-198-38	ADSVKGRFTISRDDSKNTLYLQ	MNSLRAEDTAVYCARDPYS	FYWGQGLTVTVSS 116 (SEQ ID NO: 539)
BMS3h-198-14	ADSVKGRFTISRDDTKNTLYLQ	MNSLRAEDTAVYCAKDPYS	FYWRQGLTVTVSS 116 (SEQ ID NO: 515)
	*****	*****	*****

INTERNATIONAL SEARCH REPORT

International application No

PCT/US2012/034519

A. CLASSIFICATION OF SUBJECT MATTER

INV. C07K16/28 A61K39/395
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EP0-Internal, BIOSIS, Sequence Search, EMBASE, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 02/28481 A2 (CHIRON CORP [US]; CHU KETING [US]; MASUOKA LORIANNE [US]) 11 April 2002 (2002-04-11) example 6 page 147	1
X	WO 2005/044294 A2 (CHIRON CORP [US]; LONG LI [US]; LUQMAN MOHAMMAD [US]; YABANNAVAR ASHA) 19 May 2005 (2005-05-19) page 147	1
X	EP 1 707 627 A1 (KIRIN BREWERY [JP] KIRIN PHARMA KK [JP]) 4 October 2006 (2006-10-04) page 131	1



Further documents are listed in the continuation of Box C.



See patent family annex.

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"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

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Date of the actual completion of the international search

4 June 2012

Date of mailing of the international search report

15/06/2012

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Authorized officer

Wagner, René

INTERNATIONAL SEARCH REPORT

International application No

PCT/US2012/034519

G(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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POLYPEPTIDOS ANTICUERPOS QUE ANTAGONIZAN CD40

Campo Técnico

Se proporcionan los anticuerpos y fragmentos de los
5 mismos que se dirigen a CD40, y que no muestran actividad
agonista de CD40, las composiciones que comprenden los
mismos, y los métodos de uso de los mismos para el
tratamiento de trastornos que involucran la actividad de
CD40.

Listado de Secuencias

La presente solicitud contiene un listado de
secuencias en formato ASCII y es incorporado en la presente en
su totalidad. La copia de ASCII, reada el 17 de abril 2012,
es nombrada 200896WO.txt y tiene 1,188,530 bytes en tamaño.

Antecedentes de la Invención

CD40 es una molécula co-estimuladora que pertenece
a la superfamilia de receptores del factor de necrosis
tumoral (TNF), que está presente sobre las células
presentadoras de antígeno (APC, por sus siglas en inglés),
20 incluyendo las células dendríticas, células B, y macrófagos.
Las APCs son activadas cuando CD40 se enlaza a su ligando,
CD154 (CD40L), sobre las células T_H. La activación de APC
mediada por CD40 está involucrada en una variedad de
respuestas inmunitarias, incluyendo la producción de
25 citocina, la supra-regulación de moléculas co-estimuladoras

(tales como CD86), y presentación de antígeno y proliferación de células B, mejoradas. CD40 puede también ser expresado por células endoteliales, células del músculo liso, fibroblastos, y células epiteliales.

5 La activación de CD40 está también involucrada en una variedad no deseada de respuestas de células T, relacionadas a la autoinmunidad, al rechazo de trasplantes, o a las respuestas alérgicas, por ejemplo. Una estrategia para controlar las respuestas no deseables de células T es
10 dirigirse a CD40 con un anticuerpo antagonista. Por ejemplo, el anticuerpo monoclonal HCD122 (Lucatumumab), antiguamente conocido como Chiron 1212, está actualmente en pruebas clínicas para el tratamiento de ciertos trastornos inflamatorios mediados por CD40. Ver "Study of HCD122
15 (Lucatumumab) and Bendamustine Combination Therapy in CD40⁺ Rituximab-Refractory Follicular Lymphoma," Clinical Trials Feeds, en la Internet en el protocolo de transferencia de hipertexto: clinicaltrialsfeeds.org/clinical-trials/show/NCT01275209 (última actualización 11 de Enero del
20 2011). Los anticuerpos monoclonales, no obstante, pueden mostrar actividad agonista. Por ejemplo, la utilidad del anticuerpo anti-CD40 Chi220 está limitada por su potencial estimulador débil. Ver Adams, et al., "Development of a chimeric anti-CD40 monoclonal antibody that synergizes with
25 LEA29Y to prolong islet allograft survival," *J. Immunol.* 174:

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Breve Descripción de la Invención

Los antagonistas del anticuerpo anti-CD40 que no poseen actividad agonista parcial son todavía necesarios en un panorama clínico. Son proporcionados los nuevos polipéptidos anticuerpos que se enlazan específicamente a un nuevo epítipo de CD40 humano. El epítipo de CD40 no se traslapa al epítipo de Chi220, como es mostrado por el análisis de competencia y por la estructura derivada de la co-cristalización de un polipéptido anticuerpo con CD40. Los polipéptidos anticuerpos ventajosamente no muestran actividad agonista de CD40. Los polipéptidos anticuerpos son útiles en el tratamiento de trastornos que involucran la activación de CD40, incluyendo los trastornos autoinmunitarios, el rechazo de trasplantes, y respuestas alérgicas. Los polipéptidos anticuerpos comprenden un dominio variable. En una modalidad, los polipéptidos anticuerpos están en la forma de un anticuerpo de dominio (dAb) que contiene un dominio variable simple. En otra modalidad más, los dAbs son reactivos bi-específicos que comprenden un segundo dominio variable que puede reticularse a la albúmina sérica humana (HSA), por ejemplo.

Se proporciona un polipéptido anticuerpo que comprende un primer dominio variable, donde el polipéptido anticuerpo se enlaza específicamente a un epítipo de CD40

humano, donde el epítopo comprende la secuencia de aminoácidos de la SEQ ID No.: 1, donde el polipéptido anticuerpo compite con el enlace del anticuerpo de dominio (dAb) BMS3h-56-269 (SEQ ID No.: 417), y donde el epítopo
5 comprende al menos un residuo de aminoácido de CD40 seleccionado del grupo que consiste de Trp109, Leu121, His122, Ser124, Ser156, Ala157, Phe158, Glu159, y His162.

Se proporciona además un polipéptido anticuerpo donde el primer dominio variable comprende la secuencia de
10 aminoácidos de uno de los polipéptidos anticuerpos seleccionados del grupo de líneas que consiste de BMS3h-37, BMS3h-38, BMS3h-56, y BMS3h-198, y donde el primer dominio variable tiene una constante de enlace aparente de 1 pM a 100 nM. Se proporciona además un polipéptido anticuerpo donde el
15 primer dominio variable tiene una constante de variable aparente de 1 pM a 10 nM.

Se proporciona también un polipéptido anticuerpo donde la secuencia de aminoácidos del primer dominio variable comprende (a) una región CDR1 que difiere de la región CDR1
20 de BMS3h-56-269 (SEQ ID No.: 417) por hasta dos aminoácidos, (b) una región CDR2 que difiere de la región CDR2 de BMS3h-56-269 (SEQ ID No.: 417) por hasta dos aminoácidos, (c) una región CDR3 que difiere de la región CDR3 de BMS3h-56-269 (SEQ ID No.: 417) por hasta dos aminoácidos, (d) una región
25 FR1 que difiere de la región FR1 de BMS3h-56-269 (SEQ ID No.:

417) por hasta dos aminoácidos, (e) una región FR2 que difiere de la región FR2 de BMS3h-56-269 (SEQ ID No.: 417) por hasta dos aminoácidos, (f) una región FR3 que difiere de la región FR3 de BMS3h-56-269 (SEQ ID No.: 417) por hasta dos aminoácidos, y (g) una región FR4 que difiere de la región FR4 de BMS3h-56-269 (SEQ ID No.: 417) por hasta dos aminoácidos.

Se proporciona también un polipéptido anticuerpo donde la secuencia de aminoácidos del primer dominio variable comprende (a) una región CDR1 que difiere de la región CDR1 de BMS3h-56-269 (SEQ ID No.: 417) por hasta dos aminoácidos, (b) una región CDR2 que difiere de la región CDR2 de BMS3h-56-269 (SEQ ID No.: 417) por hasta dos aminoácidos, (c) una región CDR3 que difiere de la región CDR3 de BMS3h-56-269 (SEQ ID No.: 417) por hasta dos aminoácidos.

Se proporciona además un polipéptido anticuerpo donde la secuencia de aminoácidos del primer dominio variable difiere de la secuencia de aminoácidos de BMS3h-56-258 (SEQ ID No.: 10) o BMS3h-56-269 (SEQ ID No.: 417) por hasta 10 aminoácidos.

Se proporciona además un polipéptido anticuerpo donde la secuencia de aminoácidos del primer dominio variable difiere de la secuencia de aminoácidos de BMS3h-56-258 (SEQ ID No.: 10) o BMS3h-56-269 (SEQ ID No.: 417) por hasta 5 aminoácidos.

Se proporciona además un polipéptido anticuerpo donde la secuencia de aminoácidos del primer dominio variable difiere de la secuencia de aminoácidos de BMS3h-56-258 (SEQ ID No.: 10) o BMS3h-56-269 (SEQ ID No.: 417) por dos aminoácidos.

Se proporciona además un polipéptido anticuerpo donde la secuencia de aminoácidos del primer dominio variable difiere de la secuencia de aminoácidos de BMS3h-56-258 (SEQ ID No.: 10) o BMS3h-56-269 (SEQ ID No.: 417) por un aminoácido.

Se proporciona además un polipéptido anticuerpo donde el polipéptido anticuerpo se selecciona del grupo de líneas de BMS3h-56, y donde la secuencia de aminoácidos del primer dominio variable comprende además: (a) una región CDR1 que tiene una secuencia X_1 -Tyr-Glu- Y_1 -Trp (SEQ ID No.: 1274), donde X_1 es Asp o Gly, y Y_1 es Met o Leu; (b) una región CDR2 que tiene una secuencia Ala-Ile-Asn-Pro- X_2 -Gly- Y_2 - Z_2 -Thr-Tyr-Tyr-Ala-Asp-Ser-Val- A_2 -Gly (SEQ ID No.: 1275), donde X_2 es Gln, Tyr, Pro, Trp, o Ala, Y_2 es Thr, Ser, Asn, Gly, Met, o Gln, Z_2 es Arg, Leu, Tyr, His, o Phe, y A_2 es Lys o Met; y (c) una región CDR3 que tiene una secuencia X_3 -Pro- Y_3 - Z_3 -Phe- A_3 - B_3 (SEQ ID No.: 1276), donde X_3 es Leu o Pro, Y_3 es Phe, Gln, Thr, o Met, Z_3 es Tyr, Pro, Leu, Thr, Ile, Phe, o Met, A_3 es Gln, His, Asp, Ser, Lys, Glu, o Gly, y B_3 es Glu, Asp, o Tyr.

Se proporciona además un polipéptido anticuerpo

donde la secuencia de aminoácidos del primer dominio variable comprende: (a) una región FR1 que tiene una secuencia Glu-Val-Gln-Leu-Leu-Glu-Ser-Gly-Gly-Gly--Leu-Val-Gln-Pro-Gly-Gly-Ser-X₁-Arg-Leu-Ser-Cys-Ala-Ala-Ser-Gly-Phe-Thr-Phe-Y₁ (SEQ ID No.: 1277), donde X₁ es Leu o Arg, y Y₁ es Arg o Ala; (b) una región FR2 que tiene una secuencia Trp-Val-Arg-X₂-Ala-Pro-Gly-Y₂-Z₂-Leu-Glu-Arg-Val-Ser (SEQ ID No.: 1278), donde X₂ es Gln o Arg, Y₂ es Lys o Arg, y Z₂ es Gly o Val; (c) una región FR3 que tiene una secuencia Arg-Phe-Thr-Ile-Ser-Arg-Asp-Asn-Ser-Lys-Asn-X₃-Lys-Tyr-Leu-Gln-Met-Asn-Ser-Leu-Arg-Ala-Y₃-Asp-Thr-Z₃-Val-Tyr-A₃-Cys-B₃-Lys (SEQ ID No.: 1279), donde X₃ es Thr o Met, Y₃ es Glu o Asp, Z₃ es Ala o Ser, A₃ es Tyr o His, y B₃ es Ala o Thr; y (d) una región FR4 que tiene una secuencia X₄-Gly-Y₄-Gly-Thr-Leu-Val-Thr-Val-Ser-Z₄ (SEQ ID No.: 1280), donde X₄ es Trp o Arg, Y₄ es Gln o Pro, y Z₄ es Ser o Asn.

Se proporciona además un polipéptido anticuerpo donde el primer dominio variable comprende la secuencia de aminoácidos de BMS3h-56-258 (SEQ ID No.: 10) o BMS3h-56-269 (SEQ ID No.: 417).

Se proporciona además un polipéptido anticuerpo donde el polipéptido anticuerpo se selecciona del grupo de líneas of BMS3h-37, donde el primer dominio variable comprende la secuencia Glu-Val-Gln-Leu-Leu-Glu-Ser-Gly-Gly-Gly-Leu-Val-X₁-Pro-Gly-Gly-Ser-Leu-Arg-Leu-Ser-Cys-Ala-Ala-

Ser-Gly-Phe-Thr-Phe-Glu-Trp-Tyr-Glu-Met-Gln-Trp-Val-Arg-Arg-Ala-Pro-Gly-Lys-Gly-Leu-Glu-Trp-Val-Ser-Ala-Ile-Ser-Gly-Asp-Gly-Tyr-Arg-Thr-Tyr-Tyr-Ala-Asp-Ser-Val-Lys-Gly-Arg-Phe-Thr-Ile-Ser-Arg-Asp-Asn-Ser-Lys-Asn-Thr-Leu-Tyr-Leu-Gln-Met-Asn-Ser-Leu-Arg-Ala-Glu-Asp-Thr-Ala-Val-Tyr-Tyr-Cys-Ala-Lys-Y₁-Leu-Z₁-A₁-Phe-Asp-Tyr-B₁-Gly-Arg-Gly-Thr-Leu-Val-Thr-Val-Ser-Ser (SEQ ID No.: 1281); y donde X₁ es Gln o Arg; Y₁ es Glu o Gly; Z₁ es Ala, Leu, o Glu; A₁ es Phe o Tyr; y B₁ es Trp o Arg.

10 Se proporciona también un polipéptido anticuerpo donde el polipéptido anticuerpo se selecciona del grupo de líneas de BMS3h-38, donde el primer dominio variable comprende la secuencia Glu-Val-Gln-Leu-Leu-Ala-Ser-Gly-Gly-Gly-Leu-Val-Gln-Pro-Gly-Gly-Ser-Leu-Arg-Leu-Ser-Cys-Ala-Ala-Ser-Gly-Phe-X₁-Phe-Glu-Glu-Glu-Glu-Met-Ile-Trp-Val-Arg-Gln-Ala-Pro-Gly-Lys-Gly-Leu-Glu-Trp-Val-Ser-Y₁-Ile-Ser-Z₁-A₁-Gly-B₁-C₁-Thr-Tyr-Tyr-Ala-Asp-Ser-Val-Lys-Gly-Arg-Phe-Thr-Ile-Ser-Arg-Asp-Asn-Ser-Lys-Asn-Thr-Leu-Tyr-Leu-Gln-Met-Asn-Ser-Leu-Arg-Ala-Glu-Asp-Thr-Ala-Val-Tyr-Tyr-Cys-Gly-Lys-Glu-Pro-Phe-D₁-Tyr-Asp-Tyr-Trp-Gly-Gln-Gly-Thr-Leu-Val-Thr-Val-Ser-Ser (SEQ ID No.: 1282); y donde X₁ es Thr o Pro; Y₁ es Ala o Ser; Z₁ es Arg o Gly; A₁ es Arg, Ser, Asn, Gln, Gly, His, o Leu; B₁ es Tyr, Phe, Trp, o Gly; C₁ es Ser o Gly; y D₁ es Arg, Met, o Pro.

25 Se proporciona también un polipéptido anticuerpo donde

el polipéptido anticuerpo se selecciona del grupo de líneas de BMS3h-198, donde el primer dominio variable comprende la secuencia Glu-Val-Gln-Leu-Leu-Glu-Ser-Gly-Gly-Gly-Leu-Val-Gln-Pro-Gly-Gly-Ser-Leu-Arg-Leu-Ser-Cys-Ala-Ala-Ser-Gly-Phe-
 5 Thr-Phe-Ala-Gly-Trp-Glu-X₁-Trp-Trp-Y₁-Arg-Gln-Ala-Pro-Gly-Lys-Gly-Leu-Glu-Arg-Val-Ser-Ala-Ile-Ser-Gly-Ser-Gly-Gly-Ser-Thr-Tyr-Tyr-Ala-Asp-Ser-Val-Lys-Gly-Arg-Phe-Thr-Ile-Ser-Arg-Asp-Z₁-A₁-Lys-Asn-Thr-Leu-Tyr-Leu-Gln-Met-Asn-Ser-Leu-Arg-Ala-Glu-Asp-Thr-Ala-Val-Tyr-B₁-Cys-Ala-C₁-D₁-Pro-Tyr-Ser-E₁-Asp-Tyr-F₁-
 10 G₁-H₁-Gly-Thr-Leu-Val-Thr-Val-Ser-Ser (SEQ ID No.: 1283); y donde X₁ es Met o Leu; Y₁ es Val o Phe; Z₁ es Asp o Asn; A₁ es Ser o Thr; B₁ es Tyr o His; C₁ es Lys o Arg; D₁ es Asp o Glu; E₁ es Tyr o Phe; F₁ es Trp o Arg; G₁ es Gly o Arg; y H₁ es Gln o His.

15 Se proporciona además un polipéptido anticuerpo donde el polipéptido anticuerpo es un anticuerpo de dominio (dAb).

Se proporciona además un polipéptido anticuerpo donde el dominio variable está fusionado a un dominio Fc.

20 Se proporciona además un polipéptido anticuerpo donde el polipéptido anticuerpo comprende además un segundo dominio variable que se enlaza específicamente un segundo antígeno, donde el segundo antígeno es un antígeno diferente del CD40 humano.

25 Se proporciona también un polipéptido anticuerpo

donde el segundo antígeno es un grupo de moléculas de diferenciación (CD) o una molécula de la Clase II del Complejo Mayor de Histocompatibilidad (MHC).

Se proporciona también un polipéptido anticuerpo
5 donde el segundo antígeno es la albúmina sérica (SA).

Se proporciona un ácido nucleico que codifica para el polipéptido anticuerpo descrito en la presente.

Se proporciona también un vector que comprende el ácido nucleico descrito en la presente.

10 Se proporciona también una célula hospedera que comprende el vector descrito en la presente.

Se proporciona una composición farmacéutica que comprende una cantidad terapéuticamente efectiva del polipéptido anticuerpo descrito en la presente y un portador
15 farmacéuticamente aceptable. Se proporciona también una composición farmacéutica que comprende además un agente inmunosupresor/inmunomodulador y/o anti-inflamatorio.

Se proporciona un método para tratar un trastorno inmunitario en un paciente en necesidad de tal tratamiento,
20 que comprende administrar al paciente una cantidad terapéuticamente efectiva de la composición farmacéutica descrita en la presente. Se proporciona también un método donde la composición farmacéutica es administrada en combinación con un agente inmunosupresor/inmunomodulador y/o
25 anti-inflamatorio.

Se proporciona un método para tratar un trastorno inmunitario donde el trastorno inmunitario es un trastorno autoinmunitario o un trastorno relacionado a injerto. Se proporciona además un método para tratar un trastorno

5 inmunitario donde el trastorno inmunitario es seleccionado del grupo que consiste de enfermedad de Addison, alergias, espondilitis anquilosante, asma, aterosclerosis, trastornos autoinmunitarios del oído, trastornos autoinmunitarios del ojo, hepatitis autoinmunitaria, parotitis autoinmunitaria,

10 colitis, trastorno cardiaco coronario, enfermedad de Crohn, diabetes, incluyendo diabetes Tipo 1 y/o Tipo 2, epididimitis, glomerulonefritis, enfermedad de Graves, síndrome de Guillain-Barre, enfermedad de Hashimoto, anemia hemolítica, púrpura trombocitopénica idiopática, enfermedad

15 inflamatoria del intestino, respuesta inmunitaria a productos farmacéuticos recombinantes, lupus eritematoso sistémico, infertilidad masculina, esclerosis múltiple, miastenia gravis, pénfigo, psoriasis, fiebre reumática, artritis reumatoide, sarcoidosis, esclerodermia, síndrome de Sjogren,

20 espondiloartropatías, tiroiditis, rechazo de trasplante, vasculitis, SIDA, alergia atópica, asma bronquial, eczema, lepra, esquizofrenia, depresión heredada, trasplantes de tejidos y órganos, síndrome de fatiga crónica, enfermedad de Alzheimer, enfermedad de Parkinson, infarto del miocardio,

25 apoplejía, autismo, epilepsia, fenómeno de Arthus,

anafilaxis, adicción al alcohol, y adicción a drogas.

Se proporciona también un método para dirigirse a CD40 utilizando un primer dominio variable que se enlaza específicamente a un epítopo de CD40 humano que comprende la
5 secuencia de aminoácidos de la SEQ ID No.: 1, donde el polipéptido anticuerpo compite con el enlace del anticuerpo de dominio (dAb) BMS3h-56-269 (SEQ ID No.:417).

Se proporciona el uso en medicina de un polipéptido anticuerpo que comprende un primer dominio variable que se
10 enlaza específicamente a un epítopo de CD40 humano, que comprende la secuencia de aminoácidos de la SEQ ID No.: 1, en donde el polipéptido anticuerpo compite con el enlace del anticuerpo de dominio (dAb) BMS3h-56-201 (SEQ ID No.: 9), o una sal farmacéuticamente aceptable del mismo.

15 Se proporciona el uso de un polipéptido anticuerpo que comprende un primer dominio variable que se enlaza específicamente a un epítopo de CD40 humano, que comprende la secuencia de aminoácidos de la SEQ ID No.: 1, en donde el polipéptido anticuerpo compite con el enlace del anticuerpo
20 de dominio (dAb) BMS3h-56-201 (SEQ ID No.: 9), o una sal farmacéuticamente aceptable del mismo, en la preparación de un medicamento para el tratamiento de un trastorno inmunitario. En algunas modalidades, la composición farmacéutica es administrada en combinación con un agente
25 inmunosupresor/inmunomodulador y/o anti-inflamatorio. En

modalidades adicionales, el trastorno inmunitario es un trastorno autoinmunitario o un trastorno relacionado al injerto. En modalidades adicionales, el trastorno inmunitario es seleccionado del grupo que consiste de

5 enfermedad de Addison, alergias, espondilitis anquilosante, asma, aterosclerosis, trastornos autoinmunitarios del oído, trastornos autoinmunitarios del ojo, hepatitis autoinmunitaria, parotitis autoinmunitaria, colitis, trastorno cardiaco coronario, enfermedad de Crohn, diabetes,

10 incluyendo diabetes Tipo 1 y/o Tipo 2, epididimitis, glomerulonefritis, enfermedad de Graves, síndrome de Guillain-Barre, enfermedad de Hashimoto, anemia hemolítica, púrpura trombocitopénica idiopática, enfermedad inflamatoria del intestino, respuesta inmunitaria a productos

15 farmacéuticos recombinantes, lupus eritematoso sistémico, infertilidad masculina, esclerosis múltiple, miastenia gravis, pénfigo, psoriasis, fiebre reumática, artritis reumatoide, sarcoidosis, esclerodermia, síndrome de Sjogren, espondiloartropatías, tiroiditis, rechazo de trasplante,

20 vasculitis, SIDA, alergia atópica, asma bronquial, eczema, lepra, esquizofrenia, depresión heredada, trasplantes de tejidos y órganos, síndrome de fatiga crónica, enfermedad de Alzheimer, enfermedad de Parkinson, infarto del miocardio, apoplejía, autismo, epilepsia, fenómeno de Arthus,

25 anafilaxis, adicción al alcohol, y adicción a drogas.

Se proporciona un polipéptido anticuerpo que comprende un primer dominio variable que se enlaza específicamente a un epítipo de CD40 humano que comprende la secuencia de aminoácidos de la SEQ ID No.: 1, en donde el polipéptido anticuerpo compite con el enlace del anticuerpo de dominio (dAb) BMS3h-56-201 (SEQ ID No.: 9), o una sal farmacéuticamente aceptable del mismo, para el uso en la preparación de un medicamento para el tratamiento de un trastorno inmunitario. El medicamento puede ser administrado, por ejemplo, en combinación con un agente inmunosupresor/inmunomodulador y/o anti-inflamatorio. El trastorno inmunitario puede ser, por ejemplo, un trastorno autoinmunitario o un trastorno relacionado al injerto. El trastorno inmunitario puede ser también seleccionado del grupo que consiste de enfermedad de Addison, alergias, espondilitis anquilosante, asma, aterosclerosis, trastornos autoinmunitarios del oído, trastornos autoinmunitarios del ojo, hepatitis autoinmunitaria, parotitis autoinmunitaria, colitis, trastorno cardíaco coronario, enfermedad de Crohn, diabetes, incluyendo diabetes Tipo 1 y/o Tipo 2, epididimitis, glomerulonefritis, enfermedad de Graves, síndrome de Guillain-Barre, enfermedad de Hashimoto, anemia hemolítica, púrpura trombocitopénica idiopática, enfermedad inflamatoria del intestino, respuesta inmunitaria a productos farmacéuticos recombinantes, lupus eritematoso sistémico,

infertilidad masculina, esclerosis múltiple, miastenia
gravis, pénfigo, psoriasis, fiebre reumática, artritis
reumatoide, sarcoidosis, esclerodermia, síndrome de Sjogren,
5 vasculitis, SIDA, alergia atópica, asma bronquial, eczema,
lepra, esquizofrenia, depresión heredada, trasplantes de
tejidos y órganos, síndrome de fatiga crónica, enfermedad de
Alzheimer, enfermedad de Parkinson, infarto del miocardio,
apoplejía, autismo, epilepsia, fenómeno de Arthus,
10 anafilaxis, adicción al alcohol, y adicción a drogas.

Breve Descripción de las Figuras

El archivo de patente o de la solicitud contiene al
menos un dibujo ejecutado a color. Las copias de esta
patente o la publicación de la solicitud de patente con
15 dibujos en color serán proporcionadas por la Oficina a
petición y con el pago de los derechos necesarios.

La Figura 1 describe los modos de enlace de dos
diferentes estructuras co-cristalinas de CD40 humano (SEQ ID
No.: 1), una con dAb BMS3h-56-5 (SEQ ID No.: 321) y una con
20 Fab' del anticuerpo Chi220. Las moléculas de BMS3h-56-5 y
Fab' de Chi220 son mostradas como caricaturas con hebras β
(representadas como flechas en dAb) y la estructura
secundaria no repetitiva (representada como bucles en dAb).
Las regiones de determinación de la complementariedad (CDRs,
25 por sus siglas en inglés) son también mostradas. CD40 es

también mostrado como una caricatura con los residuos del epítopo de BMS3h-56-5 de CD40 humano. Son también mostrados los residuos del epítopo de Chi220. Son también mostrados los enlaces disulfuro. El extremo N (N) y el extremo C (C) de CD40 están etiquetados.

La Figura 2 describe un modelo de relleno de espacio de BMS3h-56-5 (SEQ ID No.: 321) que pone en contacto el CD40 humano (SEQ ID No.: 1), el cual es mostrado como una caricatura. Los residuos superficiales del dAb BMS3h-56-5 que hacen contacto con CD40, son también mostrados. La región CDR3 de BMS3h-56-5 y los residuos de FR-2 Leu45, Arg47, Arg56 y Phe99 están etiquetados. La numeración de Kabat (Kabat et al., *Sequences of Immunological Interest*, 5th ed., U.S. Dept. Health & Human Services, Washington, D.C. (1991)) es utilizada en este diagrama y difiere de la numeración secuencial en que los residuos de inserción son utilizados para mantener idéntica la numeración de los residuos de las hebras β . De este modo para BMS3h-56-5, el residuo secuencial 53 se vuelve el residuo 52A, los residuos secuenciales 84, 85, y 86 se vuelven, respectivamente, 82A, 82B, 82C y el residuo de Kabat número 100 está ausente (éste estaría entre los residuos secuenciales 103 y 104); CD40 es también representado como una caricatura con estructura secundaria no repetitiva y el epítopo BMS3h-56-5. Los residuos de CD40 que difieren entre el humano y *Macaca*

fascicularis (mono cynomolgus), Ala115, Phe99, Ser126, His162, Leu121, y Trp109, se muestran en representación de barras. Los residuos CD40 que difieren entre el humano y el mono cynomolgus que son parte del epítipo BMS3h-56-5 son

5 Trp109, Leu121, y His162. Los residuos CD40 Trp109 y Leu121 yacen en una hendidura entre el CDR3 y FR-2 de BMS3h-56-5. La mutación de Trp109 ya sea que reduce en gran medida o bien abate la actividad de BMS3h-56-5.

La Figura 3 describe el enlace de un dAb anti-CD40 humano, PEGilado, BMS3h38-2C-P40Br, en muestras de sangre

10 provenientes de humano y especies de primate. La Figura 3A muestra el enlace de BMS3h38-2C-P40Br a células B de humano y de cynomolgus; la Figura 3B muestra el enlace de BMS3h38-2C-P40Br a células B de humano, de rhesus, y de chimpancé.

La Figura 4, la Figura 5, la Figura 6, y la Figura 7 muestran alineamientos ClustalW2 de los polipéptidos anticuerpos de dominio, representativos provenientes de las

15 líneas BMS3h-56, BMS3h-37, BMS3h-38, y BMS3h-198, respectivamente.

20 **Descripción Detallada de la Invención**

Se proporcionan los polipéptidos anticuerpos que se enlazan específicamente al CD40 humano. Los polipéptidos anticuerpos no muestran actividad agonista de CD40, y los polipéptidos anticuerpos son útiles en el tratamiento de

25 trastornos que involucran la activación de CD40, tales como

los trastornos autoinmunitarios. Los polipéptidos anticuerpos pueden ser seleccionados utilizando una selección primaria que utiliza el ensayo de enlace a células, seguido por una o más rondas de maduración de afinidad dirigida al oligonucleótido, degenerado o propenso a errores. Como resultado, se proporciona un género de los polipéptidos anticuerpos que se enlazan específicamente a un epítipo de CD40 simple.

Una "línea" es un grupo de polipéptidos anticuerpos relacionados que fueron preparados a partir de un precursor común mediante maduración de afinidad dirigida al oligonucleótido, degenerada o propensa a error, como se describe en los ejemplos siguientes, y que se espera se enlace al mismo epítipo de CD40. La nomenclatura de los polipéptidos anticuerpos es utilizada para designar las diversas líneas. La nomenclatura "BMS3h-56," por ejemplo, se refiere a los polipéptidos anticuerpos de la línea 56, que fueron producidos contra CD40 humano. Los polipéptidos anticuerpos de la "Línea BMS3h-56" incluyen BMS3h-56-1 a BMS3h-56-33, y BMS3h-56-202 a BMS3h-56-288.

En consecuencia, en un aspecto, un polipéptido anticuerpo comprende un dominio variable que se enlaza específicamente a CD40 humano, donde el polipéptido anticuerpo compite con el enlace de cualquiera de los anticuerpos de dominio (dAbs) listados en la TABLA 3. Por

ejemplo, el dAb puede pertenecer a una línea seleccionada del grupo que consiste de BMS3h-37, BMS3h-38, BMS3h-41, BMS3h-43, BMS3h-56, BMS3h-131, BMS3h-198, y BMS3h-202, tal como el dAb BMS3h-56-5, BMS3h-56-201, o BMS3h-56-258, por ejemplo. En otro aspecto más, un polipéptido anticuerpo se enlaza específicamente al mismo epítipo de CD40 humano que cualquiera de los dAbs listados en la TABLA 3. Por ejemplo, el polipéptido anticuerpo puede comprender un dominio variable que se enlaza específicamente al mismo epítipo de CD40 humano que dAb BMS3h-56-5, BMS3h-56-201, o BMS3h-56-258, por ejemplo. Como se describe más adelante, el epítipo de CD40 humano puede comprender el residuo de aminoácido Trp109 de la SEQ ID No.: 1, por ejemplo.

Los polipéptidos anticuerpos pueden ser anticuerpos de dominio que contienen un dominio variable simple. Los polipéptidos anticuerpos pueden también comprender dominios adicionales, tales como un dominio Fc. Por ejemplo, el polipéptido anticuerpo puede comprender un segundo dominio variable que se enlaza específicamente a la albúmina sérica humana (HSA). Tales polipéptidos anticuerpos específicos dobles pueden tener una vida media incrementada, por ejemplo.

En el Listado de Secuencias, la SEQ ID No.: 1 es la secuencia de aminoácidos de CD40 humano; la SEQ ID No.: 2 es la secuencia de aminoácidos de CD40 de *Macaca fascicularis*. La secuencia de aminoácidos del anticuerpo de dominio

BMS3h-56-5 es la SEQ ID No.: 321.

Como se utiliza en la presente, "enlace específico" se refiere al enlace de un antígeno por un polipéptido anticuerpo con una constante de disociación (K_d) de aproximadamente 1 μ M o menor como se mide, por ejemplo, mediante resonancia de plasmón superficial. Los sistemas de ensayo adecuados incluyen el sistema de resonancia de BIAcore^{MR} y el software de evaluación cinética BIAcore^{MR} (por ejemplo, versión 2.1). La afinidad o la K_d para una interacción de enlace específico puede ser de aproximadamente 500 nM o menor o de aproximadamente 300 nM o menor.

El término "aproximadamente" será entendido por las personas de experiencia ordinaria en la técnica y variará en cierto grado en el contexto en el cual se utiliza. En general, "aproximadamente" abarca un intervalo de valores que son más/menos 10% de un valor referido.

De acuerdo con la descripción detallada, se aplican las siguientes abreviaturas y definiciones. Se debe notar que como se utiliza en la presente, las formas singulares "un", "uno", "una", y "el" y "la", incluyen los referentes plurales a no ser que el contexto lo dicte claramente de otro modo. De este modo, por ejemplo, la referencia a "un anticuerpo" incluye una pluralidad de tales anticuerpos y la referencia a "la dosis" incluye la referencia a una o más dosis y equivalentes de las mismas conocidas por aquellos

expertos en la materia, y así sucesivamente.

1. CD40 y Actividades de CD40

Son proporcionados los polipéptidos anticuerpos que se enlazan a CD40 humano. CD40 es también conocido como el
 5 antígeno CD40 de la superficie de las células B, Bp50, receptor de CD40L, CDw40, CDW40, MGC9013, p50, TNFRSF5, y el miembro 5 de la superfamilia de receptores del factor de necrosis tumoral. La información estructural relevante para el CD40 humano puede ser encontrada, por ejemplo, en UniProt
 10 Números de Acceso P25942, Q9BYU0, y Q53GN5. "CD40 humano" se refiere al CD40 que comprende la siguiente secuencia de aminoácidos:

	MVRLPLQCVL	WGCLLTAVHP	EPPTACREKQ	YLINSQCCSL	CQPGQKLVSD
	CTEFTETECL	PCGESEFLDT	WNRETHCHQH	KYCDPNLGLR	VQQKGTSETD
15	TICTCEEGWH	CTSEACESCV	LHRSCSPGFG	VKQIATGVSD	TICEPCPVGF
	FSNVSSAFEK	CHPWTSCETK	DLVVQQAGTN	KTDVVCGPQD	RLRALVVIPI
	IFGILFAILL	VLVFIKKVAK	KPTNKAPHPK	QEPQEINFPD	DLPGSNTAAP
	VQETLHGCQP	VTQEDGKESR	ISVQERQ (SEQ ID No.: 1).		

CD40 también ha sido secuenciado en *Mus musculus*,
 20 *Sus scrofa*, *Bos taurus*, *Gallus gallus*, *Canis familiaris*, *Macaca fascicularis* (mono cynomolgus), *Ovis aries*, *Equus caballus*, y *Rattus norvegicus*.

El enlace de los presentes polipéptidos anticuerpos a CD40 antagoniza la actividad de CD40. Las "actividades de
 25 CD40" incluyen, pero no están limitadas a, la activación de

células T (por ejemplo, la inducción de la proliferación de células T o la secreción de citocinas), la activación de macrófagos (por ejemplo, la inducción de especies de oxígeno reactivo y óxido nítrico en el macrófago), y la activación de células B (por ejemplo, la proliferación de células B, el cambio de isotipo de anticuerpo, o la diferenciación a células plasmáticas). Las actividades de CD40 pueden ser mediadas por la interacción con otras moléculas. Las "actividades de CD40" incluyen la interacción funcional entre CD40 y las siguientes moléculas, las cuales son identificadas por su Número de Acceso niprot en paréntesis:

	CALR	(P27797);
	ERP44	(Q9BS26);
	FBL	(P22087);
15	POLR2H	(P52434);
	RFC5	(P40937);
	SGK1	(O00141);
	SLC30A7	(Q8NEW0);
	SLC39A7	(Q92504);
20	TRAF2	(Q5T1L5);
	TRAF3	(Q13114);
	TRAF6	(Q9Y4K3);
	TXN	(Q5T937);
	UGGT1	(Q9NYU2); y
25	USP15	(Q9Y4E8).

Por ejemplo, una "actividad" de CD40 incluye una interacción con TRAF2. La interacción CD40/TRAF2 activa NF- κ B y JNK. Ver Davies et al., *Mol. Cell Biol.* 25: 9806-19 (2005). Esta actividad de CD40 puede ser determinada de este modo por la activación de NF- κ B y JNK celulares, dependientes de CD40 con relación a una referencia.

Como se utilizan en la presente, los términos "activan," "activa," y "activado" se refieren a un incremento en una actividad dada de CD40, mensurable, por al menos 10% con relación a una referencia, por ejemplo, al menos 10%, 25%, 50%, 75%, o incluso 100%, o más. Una actividad de CD40 es "antagonizada" si la actividad es reducida por al menos 10%, y en una modalidad ejemplar, al menos aproximadamente 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 97%, o incluso 100% (por ejemplo, sin actividad detectable), con relación a la ausencia del antagonista. Por ejemplo, un polipéptido anticuerpo puede antagonizar alguna o toda la actividad de CD40, mientras que no activa a CD40. En una modalidad, el polipéptido anticuerpo no activa la proliferación de células B. En otra modalidad más, el polipéptido anticuerpo no activa la secreción de citocina por las células T, en donde la citocina es al menos una citocina seleccionada del grupo que consiste de IL-2, IL-6, IL-10, IL-13, TNF- α , IFN- γ .

2. El Epítipo de CD40

La cristalografía de rayos X de un complejo entre

CD40 humano (SEQ ID No.: 1) y el dAb BMS3h-56-5 (SEQ ID No.: 321) se utilizó para revelar un epítipo reconocido por los polipéptidos anticuerpos de la descripción. Los modelos estructurales de CD40 y BMS3h-56-5 fueron ajustados a los
5 datos de densidad electrónica para producir siete modelos o versiones del complejo CD40/BMS3h-56-5, los cuales vienen de tres complejos cristalográficamente independientes en una forma cristalina y cuatro complejos cristalográficamente independientes en una segunda forma cristalina. Las
10 versiones tienen coeficientes reales de correlación espacial de aproximadamente 0.92 para los átomos de la cadena principal y de 0.80 para los átomos de la cadena lateral. La molécula de CD40 tiene una cierta cantidad de flexibilidad en las siete versiones, pero la naturaleza general de la
15 interacción CD40/BMS3h-56-5 es conservada en todas las versiones. Las versiones difieren en la interacción entre el residuo Trp109 de CD40 y el residuo Trp103 de BMS3h-56-5 (Numeración de Kabat, ver más adelante). Trp103 de BMS3h-56-5 forma una interacción borde a cara con Trp109 de CD40 en
20 una versión, mientras que forma una interacción de apilamiento desplazado (por ejemplo, cara a cara) en otras versiones.

La estadística de complementariedad de forma, Sc , para las siete versiones está en el intervalo de 0.70-0.77, lo
25 cual muestra un más alto grado de complementariedad de forma

que para los complejos típicos anticuerpo/antígeno. Por ejemplo, estos valores se comparan a los intervalos de 0.71-0.76 para cuatro complejos de inhibidor de proteasa/proteína, 0.70-0.74 para cinco interfaces oligoméricas, y 0.64-0.68 para
 5 seis complejos anticuerpo/antígeno. Ver Lawrence et al., "Shape Complementarity at Protein/Protein Interfaces," *J. Mol. Biol.* 234: 946-950 (1993).

Un modelo del complejo CD40 humano/BMS3H-56-5 es mostrado en la Figura 1. Un BMS3h-56-5 dAb se enlaza a una
 10 molécula de CD40. El epítipo de BMS3h-56-5 no se traslapa con el epítipo del fragmento Fab' de Chi220. Todas las versiones del complejo definen un grupo de residuos de CD40 que hacen contacto con BMS3h-56-5: Trp109, Leu121, His122, Ser124, Ser156, Ala157, Phe158, Glu159, y His162 (con
 15 referencia a la SEQ ID No.: 1). Los residuos de CD40 que hacen contacto con BMS3h-56-5 en algunas versiones del complejo son Pro85, Asn86, Leu87, Gly88, Glu106, Glu107, Gly108, His110, Thr112, Cys119, Val120, Gln133, Ile134, Ala135, Thr136, Ser155, y Lys160. Val154 es un residuo de
 20 CD40 enterrado en todas las versiones. Otros residuos de CD40 enterrados en algunas versiones son Ser118, Arg123, Thr141, Phe151, Asp153, Cys161, y Pro163.

Como se utiliza en la presente, el término "en contacto" se refiere a una distancia interatómica cuyo máximo
 25 es determinado por una dependencia de distancia tipo atómica

como se define por Sheriff *et al.*, *J. Mol. Biol.* 197: 273-296 (1987) y Sheriff, *Immunomethods* 3: 191-196 (1993).

Como se utiliza en la presente, el término "enterrado" se refiere a un residuo que tiene al menos un átomo con área superficial definida por el programa MS (Connolly, *J. Appl. Crystallogr.* 16: 548-558 (1983)), una esfera de sonda de 1.7 Å, y radios de Van der Waals dependientes del tipo de átomo como se define por Sheriff, *Immunomethods* 3: 191-196 (1993).

La Figura 2 muestra la superficie de BMS3h-56-5 (SEQ ID No.: 321) incluyendo los residuos de contacto y los residuos enterrados. CD40 (SEQ ID No.: 1) es representado como un diagrama de listones con el color naranja que representa la estructura secundaria no repetitiva y el color magenta que representa los residuos de epítipo. Los residuos de CD40 Trp109, Ala115, Leu121, Ser126, y His162, los cuales son mostrados, difieren en diversas secuencias de primate no humano. Los residuos de CD40 Ala115 y Ser126 están sobre el lado opuesto del sitio de enlace a BMS3h-56-5. Trp109 y Leu121 se enlazan en una hendidura que yace entre CDR3 y FR-2 (residuos Leu45 y Arg47) de BMS3h-56-5. His162 interactúa con los residuos en CDR2 de BMS3h-56-5, especialmente Lys 56. En resumen, el epítipo de CD40 comprende uno o más residuos listados en la TABLA 1, con referencia a la numeración utilizada en la SEQ ID No.: 1.

TABLA 1

Residuos de CD40 que hacen contacto con BMS3h-56-5:
Trp109, Leu121, His122, Ser124, Ser156, Ala157, Phe158, Glu159, His162

5

BMS3h-56-5, como los otros dAbs listados en la TABLA 3, fue preparado por un método de selección y de maduración por afinidad, descrito con más detalle más adelante, utilizando el CD40 humano como el antígeno. Se

10 espera que los dAbs creados por la maduración de afinidad a partir de un dAb precursor común se enlazarán al mismo epítipo de CD40 humano. Los estudios de competencia descritos más adelante, por ejemplo, indican que los dAbs generados a partir de un dAb precursor común mediante

15 maduración de afinidad, compiten por el enlace uno con el otro al CD40 humano. Los mismos estudios de competencia, no obstante, muestran que los dAb no compiten con al menos los anticuerpos Chi220 o G28-5.

3. Polipéptidos anticuerpos

20

Los polipéptidos anticuerpos comprenden un dominio variable. En una modalidad, los polipéptidos anticuerpos están en la forma de un dAb que contiene un dominio variable simple. Los polipéptidos anticuerpos pueden ser moléculas de inmunoglobulina anti-CD40 de longitud completa que comprenden

25

dos cadenas pesadas (H) y dos cadenas ligeras (L) interconectadas por enlaces disulfuro. En esta modalidad, una porción amino-terminal de cada cadena incluye un dominio variable (V_L o V_H) de aproximadamente 100-110 aminoácidos, principalmente responsable del reconocimiento del antígeno vía las regiones de determinación de la complementariedad (CDRs, por sus siglas en inglés) contenidas en éstas. La "mitad" carboxilo-terminal de cada cadena pesada define una región constante (F_c) principalmente responsable por la función efectora.

Los polipéptidos anticuerpos también pueden ser "fragmentos" que comprenden una porción de la molécula de inmunoglobulina anti-CD40, de longitud completa, que comprende un dominio variable que se enlaza específicamente a CD40. De este modo, el término "polipéptidos anticuerpos" incluye una cadena pesada que se enlaza al antígeno, la cadena ligera, el dímero de cadena pesada-cadena ligera, el fragmento Fab, el fragmento $F(ab')_2$, el fragmento Fv, Fv de cadena simple (scFv), y dAb, por ejemplo. El término "polipéptidos anticuerpos" incluyen de este modo los polipéptidos elaborados mediante ingeniería recombinante y la expresión recombinante, así como los anticuerpos monoclonales producidos mediante recombinación y secreción naturales por clones de células hibridomas.

Las cadenas ligeras son clasificadas como kappa (κ)

o lambda (λ), y están caracterizadas por una región constante particular, C_L , como es conocida en la técnica. Las cadenas pesadas son clasificadas como γ , μ , α , δ , o ϵ , y definen el isotipo de un anticuerpo como IgG, IgM, IgA, IgD, o IgE, respectivamente. La región constante de cadena pesada está comprendida de tres dominios (CH1, CH2, y CH3) para IgG, IgD, e IgA; y cuatro dominios (CH1, CH2, CH3, y CH4) para IgM e IgE. Los anticuerpos anti-CD40 pueden tener una región constante de cadena pesada seleccionada de cualquiera de las clases de inmunoglobulinas (IgA, IgD, IgG, IgM, e IgE).

Cada dominio variable de cadena ligera (V_L) y cada dominio variable de cadena pesada (V_H) está compuesto de tres CDRs y cuatro regiones estructurales (FRs), acomodadas del amino terminal al carboxilo terminal en el siguiente orden: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. Las tres CDRs de la cadena ligera son denominadas como "LCDR1, LCDR2, y LCDR3" y las tres CDRs de la cadena pesada son denominadas como "HCDR1, HCDR2, y HCDR3."

Como se utiliza en la presente, el término "dominio Fc" se refiere a las secuencias de anticuerpo de región constante que comprenden los dominios constantes CH2 y CH3 como son delimitados de acuerdo a Kabat et al., *Sequences of Immunological Interest*, 5th ed., U.S. Dept. Health & Human Services, Washington, D.C. (1991). La región Fc puede ser derivada de una IgG1 o una región Fc de IgG4 Fc, por ejemplo.

Un dominio variable puede ser fusionado a un dominio Fc. En este caso, el carboxilo terminal del dominio variable (ya sea el dominio V_L o V_H, incluyendo los dAbs) puede ser enlazado o fusionado al amino terminal del dominio CH2 de Fc. Alternativamente, el carboxilo terminal del dominio variable puede ser enlazado o fusionado al amino terminal de un dominio CH1, el cual por sí mismo está fusionado al dominio CH2 de Fc. La proteína puede comprender la región de bisagra entre los dominios CH1 y CH2 total o parcialmente.

Las CDRs contienen la mayoría de los residuos que forman interacciones específicas con el antígeno. Como se muestra en la Figura 2, por ejemplo, CDR2 y CDR3, más el residuo Trp103 de FR4, forman la mayoría de los contactos entre CD40 y el dAb BMS3h-56-5. Por ejemplo, el dominio variable de un polipéptido anticuerpo comprende las regiones CDR1, CDR2, y CDR3 que tienen las mismas secuencias de aminoácidos que las regiones CDR1, CDR2, y CDR3 de uno de los dAbs listados en la TABLA 3 o que cada uno difieren de las regiones CDR1, CDR2, y CDR3 regiones por uno o dos aminoácidos. Por ejemplo, el polipéptido anticuerpo puede comprender las regiones CDR1, CDR2, y CDR3 que tienen la misma secuencia de aminoácidos que las regiones CDR1, CDR2, y CDR3 de BMS3h-56-5, BMS3h-56-258, o BMS3h-56-201, por ejemplo.

Un "anticuerpo de dominio" (dAb) comprende un

dominio variable simple (V_L o V_H) que es capaz de reticularse específicamente y de manera monovalente a un antígeno, tal como CD40. Por ejemplo, un dAb puede tener una estructura V_{HH} , característica de un dAb camélido. Un "dominio V_H " como
5 se utiliza en la presente, se entiende que incluye una estructura de V_{HH} . En otra modalidad más, los dominios V_H de la presente invención (incluyendo todas las características y combinación de características presentadas como modalidades en la presente) son diferentes de los dominios de V_{HH} . Los
10 dAbs pueden formar homo- o heterodímeros en solución. Se cree que los anticuerpos bivalentes anti-CD40 muestra actividad agonista debido a la habilidad para reticularse a las moléculas de CD40 enlazadas, sobre la superficie celular. Mientras que no se está limitado por ninguna teoría
15 particular, se cree que los dAbs monovalentes no activan CD40, debido a que los dAbs no reticulan CD40.

Como se utiliza en la presente, el término "dominio variable" se refiere a los dominio variables de inmunoglobulina, definidos por Kabat et al., *Sequences of*
20 *Immunological Interest*, 5th ed., U.S. Dept. Health & Human Services, Washington, D.C. (1991). La numeración y la colocación de los residuos de aminoácidos de CDR dentro de los dominios variables está de acuerdo con la convención de numeración de Kabat. Por ejemplo, la numeración de Kabat
25 para BMS3h-56-5 (SEQ ID No.: 321) es comparada en la TABLA 2

[illegible]

25 El término "humano", cuando se aplica a los polipéptidos

anticuerpos, significa que el polipéptido anticuerpo tiene una secuencia, por ejemplo, los dominios de FR y/o CH, derivados de una inmunoglobulina humana. Una secuencia es "derivada de" una secuencia de codificación de inmunoglobulina humana cuando la secuencia es ya sea: (a) aislada de un individuo humano o una célula o línea celular proveniente de un individuo humano; (b) aislada de una biblioteca de secuencias de genes de anticuerpos humanos, clonados o de secuencias de dominio de anticuerpo humano; o (c) diversificada por mutación y selección a partir de uno o más de los polipéptidos anteriores. Un compuesto "aislado" como se utiliza en la presente significa que el compuesto es removido de al menos un componente con el cual el compuesto está naturalmente asociado en la naturaleza.

Los polipéptidos anticuerpos pueden ser administrados a pacientes humanos mientras que se evita en gran medida la respuesta inmunitaria anti-anticuerpos a menudo provocada por la administración de anticuerpos provenientes de otras especies, por ejemplo, de ratón. Por ejemplo, los anticuerpos murinos pueden ser "humanizados" mediante injerto de CDRs murinas sobre una FR de dominio variable humano, de acuerdo a los procedimientos bien conocidos en la técnica. Los anticuerpos humanos como se describen en la presente, no obstante, pueden ser producidos sin la necesidad para la manipulación genética de una

secuencia de anticuerpo murino.

Los dominios variables pueden comprender una o más regiones estructurales (FR) con la misma secuencia de aminoácidos que una región estructural correspondiente
 5 codificada por un segmento génico de anticuerpo humano de línea germinal. Por ejemplo, un anticuerpo de dominio puede comprender los segmentos génicos de línea germinal de V_H , DP47, DP45, o DP38, el segmento DPK9 del gen de línea germinal de V_K , el segmento JH4b de J_H , o el segmento J_K1 de
 10 J_K .

Pueden ser realizados cambios a las secuencias del polipéptido anticuerpo mientras que se conserva la habilidad de reticularse a CD40 específicamente. Específicamente, los polipéptidos anticuerpos (por ejemplo, un dAb) pueden
 15 comprender un dominio variable variante que conserva la función de reticularse específicamente al mismo epítipo de CD40 que el dAb BMS3h-56-5. Ver TABLA 1. Es decir, el dominio variable variante puede reticularse a un epítipo de CD40 humano que comprende al menos uno de Trp109, Leu121,
 20 His122, Ser124, Ser156, Ala157, Phe158, Glu159, y His162 de la SEQ ID No.: 1. En una modalidad, el epítipo del dominio variable variante puede comprender Trp109, Leu121, His122, Ser124, Ser156, Ala157, Phe158, Glu159, y His162. Alternativamente, el dominio variable variante puede
 25 reticularse específicamente a un epítipo de CD40 que

comprende el residuo Trp109 de CD40. En otra modalidad más, el dominio variable variante puede competir con BMS3h-56-5 por el enlace específico a CD40. La maduración por afinidad propensa a errores, como se describe en los ejemplos más
5 adelante, proporciona un método ejemplar para elaborar e identificar polipéptidos anticuerpos con secuencias variantes que se enlazan específicamente al mismo epítipo de CD40.

Por ejemplo, un dominio variable variante puede diferir de los dominios variables listados en la TABLA 3 por
10 hasta 10 aminoácidos o cualquier valor integral entre éstos, donde el dominio variable variante se enlaza específicamente a CD40. Alternativamente, el dominio variable variante puede tener al menos 90% de identidad secuencial (por ejemplo, al menos 92%, 95%, o 98% de identidad secuencial) con relación a
15 una secuencia listada en el presente Listado de Secuencias. Los residuos de aminoácidos no idénticos o los aminoácidos que difieren entre dos secuencias pueden representar sustituciones, adiciones o supresiones de aminoácidos. Los residuos que difieren entre dos secuencias aparecen como
20 posiciones no idénticas, cuando las dos secuencias están alineadas por cualquier algoritmo de alineamiento de secuencia de aminoácidos apropiados, tal como BLAST.

Se proporciona que las sustituciones de aminoácidos pueden ser realizadas a las regiones FR individuales, tal que
25 una o más FR comprenden hasta dos diferentes aminoácidos con

relación a la secuencia de aminoácidos de la FR correspondiente, codificada por un segmento génico de anticuerpo de línea germinal humana. Se proporciona además que el dominio variable variante puede contener una o dos
5 sustituciones de aminoácidos en una o más CDR. Los dominios variables representativos que se enlazan específicamente a CD40 son listados en la TABLA 3.

Los alineamientos ClustalW2 entre los dominios variables representativos de los polipéptidos anticuerpos
10 provenientes de las líneas BMS3h-56, BMS3h-37, BMS3h-38, y BMS3h-198 son mostrados en la Figura 4, la Figura 5, la Figura 6, y la Figura 7, respectivamente. Como una regla general, el grado al cual un aminoácido es conservado en un alineamiento de secuencias de proteínas relacionadas, es
15 proporcional a la importancia relativa de la posición del aminoácido para la función de la proteína. Es decir, los aminoácidos que son comunes en todas las secuencias relacionadas probablemente juegan un papel importante y no pueden ser fácilmente sustituidos. Por otra parte, las
20 posiciones que varían entre las secuencias probablemente pueden ser sustituidas con otros aminoácidos o de otro modo modificados, mientras que se mantiene la actividad de la proteína. Los alineamientos mostrados en la Figura 4, la Figura 5, la Figura 6, y la Figura 7 y las relaciones
25 estructurales averiguadas de la Figura 1 y la Figura 2, por

ejemplo, pueden guiar la construcción de los polipéptidos anticuerpos variantes que se enlazan específicamente a un epítipo de CD40 humano que comprende la secuencia de aminoácidos de la SEQ ID No.: 1, en donde el polipéptido anticuerpo compite con el enlace del dAb BMS3h-56-201 (SEQ ID No.: 9). Tales polipéptidos anticuerpos variantes incluyen, pero no están limitados a, aquellos con una modificación de aminoácido correspondiente a una sustitución, inserción o supresión con referencia a cualquiera de los dominios variables listados en la TABLA 3. Los polipéptidos anticuerpos variantes también incluyen aquellos con una modificación de aminoácido correspondiente a una modificación de aminoácido conservada entre las secuencias listadas en la TABLA 3.

La información con respecto a los límites de los dominios V_L o V_H de los genes de cadena pesada y ligera puede ser utilizada para diseñar cebadores de PCR, para amplificar el dominio variable a partir de una secuencia de codificación de la cadena pesada o la cadena ligera, clonada, que codifica para un polipéptido anticuerpo que se sabe se enlaza a CD40. El dominio variable amplificado puede ser insertado dentro de un vector de expresión adecuado, por ejemplo, pHEN-1 (Hoogenboom et al. (1991) *Nucleic Acids Res.* 19:4133-4137) y expresado, ya sea solo o como una fusión, con otra secuencia polipeptídica, utilizando técnicas bien conocidas en la

materia. Con base en las secuencias descritas de aminoácidos y de polinucleótidos, la proteína de fusión puede ser producida y purificada utilizando únicamente habilidad ordinaria en cualquier línea celular hospedera de mamífero, adecuada, tal como CHO, 293, COS, NSO, y similares, seguido por la purificación utilizando uno o una combinación de métodos, incluyendo la cromatografía de afinidad de proteína A, intercambio iónico, técnicas de fase inversa, o similares.

En un aspecto, el polipéptido anticuerpo es un polipéptido anticuerpo "específico doble" que comprende un primer dominio variable que se enlaza específicamente a CD40 humano que comprende la secuencia de aminoácidos de la SEQ ID No.: 1. Los polipéptidos anticuerpos específicos dobles comprenden un segundo dominio variable que se enlaza específicamente a un segundo antígeno que es diferente del CD40 humano.

En otra modalidad más, el segundo antígeno puede ser una molécula de la superficie celular de una célula inmunitaria efectora o una molécula soluble tal como una citocina, por ejemplo. El enlace del polipéptido anticuerpo de especificidad doble podría ser utilizado para antagonizar CD40 y antagonizar una actividad biológica del segundo antígeno. Las moléculas de la superficie celular de las células efectoras inmunitarias incluyen el grupo de moléculas de diferenciación (CD). Los marcadores de CD representativos

son listados en la Internet en el protocolo de transferencia de hipertexto en wikipedia.org/wiki/List_of_human_clusters_of_differentiation (última modificación el 22 de Febrero del 2012). Las moléculas de la superficie celular de las células efectoras inmunitarias también incluyen las moléculas de la Clase II del Complejo Mayor de Histocompatibilidad (MHC). Los anticuerpos contra estas moléculas de la superficie celular son conocidos en la técnica y pueden ser utilizados como una fuente de un dominio variable para construir un polipéptido anticuerpo específico doble.

En una modalidad, los polipéptidos anticuerpos de un ligando específico doble pueden ser enlazados por un "ligador de aminoácido" o "ligador". Por ejemplo, un dAb puede ser fusionado al extremo N de un ligador de aminoácido, y otro dAb puede ser fusionado al extremo C del ligador. Aunque los ligadores de aminoácidos pueden ser de cualquier longitud y pueden consistir de cualquier combinación de aminoácidos, la longitud del ligador puede ser relativamente corta (por ejemplo, cinco o menos aminoácidos) para reducir las interacciones entre los dominios enlazados. La composición de aminoácidos del ligador puede ser también ajustada para reducir el número de aminoácidos con cadenas laterales voluminosas o los aminoácidos que probablemente introducen estructura secundaria. Los ligadores de

aminoácidos adecuados incluyen, pero no están limitados a, aquellas hasta de 3, 4, 5, 6, 7, 10, 15, 20, ó 25 aminoácidos de longitud. Las secuencias ligadoras de aminoácidos representativas incluyen (GGGGS)_n (SEQ ID No.: 4), donde n
5 puede ser cualquier número entero entre 1 y 5. Otras secuencias ligadoras adecuadas pueden ser seleccionadas del grupo que consiste de AST (SEQ ID No.: 5), TVAAPS (SEQ ID No.: 6), TVA (SEQ ID No.: 7), y ASTSGPS (SEQ ID No.: 8).

El enlace del segundo antígeno puede incrementar la
10 vida media *in vivo* del polipéptido anticuerpo. Por ejemplo, el segundo dominio variable del polipéptido anticuerpo específico doble puede reticularse específicamente a la albúmina sérica (SA), por ejemplo, la albúmina sérica humana (HSA). El polipéptido anticuerpo formateado para reticularse
15 a HSA puede tener una vida media t- α *in vivo* ("vida media alfa") o t- β ("vida media beta") incrementadas, con relación al mismo polipéptido anticuerpo no formateado. Las vidas medias t- α y t- β miden qué tan rápido una sustancia es distribuida en y eliminada del cuerpo. El enlace a HSA puede
20 ser logrado mediante la fusión del polipéptido anticuerpo con un segundo dominio variable capaz de reticularse específicamente a HSA, por ejemplo. Los anticuerpos anti-albúmina sérica humana son bien conocidos en la técnica. Ver *por ejemplo*, Abcam®, anticuerpos para albúmina sérica humana
25 ab10241, ab2406, y ab8940, disponibles en la Internet en el

protocolo de transferencia de hipertexto
www.abcam.com/index.html, o GenWay. El anticuerpo ALB,
disponible en la Internet en el protocolo de transferencia de
hipertexto www.genwaybio.com. Los dominios variables que se
5 enlazan específicamente a HSA pueden ser obtenidos de
cualquiera de estos anticuerpos, y luego fusionados a un
polipéptido anticuerpo de la descripción utilizando técnicas
recombinantes que son bien conocidas en la materia.

Alternativamente, el enlace del polipéptido
10 anticuerpo a HSA puede ser logrado al fusionar directamente
la secuencia del polipéptido anticuerpo a una secuencia de
codificación de HSA utilizando técnicas bien conocidas por el
experto en la materia. Las secuencias de codificación de HSA
pueden ser obtenidas mediante PCR utilizando cebadores de la
15 secuencia de cADN disponible de GenBank Acceso No. NM000477,
por ejemplo.

En una modalidad, la vida media t_{α} de la
composición de anticuerpo de dominio enlazado a HSA, es
incrementada por 10% o más. En otra modalidad más, la vida
20 media t_{α} de la composición del anticuerpo de dominio enlazado
a HSA está en el intervalo de 0.25 horas a 6 horas. En otra
modalidad más, la vida media t_{β} de la composición del
anticuerpo de dominio enlazado a HSA es incrementada por 10%
o más. En otra modalidad más, vida media t_{β} de la
25 composición del anticuerpo de dominio enlazado a HSA está en

el intervalo de 12 a 48 horas.

En otra modalidad más, un polipéptido anticuerpo puede ser formateado para incrementar su vida media *in vivo* por PEGilación. En una modalidad, el PEG es covalentemente
5 enlazado. En otra modalidad más, el PEG es enlazado al polipéptido anticuerpo en un residuo de cisteína o de lisina. En otra modalidad más, el polipéptido anticuerpo enlazado al PEG tiene un tamaño hidrodinámico de al menos 24 kD. En otra modalidad más, el tamaño de PEG total es de 20 a 60 kD,
10 inclusive. En otra modalidad más, el anticuerpo de dominio enlazado a PEG tiene un tamaño hidrodinámico de al menos 200 kD.

La PEGilación puede ser lograda utilizando varias porciones de enlace a PEG, incluyendo, pero no limitadas al
15 éster activo de N-hidroxilsuccinimida, propionato de succinimidilo, maleimida, vinilsulfona, o tiol. Un polímero de PEG puede ser enlazado a un polipéptido anticuerpo ya sea en una posición predeterminada, o bien puede ser aleatoriamente enlazado a la molécula del anticuerpo de
20 dominio. La PEGilación puede ser también mediada a través de un mediador peptídico enlazado a un anticuerpo de dominio. Es decir, la porción de PEG puede ser enlazada a un ligador peptídico fusionado a un polipéptido anticuerpo, donde el ligador proporciona el sitio (por ejemplo, una cisteína o
25 lisina libre) para acoplamiento del PEG. Los métodos de

PEGilación de los anticuerpos son bien conocidos en la técnica, como se describe en Chapman, et al., "PEGylated antibodies and antibody fragments for improved therapy: a review", *Adv. Drug Deliv. Rev.* 54(4):531-45 (2002), por ejemplo.

Los polipéptidos anticuerpos pueden ser también diseñados para formar un dímero, trímero, tetrámero u otro multímero. Los polipéptidos anticuerpos, por ejemplo, los dAbs, pueden ser enlazados para formar un multímero mediante varios métodos conocidos en la técnica, incluyendo, pero no limitados a, la expresión de monómeros como una proteína de fusión, el enlace de dos o más monómeros vía un enlazador peptídico entre monómeros, o al unir químicamente los monómeros después de la traducción, ya sea uno al otro directamente, o a través de un ligador por enlaces disulfuro, o mediante enlace a una porción de enlace di-, tri- o multivalente (por ejemplo, un PEG de brazos múltiples). En una modalidad, el multímero puede reticularse a una molécula simple de CD40.

20 **4. Composiciones Farmacéuticas y Métodos de Tratamiento**

Una composición farmacéutica comprende una cantidad terapéuticamente efectiva de uno o más polipéptidos anticuerpos y opcionalmente un portador farmacéuticamente aceptable. Los portadores farmacéuticamente aceptables incluyen, por ejemplo, agua, solución salina, solución salina

amortiguada con fosfato, dextrosa, glicerol, etanol y similares, así como combinaciones de los mismos. Los portadores farmacéuticamente aceptables pueden además comprender cantidades menores de sustancias auxiliares, tales como agentes humectantes o emulsificantes, conservantes, o amortiguadores que mejoran la vida de anaquel o la efectividad de la proteína de fusión. Las composiciones pueden ser formuladas para proporcionar liberación rápida, sostenida o retardada del o de los ingredientes activos después de la administración. Las composiciones farmacéuticas y los procesos adecuados para prepararlos son bien conocidos en la técnica. Ver, *por ejemplo*, Remington, THE SCIENCE Y PRACTICE OF PHARMACY, A. Gennaro, et al., eds., 21st ed., Mack Publishing Co. (2005).

La composición farmacéutica puede comprender además un agente inmunosupresor/inmunomodulador y/o anti-inflamatorio. Un método para tratar un trastorno inmunitario en un paciente en necesidad de tal tratamiento puede comprender administrarle al paciente una cantidad terapéuticamente efectiva de la composición farmacéutica. El antagonismo de la activación de células T mediado por CD40, podría inhibir las respuestas de células T no deseadas, que ocurren durante la autoinmunidad, en rechazo de trasplantes o las respuestas alérgicas, por ejemplo. La inhibición de las células T mediada por CD40, podría moderar la progresión y/o

la severidad de estos trastornos.

Como se utiliza en la presente, un "paciente" significa un animal, por ejemplo, un mamífero, incluyendo humanos. El paciente puede ser diagnosticado con un trastorno inmunitario. "Tratamiento" o "trato" o "tratar" se refiere al proceso que involucra aliviar la progresión o la severidad de un síntoma, trastorno, condición o enfermedad. Un "trastorno inmunitario" se refiere a cualquier trastorno asociado con el desarrollo de una reacción inmunitaria en un individuo, incluyendo una reacción inmunitaria celular y/o humoral. Los ejemplos de trastornos inmunitarios incluyen, pero no están limitados a, inflamación, alergia, trastornos autoinmunitarios o trastornos relacionados a injerto. El trastorno autoinmunitario puede ser seleccionado del grupo que consiste de lupus eritematoso sistémico, esclerosis múltiple, artritis reumatoide, diabetes, psoriasis, esclerodermia, aterosclerosis, enfermedad inflamatoria del intestino y colitis ulcerativa.

Los trastornos que pueden ser tratados por administración de la composición farmacéutica pueden ser seleccionados del grupo que consiste de enfermedad de Addison, alergias, espondilitis anquilosante, asma, aterosclerosis, trastornos autoinmunitarios del oído, trastornos autoinmunitarios del ojo, hepatitis autoinmunitaria, parotitis autoinmunitaria, colitis,

trastorno cardiaco coronario, enfermedad de Crohn, diabetes, incluyendo diabetes Tipo 1 y/o Tipo 2, epididimitis, glomerulonefritis, enfermedad de Graves, síndrome de Guillain-Barre, enfermedad de Hashimoto, anemia hemolítica, 5 púrpura trombocitopénica idiopática, enfermedad inflamatoria del intestino, respuesta inmunitaria a productos farmacéuticos recombinantes (por ejemplo, Factor VII en hemofílicos), lupus eritematoso sistémico, infertilidad masculina, esclerosis múltiple, miastenia gravis, pénfigo, 10 psoriasis, fiebre reumática, artritis reumatoide, sarcoidosis, esclerodermia, síndrome de Sjogren, espondiloartropatías, tiroiditis, rechazo de trasplantes y vasculitis. Las condiciones mediadas autoinmunitariamente incluyen, pero no están limitadas a, condiciones en las 15 cuales el tejido afectado es el objetivo primario, y en algunos casos, el objetivo secundario. Tales condiciones incluyen, pero no están limitadas a, SIDA, alergia tópica, asma bronquial, eczema, lepra, esquizofrenia, depresión heredada, trasplante de tejidos y órganos, síndrome de fatiga 20 crónica, enfermedad de Alzheimer, enfermedad de Parkinson, infarto del miocardio, apoplejía, autismo, epilepsia, fenómeno de Arthus, anafilaxis, adicción al alcohol, y adicción a drogas.

La composición farmacéutica puede ser administrada 25 sola o en terapia de combinación, (por ejemplo, simultánea o

secuencialmente) con un agente inmunosupresor/inmunomodulador y/o anti-inflamatorio. Los diferentes trastornos inmunitarios pueden requerir el uso de compuestos auxiliares específicos útiles para tratar trastornos inmunitarios, los cuales pueden ser determinados en una base de paciente por paciente. Por ejemplo, la composición farmacéutica puede ser administrada en combinación con uno o más adyuvantes adecuados, por ejemplo, citocinas (IL-10 y IL-13, por ejemplo) u otros estimuladores del sistema inmunitario, por ejemplo, quimiocinas, antígenos asociados al tumor, y péptidos. Los adyuvantes adecuados son conocidos en la técnica.

Cualquier método o ruta adecuada pueden ser utilizados para administrar el polipéptido anticuerpo o la composición farmacéutica. Las rutas de administración incluyen, por ejemplo, la administración oral, intravenosa, intraperitoneal, subcutánea, o intramuscular. Una dosis terapéuticamente efectiva del o de los polipéptidos anticuerpos administrados, depende de numerosos factores, incluyendo, por ejemplo, el tipo y la severidad del trastorno inmunitario que se trate, el uso de la terapia en combinación, la ruta de administración de o de los polipéptidos anticuerpos o la composición farmacéutica, y el peso del paciente. Un intervalo no limitante para una cantidad terapéuticamente efectiva de un anticuerpo de

dominio es de 0.1-20 mg/kg, y en un aspecto, de 1-10 mg/kg, con relación al peso corporal del paciente. La dosis del o de los polipéptidos anticuerpos puede ser además guiada por la cantidad del o de los polipéptidos anticuerpos, requerida para el antagonismo de CD40 en modelos *in vitro* y/o *in vivo* de los estados de enfermedad. Los modelos representativos son descritos más adelante y en los ejemplos.

5. Modelos *In Vitro* y *In Vivo*

La habilidad de los polipéptidos anticuerpos de la descripción para antagonizar CD40, puede ser probada en uno de varios sistemas modelo *in vitro* o *in vivo*, disponibles. Los sistemas modelo animales y celulares, apropiados, se describen más adelante. Los sistemas de ensayo celular adicionales son descritos en los ejemplos.

5.1. Modelos de Enfermedad Inflamatoria del Intestino (IBD) :

La IBD es un trastorno inmunitario multifactorial de etiología incierta. Varios modelos de ratón de inflamación mucosal que se asemejan a IBD han proporcionado una introspectiva hacia los mecanismos que gobiernan la función inmunitaria mucosal normal y patológica. Los modelos de IBD incluyen el uso de inmunidad mucosal y el sistema de inflamación de De Winter et al., *Am. J. Physiol.* 276: G1317-1321 (1999). En un aspecto, la inyección dentro de ratones inmunodeficientes de un subgrupo de linfocitos T CD4(+), las

células CD4(+)CD45RB^{high}, conduce a la inflamación del intestino. La patogénesis es debida, en parte, a la secreción de las citocinas proinflamatorias. La inducción de la colitis puede ser prevenida mediante co-transferencia de otra subpoblación CD4(+), las células CD4(+)CD45RB^{low}. Esta población se comporta análogamente a la población CD4(+)CD45RB^{high} en términos de la adquisición de marcadores de activación y al alojamiento en el intestino del hospedero. Sin embargo, su perfil de linfocina cuando se activa es diferente, y las citocinas anti-inflamatorias secretadas y/o inducidas por las células T CD4(+)CD45RB^{low} previenen la colitis. De Winter et al. proporcionan una descripción del modelo de transferencia adoptiva y los factores que promueven y previenen la patogénesis de la colitis.

15 **5.2. Modelos de Artritis Espontánea:**

Un modelo de trastorno específico de órganos, provocado por la autoinmunidad sistémica, es proporcionado por Kouskoff et al., *Cell* 87: 811-822 (1996). La artritis reumatoide (RA) es un trastorno crónico de las articulaciones caracterizado por invasión de leucocitos y activación de sinoviocitos, seguido por destrucción del cartílago y del hueso. Kouskoff et al. describen un modelo de RA espontáneo de ratón, generado mediante el cruce de una línea transgénica del receptor de células T (TCR) con la cepa NOD. Toda la progenie desarrolla un trastorno de las articulaciones

altamente reminisciente de RA en humanos. El disparador para el trastorno murino es el reconocimiento probabilístico de una molécula de la clase II del complejo mayor de histocompatibilidad (MHC) derivada de NOD mediante TCR transgénica; la progresión hacia la artritis involucra células T, B y probablemente mieloides, CD4+.

5.3. Modelo de Artritis Inducida por Colágeno (CIA) :

Un modelo en ratón de artritis inducida por colágeno es proporcionado por Brand et al., *Methods Mol. Med.* 102: 295-312 (2004). La artritis inducida por colágeno (CIA) es un trastorno autoinmunitario que puede ser promovido en cepas susceptibles de roedores (rata y ratón) y primates no humanos por inmunización con colágeno tipo II (CII), la proteína constituyente principal del cartílago articular. Después de la inmunización, los animales desarrollan una poliartritis autoinmunitaria que comparte varias características clínicas e histológicas con RA. La susceptibilidad a CIA en roedores está vinculada a las moléculas de la clase II del complejo mayor de histocompatibilidad (MHC), y la respuesta inmunitaria a CII está caracterizada por estimulación de las células T específicas del colágeno, y la producción de títulos altos del anticuerpo específico para el inmunógeno (CII heterólogo) y el autoantígeno (CII de ratón). La CIA murina,

histológicamente, está caracterizada por una sinovitis intensa que corresponde con el inicio clínico de la artritis. Estos datos experimentales son útiles para evaluar CIA debido a las similitudes patológicas entre CIA y RA.

5 **5.4. Modelo *In Vivo* Inducido por Antígeno de Proliferación de Células T:**

El uso de la transferencia adoptiva de las células T transgénicas del receptor de las células T (TCR) proporciona un modelo *in vivo* para la proliferación de
10 células T, inducida por antígeno. Pape et al., *Immunol. Rev.* 156: 67-78 (1997) describen la transferencia adoptiva de las células T transgénicas una TCR que expresan uniformemente una TCR identificable de una especificidad conocida de péptido/MHC. El modelo puede ser utilizado para monitorizar
15 el comportamiento *in vivo* de las células T específicas del antígeno. Las células T intactas, son inicialmente activadas dentro de zonas de las células T del tejido linfoide secundario para proliferar de una manera dependiente de B7. Si están presentes adyuvantes o citocinas inflamatorias
20 durante este periodo, números aumentados de células T se acumulan, migran hacia los folículos ricos en células B, y adquieren la capacidad para producir IFN- γ y ayudar a las células B a producir IgG2a. Si la inflamación es efectivamente antagonizada, la mayoría de las células T
25 específicas del antígeno, inicialmente activadas, desaparecen

sin entrar a los folículos, y las sobrevivientes son productoras pobres de IL-2 e IFN- γ .

EJEMPLOS

La TABLA 3 lista las secuencias de aminoácidos del dominio variable anti-CD40 humano, representativas, útiles para los polipéptidos anticuerpos de la descripción. La TABLA 4 describe los ácidos nucleicos representativos que codifican para las secuencias del dominio variable listadas en la TABLA 3. Como es bien conocido en la técnica, múltiples codones pueden codificar para el mismo aminoácido. Los ácidos nucleicos que codifican para una secuencia de proteínas que incluyen ácidos nucleicos que tienen degeneración de codón. Los polipéptidos anticuerpos descritos en la TABLA 3 se enlazan específicamente a CD40 y fueron elaborados utilizando la selección inicial/primaria reiterativa y las metodologías de maduración por afinidad descritas en los ejemplos siguientes.

TABLA 3

Secuencias de Aminoácidos del Dominio Variable Anti-CD40 Humano.

BMS3h-56-201

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA

DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFQEWGQGTLTVSS (SEQ

ID NO: 9)

BMS3h-56-258

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGTLVTVSS (SEQ
ID NO: 10)

5 BMS3h-37

EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKELGYFDYWGQGTLVTVSS (SEQ
ID NO: 11)

BMS3h-38

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISGSGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPFRFDYWGQGTLVTVSS (SEQ
ID NO: 12)

BMS3h-41

EVQLLESGGGLVQPGGSLRLSCAASGFTFTEYEMIWVRQAPGKGLEWVSSISGNGANTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPLRFDYWGQGTLVTVSS (SEQ
ID NO: 13)

BMS3h-43

EVQLLESGGGLVQPGGSLRLSCTASGFTFNMYEMSWVRQAPGKGLEWVSGISRRGFTTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPITYAMRYARFDYWGQGTLVTVS
20 S (SEQ ID NO: 14)

BMS3h-56

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFT
ISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFIFDYWGQGTLVTVSS (SEQ ID NO: 15)

BMS3h-106

25 EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYHMQWVRQAPGKGLEWVSMIDADGLGTYYA

DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKPGPQFGQFDYWGQGTLVTVSS

(SEQ ID NO: 16)

BMS3h-107

EVQLLESGGGLVQPGGSLRLSCAASGFTFSGYDMQWVRQAPGKGLEWVSTISASGVFTYYA

5 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKYPNRFALNNFDYWGQGTLVTVSS

(SEQ ID NO: 17)

BMS3h-131

DIQMTQSPSSLSASVGDRVITITCRANSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSR

FSGSGSGTDFTLTISLQPEDFATYYCVQNA GWPGTFGQGTKVEIKR (SEQ ID NO:

10 18)

BMS3h-193

DIQMTQSPSSLSASVGDRVITITCRASQTIERRLN WYQQKPGKAPKLLIYLASRLQSGVPSRFSG

SGSGTDFTLTISLQPEDFATYYCHQYASPLTFGQGTKVEIKR (SEQ ID NO: 19)

BMS3h-198

15 EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMWVRQAPGKGLERVSAISGSGGSTYYA

DSVKGRFTISRDD SKNTLYLQMNSLRAEDTAVYYCAKDPYSFDYWGQGTLVTVSS (SEQ
ID NO: 20)

BMS3h-202

EVQLLESGGGLVQPGGSLRLSCAASGFTFPTAEMWVRQAPGKGLEWVSSISASGGSTYYA

20 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPVSYVATFDYWGQGTLVTVSS

(SEQ ID NO: 21)

BMS3h-217

DIQMTQSPSSLSASVGDRVITITCRASHFIGTLLSWYQQKPGKAPKLLITYGSLQSGVPSR

FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO:

25 22)

BMS3h-1

EVQLLESGGGLVQPGGSLRLSCAASGFTTFPKNEMTWVRQAPGKGLEWVSAIESDGQATYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKNRIPDLVFDYWGQGTLVTVSS
(SEQ ID NO: 23)

5 BMS3h-2

EVQLLESGGGLVQPGGSLRLSCAASGFTFDAGAMTWVRQAPGKGLEWVSSIDKEGLSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGRI PGLVFDYWGQGTLVTVSS
(SEQ ID NO: 24)

BMS3h-3

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFGDAAMTWVRQAPGKGLEWVSAIQPMGDGTYADSVKGRFTVS
RDNSKNTLYLQMNSLRAEDTAVYYCAKGRIPTLQFDYWGQGTLVTVSS (SEQ ID NO: 25)

BMS3h-4

EVQLLESGGGLVQPGGSLRLSCAASGFTFEDSPMTWVRQAPGKGLEWVSAITSNGYETYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGRIPTLHFDYWGQGTLVTVSS

15 (SEQ ID NO: 26)

BMS3h-5

EVQLLESGGGLVQPGGSLRLSCAASGFTFDEHMSWVRQAPGKGLEWVSRIGPDGFHTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGRIPTLHFDYWGQGTLVTVSS
(SEQ ID NO: 27)

20 BMS3h-6

EVQLLESGGGLVQPGGSLRLSCAASGFTFGEYHMSWVRQAPGKGLEWVSRITPLGTLTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGRI PSLTFDYWGQGTLVTVSS
(SEQ ID NO: 28)

BMS3h-7

25 EVQLLESGGGLVQPGGSLRLSCAASGFTFGTNAMSWVRQAPGKGLEWVSRISPGGDYTYA

DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGRVPDLLFDYWGQGTLVTVSS

(SEQ ID NO: 29)

BMS3h-8

EVQLLES GGGGLVQPGGSLRLSCAASGFTFPSEEMSWVRQAPGKGLEWVSRISADGANTYYA

5 DSVKGRFTISRDN SKNTLYLQMNSLRAEDAAVYYCAKGRVPDLLFDYWGQGTLVTVSS

(SEQ ID NO: 30)

BMS3h-9

EVQLLES GGGGLVQPGGSLRLSCAASGFTFAEDDMTWVRQAPGKGLEWVSRIAVDGDRITYYA

DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGKVP SLHFDYWGQGTLVTVSS

10 (SEQ ID NO: 31)

BMS3h-10

EVQLLES GGGGLVQPGGSLRLSCAASGFTFRTMDMSWVRQAPGKGLEWVSRITGDGMNTYYA

DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGVTPDLTFDYWGQGTLVTVSS

(SEQ ID NO: 32)

15 BMS3h-11

EVQLLES GGGGLVQPGGSLRLSCAASGFTFERDDMTWVRQAPGKGLEWVSRINAGGVHTYYA

DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGVTPDLTFDYWGQGTLVTVSS

(SEQ ID NO: 33)

BMS3h-12

20 EVQLLES GGGGLVQPGGSLRLSCAASGFTFDDDSMTWVRQAPGKGLEWVSRISSDGASTYYA

DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGVTPDLTFDYWGQGTLVTVSS

(SEQ ID NO: 34)

BMS3h-13

EVQLLES GGGGLVQPGGSLRLSCAASGFTFTEEDMTWVRQAPGKGLEWVSRIDSVGEGTYYA

25 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGVTPDLTFDYWGQGTLVTVSS

(SEQ ID NO: 35)

BMS3h-14

EVQLLESGGGLVQPGGSLRLSCAASGFTFSDSAMSWVRQAPGKGLEWVSRIDNPGQHTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGTVP TLEFDYWGQGT LVTVSS

5 (SEQ ID NO: 36)

BMS3h-15

EVQLLESGGGLVQPGGSLRLSCAASGFTFGQHSMTWVRQAPGKGLEWVSRIDGGGYNTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGEV PRLHFDYWGQGT LVTVSS

(SEQ ID NO: 37)

10 BMS3h-16

EVQLLESGGGLVQPGGSLRLSCAASGFTFGQEPMTWVRQAPGKGLEWVSRIAYNGGDTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGIT PNLTFDYWGQGT LVTVSS

(SEQ ID NO: 38)

BMS3h-17

15 EVQLLESGGGLVQPGGSLRLSCAASGFTFENYPMSWVRQAPGKGLEWVSRINATGSITYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGVIP HLMFDYWGQGT LVTVSS

(SEQ ID NO: 39)

BMS3h-18

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYDMSWVRQAPGKGLEWVSRITGTGNSTYYA
20 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAQGVVP YLAFDYWGQGT LVTVSS

(SEQ ID NO: 40)

BMS3h-19

EVQLLESGGGLVQPGGSLRLSCAASGFTFEADAMTWVRQAPGKGLEWVSRINVDG
DRYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGTVP TLEFDYWG

25 QGT LVTVSS (SEQ ID NO: 41)

BMS3h-21

EVQLLESGGGLVQPGGSLRLSCAASGFTFDRADMTWVRQAPGKGLEWVSRISGEGKCTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGMV PNLVFDYWGQGTLVTVSS
(SEQ ID NO: 42)

5 BMS3h-22

EVQLLESGGGLVQPGGSLRLSCAASGFTFHWEPMSWVRQAPGKGLEWVSRINSSGWD TYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGMV PNLVFDYWGQGTLVTVSS
(SEQ ID NO: 43)

BMS3h-24

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFADEPMTWVRQAPGKGLEWVSRIPPEGAP TYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGITPNLTFDYWGQGTLVTVSS
(SEQ ID NO: 44)

BMS3h-26

EVQLLESGGGLVQPGGSLRLSCAASGFTFHNHDM SWVRQAPGKGLEWVSRISRGGLQ TYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGIVPDLHFDYWGQGTLVTVSS
(SEQ ID NO: 45)

BMS3h-27

EVQLLESGGGLVQPGGSLRLSCAASGFTFNEYPM SWVRQAPGKGLEWVSRINGDGANT YYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGII PAMQFDYWGQGTLVTVSS
20 (SEQ ID NO: 46)

BMS3h-28

EVQLLESGGGLVQPGGSLRLSCAASGFTFGDVPMS WVRQAPGKGLEWVSRIDPYGSNT YYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGIMPSLTFDYWGQGTLVTVSS
(SEQ ID NO: 47)

BMS3h-29

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFADYDMSWVRQAPGKGLEWVSRISALGATTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGQLPALEFDYWGQGTLVTVSS
(SEQ ID NO: 48)

5 BMS3h-30

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFKRYYMTWVRQAPGKDLEWVSGIVPSGNRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGRI PDLHFDYWGQGTLVTVSS
(SEQ ID NO: 49)

BMS3h-31

10 EVQLLES GGGGLVQP GGSRLRLSCAASGFTFADYDMTWVRQAPGKGLEWVSRISPTGGQTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGVIPYLSFSPFDYWGQGTLVTVSS
(SEQ ID NO: 50)

BMS3h-32

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFSKYWMGWARQAPGKGLEWVSSIDSHGAGTYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRVEDTAVYYCAKGAPKFMTTYTFDYWGQGTLVTVSS
(SEQ ID NO: 51)

BMS3h-33

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFLSYPMHWVRQAPGKGLEWVSSIDSRGSVTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGHSWTFDYWGQGTLVTVSS (SEQ
20 ID NO: 52)

BMS3h-34

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFANSNMTWVRQAPGKGLEWVSRINPDGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAEGRIPTLHFDYWGQGTLVTVSS
(SEQ ID NO: 53)

BMS3h-35

EVQLLESGGGLVQPGGSLRLSCAASGFTFGPRRMGWRQAPGKGLEWVSSIDDIGRRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAEGAQGVL LFDYWGQGTLVTVSS
(SEQ ID NO: 54)

5 BMS3h-36

EVQLLESGGGLVQPGGSLRLSCAASGFTFEDYRMVWVRQAPGKGLEWVSSISTSGELTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAETAGQFFDYWGQGTLVTVSS (SEQ
ID NO: 55)

BMS3h-39

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFPEYEMVWVRQAPGKGLEWVSAISREGRATYYA
DSVKGRFTISRDN SKNTLYLQMNNLRAEDTAVYYCAKEPVRFDYWGQGTLVTVSS (SEQ
ID NO: 56)

BMS3h-40

EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYEMLWVRQAPGKGLEWVSSISSSGNYTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPLMFDYWGQGTLVTVSS (SEQ
ID NO: 57)

BMS3h-42

EVQLLESGGGLVQPGGSLRLSCAASGFTFDTEEMSWVRQAPGKGLEWVSAISPNGAFTFYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPILFDYWGQGTLVTVSS (SEQ
20 ID NO: 58)

BMS3h-44

EVQLLESGGGLVQPGGSLRLSCAASGFTFGHYDMVWVRQAPGRGLEWVSTINGAGLNTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAQSASRIFDYWGQGTLVTVSS (SEQ
ID NO: 59)

BMS3h-45

EVQLLESGGGLVQPGGSLRLSCAASGFTFRSYEMAWVRQAPGKGLEWVSSISTLGTKTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAQSSTHIFDYWGQGLTVTVSS (SEQ
ID NO: 60)

5 BMS3h-46

EVQLLESGGGLVQPGGSLRLSCAASGFTFIRYEMAWVRQAPGKGLEWVSSISSSGWTTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKSDAHIFDYWGQGLTVTVSS (SEQ
ID NO: 61)

BMS3h-47

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFYAYEMAWVRQAPGKGLEWVSSISDDGTRTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDLGQGFYWGQGLTVTVSS (SEQ
ID NO: 62)

BMS3h-48

EVQLLESGGGLVQPGGSLRLSCAASGFTFADHGMTWVRQAPGKGLEWVSGIGPSGEATYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDRI PNLFYWGQGLTVTVSS
(SEQ ID NO: 63)

BMS3h-49

EVQLLESGGGLVQPGGSLRLSCAASGFTFESQDMSWVRQAPGKGLEWVSGISPNGWDTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDRSDFDYWGQGLTVTVSS (SEQ
20 ID NO: 64)

BMS3h-50

EVQLLESGGGLVQPGGSLRLSCAASGFTFGDYDMWWVRQAPGKGLEWVSRIRHPGGVTTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKAVPKGFYWGQGLTVTVSS (SEQ
ID NO: 65)

BMS3h-51

EVQLLESGGGLVQPGGSLRLSCAASGFTFRVYWMTWVRQAPGKGLEWVSSIDPQGGMTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKARIPNLEFDYWGQGTLVTVSS
(SEQ ID NO: 66)

5 BMS3h-52

EVQLLESGGGLVQPGESLRLSCAASGFTFSAYDMTWVRQAPGKGLEWVSRINPTGSYTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKAKIPNLVFDYWGQGTLVTVSS
(SEQ ID NO: 67)

BMS3h-53

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFADSEMMWVRQAPGKGLEWVSGIAHNGGHTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKAGHPQQTEAFDYWGQGTLVTVSS
(SEQ ID NO: 68)

BMS3h-54

EMQLLESGGGLVQPGGSLRLSCAASGFTFATYDMYWVRQAPGKGLEWVSKISPNGWSTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKYQTHFDYWGQGTLVTVSS (SEQ
ID NO: 69)

BMS3h-55

EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYDMRWVRQAPGKGLEWVSTISSSGTYTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKYPKNFDYWGQGTLVTVSS (SEQ
20 ID NO: 70)

BMS3h-57

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHEDMTWVRQAPGKGLEWVSSISPNGWDTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKRTRSKFDYWGQGTLVTVSS (SEQ
ID NO: 71)

BMS3h-58

EVQLLESGGGLVQPGGSLRLSCAASGFTFEKYIMGWARQAPGKGLEWVSTIDYWGQHTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKRSHLIPLQFDYWGQGTLVTVSS
(SEQ ID NO: 72)

5 BMS3h-59

EVQLLESGGGLVQPGGSLRLSCAASGFTFSDYAMGWVRQAPGKGLEWVSTISYVGYYTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKKALRGEAFTERFDYWGQGTLVTVS
S (SEQ ID NO: 73)

BMS3h-60

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFGPYMMHWVRQAPGKGLEWVSTIEVNGNRITYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKWVGSKTSSDKSFDYWGQGTLVTVS
S (SEQ ID NO: 74)

BMS3h-61

EVQLLESGGGLVQPGGSLRLSCAASGFTFGTTEMAWVRQAPGKGLEWVSSIGSAGAWTYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKIGGHPQGQFDYWGQGTLVTVSS
(SEQ ID NO: 75)

BMS3h-62

EVQLLESGGGLVQPGGSLRLSCAASGFTFPREWMAWVRQAPGKGLEWVSSIQPMGQTTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKYSRNKGFFDYWGQGTLVTVSS
20 (SEQ ID NO: 76)

BMS3h-63

EVQLLESGGGLVQPGGSLRLSCAASGFTFTSEYMGWVRQAPGKGLEWVSSIQRYGSTTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHESNWETFDYWGQGTLVTVSS
(SEQ ID NO: 77)

BMS3h-70

EVQLLESGGGLVQPGGSLRLSCAASGFTFSVYSMQWVRQAPGKGLEWVSAITPNGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKTLGRGSYPGVDFDYWGQGTLVTVS
S (SEQ ID NO: 78)

5 BMS3h-71

EVQLLESGGGLVQPGGSLRLSCAASGFTFPSYAMTWVRQAPGKGLEWVSRITADGTVTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGSIPMLTFDYWGQGTLVTVSS
(SEQ ID NO: 79)

BMS3h-72

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFSTYDMIWVRQAPGKGLEWVSAISPNGTGIYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKNQSVHHAVFDYWGQGTLVTVSS
(SEQ ID NO: 80)

BMS3h-73

EVQLLESGGGLVQPGGSLRLSCAASGFTFENYEMTWVRQAPGKGLEWVSRIAPHGRLTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGQIPMLDFDYWGQGTLVTVSS
(SEQ ID NO: 81)

BMS3h-74

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYMMMWVRQAPGKGLEWVSTISHFGDITYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKNDMMKNGGFDYWGQGTLVTVSS
20 (SEQ ID NO: 82)

BMS3h-75

EVQLLESGGGLVQPGGSLRLSCAASGFTFERYDMSWVRQAPGKGLEWVSRIDSRGWSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGLVPHLRFDYWGQGTLVTVSS
(SEQ ID NO: 83)

BMS3h-76

EVQLLESGGGLVQPGGSLRLSCAASGFTFANAQMTWVRQAPGKGLEWVSRIDAMGDATYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGKVP SIDYWGQGT LVTVSS (SEQ
ID NO: 84)

5 BMS3h-77

EVQLLESGGGLVQPGGSLRLSCAASGFTFANAQMTWVRQAPGKGLEWVSRIDAMGDATYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGVIPAFDYWGQGT LVTVSS (SEQ
ID NO: 85)

BMS3h-78

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFQNDRMHWVRQAPGKGLEWVSSISATGGDTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKQTGTNRFDYWGQGT LVTVSS
(SEQ ID NO: 86)

BMS3h-79

EVQLLESGGGLVQPGGSLRLSCAASGFTFNQPYMSWVRQAPGKGLEWVSSIDASGGTTYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDAAVYYCAKDRI PNLVFDYWGQGT LVTVSS
(SEQ ID NO: 87)

BMS3h-80

EVQLLESGGGLVQPGGSLRLSCAASGFTFDNENMTWVRQAPGKGLEWVSRIDGGGYNTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGQVPELLFDYWGQGT LVTVSS
20 (SEQ ID NO: 88)

BMS3h-81

EVQLLESGGGLVQPGGSLRLSCAASGFTFVSSNMTWVRQAPGKGLEWVSAISGSGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGRIPTLVFDYWGQGT LVTVSS
(SEQ ID NO: 89)

BMS3h-82

EVQLLESGGGLVQPGGSLRLSCAASGFTFVSSNMTWVRQAPGKGLEWVSAISGSGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDRIPNLVFDYWGQGTLVTVSS
(SEQ ID NO: 90)

5 BMS3h-83

EVQLLESGGGLVQPGGSLRLSCAASGFTFSDDSMSWVRQAPGKGLEWVSRINDAGSSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGTIPLLEFDYWGQGTLVTVSS
(SEQ ID NO: 91)

BMS3h-84

10 EMQLLESGGGLVQPGGSLRLSCAASGFTFVSDTMSWVRQAPGKGLEWVSRIDGTGGDTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAGDTAVYYCAKGLIPDLQFDYWGQGTLVTVSS
(SEQ ID NO: 92)

BMS3h-85

EVQLLESGGGLVQPGGSLRLSCAASGFTFDEEEMTWVRQAPGKGLEWVSRIIGGGHETYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGTIPLLEFDYWGQGTLVTVSS
(SEQ ID NO: 93)

BMS3h-86

EVQLLESGGGLVQPGGSLRLSCAASGFTFDNENMTWVRQAPGKDLEWVSRITERGDVTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGTVP TLEFDYWGQGTLVTVSS
20 (SEQ ID NO: 94)

BMS3h-87

EVQLLESGGGLVQPGGSLRLSCAASGFTFDEEEMTWVRQAPGKGLEWVSRIIGGGHETYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGTVP TLEFDYWGQGTLVTVSS
(SEQ ID NO: 95)

BMS3h-88

EVQLLESGGGLVQPGGSLRLSCAASGFTTFHETEMTWVRQAPGKGLEWVSAINRLGQDTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGRI PGLVFDYWGQGTLVTVSS
(SEQ ID NO: 96)

5 BMS3h-89

EVQLLESGGGLVQPGGSLRLSCAASGFTFSDDSMSWVRQAPGKGLEWVSRINDAGSSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGTVP TLEFDYWGQGTLVTVSS
(SEQ ID NO: 97)

BMS3h-90

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFDNENMTWVRQAPGKDLEWVSRITERGDVTTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGRI PTLVFDYWGQGTLVTVSS
(SEQ ID NO: 98)

BMS3h-91

EVQLLESGGGLVQPGGSLRLSCAASGFTFSDDSMSWVRQAPGKGLEWVSRINDAGSSTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGITPNLTFDYWGQGTLVTVSS
(SEQ ID NO: 99)

BMS3h-92

EVQLLESGGGLVQPGGSLRLSCAASGFTFADEPMTWVRQAPGKGLEWVSRIPPEGAPTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGLIPDLQFDYWGQGTLVTVSS
20 (SEQ ID NO: 100)

BMS3h-93

EVQLLESGGGLVQPGGSLRLSCAASGFTFQDSDMTWVRQAPGKGLEWVSAIAAPGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDRI PNLRFDYWGQGTLVTVSS
(SEQ ID NO: 101)

BMS3h-94

EVQLLESGGGLVQPGGSLRLSCAASGFTFVSDTMSWVRQAPGKGLEWVSRIDGTGGDTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGQVPELLFDYWGQGTLVTVSS
(SEQ ID NO: 102)

5 BMS3h-95

EVQLLESGGGLVQPGGSLRLSCAASGFTFQSDMTWVRQAPGKGLEWVSAIAAPGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDRI PNLFVDYWGQGTLVTVSS
(SEQ ID NO: 103)

BMS3h-96

10 EVQLLESGGGLVQPGGSLRLSCAAAGFTFDLAEMTWVRQAPGKGLEWVSRIDEDGASTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDAAVYYCAEGVIPSLTFDYWGQGTLVTVSS
(SEQ ID NO: 104)

BMS3h-97

EVQLLESGGGLVQPGGSLRLSCAASGFTFTDKHMSWVRQAPGKGLEWVSRISPDGTYTYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDAAVYYCAEGVIPSLTFDYWGQGTLVTVSS
(SEQ ID NO: 105)

BMS3h-98

EVQLLESGGGLVQPGGSLRLSCAASGFTFAEDDMTWVRQAPGKGLEWVSRIAVDGDRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRTEDTAVYYCAKGKTPHLVFDYWGQGTLVTVSS
20 (SEQ ID NO: 106)

BMS3h-99

EVQLLESGGGLVQPGGSLRLSCAAAGFTFDLAEMTWVRQAPGKGLEWVSRIDEDGASTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGQVPALVFDYWGQGTLVTVSS
(SEQ ID NO: 107)

BMS3h-100

EVQLLESGGGLVQPGGSLRLSCAASGFTTFEDSMMSWVRQAPGKGLEWVSRIDPGGAQTYYA
 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGVTPDLTFDYWGQGTLVTVSS
 (SEQ ID NO: 108)

5 BMS3h-101

EVQLLESGGGLVQPGGSLRLSCAASGFTTFEHADMSWVRQASGKGLEWVSRIDNSGQSTYYA
 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGVTPDLTFDYWGQGTLVTVSS
 (SEQ ID NO: 109)

BMS3h-102

10 EVQLLESGGGLVQPGGSLRLSCAASGFTTFSEAEMNWVRQAPGKGLEWVSRITTDGDSTYYA
 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGRIPTLHFDYWGQGTLVTVSS
 (SEQ ID NO: 110)

BMS3h-103

EVQLLESGGGLVQPGGSLRLSCAASGFTTFDDSDMTWVRQAPGKSLEWVSYIRGDDDETYYA
 15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKNRIPDLVFDYWGQGTLVTVSS
 (SEQ ID NO: 111)

BMS3h-108

EVQLLESGGGLVQPGGSLRLSCAASGFTTFNVADMQWVRQAPGKGLEWVSSISPNGWDTYYA
 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKHASTEPTAFDYWGQGTLVTVSS
 20 (SEQ ID NO: 112)

BMS3h-109

EVQLLESGGGLVQPGGSLRLSCAASGFTTFGPYDMGWVRQAPGKGLEWVSWISAHGSFTYYA
 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKWPKFDYWGQGTLVTVSS (SEQ
 ID NO: 113)

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BMS3h-110

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFGSGSMSWVRQAPGKGLEWVSRIGSNGADTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGMV PNLVFDYWGQGTLVTVSS
(SEQ ID NO: 114)

5 BMS3h-111

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFNRFDMTWVRQAPGKGLEWVSAISGSGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDRI PNLVFDYWGQGTLVTVSS
(SEQ ID NO: 115)

BMS3h-112

10 EVQLLES GGGGLVQP GGSRLRLSCAASGFTFGESDMKWVRQAPGKGLEWVSSISPNGWDTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKSPSSRLKF DYWGQGTLVTVSS
(SEQ ID NO: 116)

BMS3h-139

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFDSSEMSWVRQAPGKGLEWVSSIENQGGATYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDRI PNLVFDYWGQGTLVTVSS
(SEQ ID NO: 117)

BMS3h-140

EVQLLES GGGGLVQP GGSRLRLSCAASGFTLDAYPMYWVRQAPGKGLEWVSWIASGGGATYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKRTKNFDYWGQGTLVTVSS (SEQ
20 ID NO: 118)

BMS3h-141

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFMSYSMAWVRQAPGKGLEWVSGITSNGNRITYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKSTGANSRNF DYWGQGTLVTVSS
(SEQ ID NO: 119)

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BMS3h-142

EVQLLES GGGGLVQP GGS LRLSCAASGFTTFEGY LMSWVRQAPGKGLEWVSSIAANGMQTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKKPRGIWDGDFDYWGQGTLVTVSS
(SEQ ID NO: 120)

5 BMS3h-143

EVQLLES GGGGLVQP GGS LRLSCAASGFTTFHESTM TWVRQAPGKGLEWVSTIRHPGEFTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAGDTAVYYCAKGLIPDLQFDYWGQGTLVTVSS
(SEQ ID NO: 121)

BMS3h-144

10 EVQLLES GGGGLVQP GGS LRLSCAASGFTTFAMYSMSWVRQAPGKGLEWVSSIAPPGGRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKQSLTGYSRSFDYWGQGTLVTVSS
(SEQ ID NO: 122)

BMS3h-145

EVQLLES GGGGLVQP GGS LRLSCAASGFTTFSQNPM SWVRHAPGKGLEWVSTIPANGRPTSYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKYSQQPGRRFDYWGQGTLVTVSS
(SEQ ID NO: 123)

BMS3h-146

EVQLLES GGGGLVQP GGS LRLSCAASGFTTFANYHMTWVRQAPGKGLEWVSSIPDSGKQTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGRIPSLLFDYWGQGTLVTVSS
20 (SEQ ID NO: 124)

BMS3h-147

EVQLLES GGGGLVQP GGS LRLSCAASGFTTFAQYHMRWVRQAPGKGLEWVSTINDIGSNTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKVGGRGSFSFDYWGQGTLVTVSS
(SEQ ID NO: 125)

BMS3h-148

EVQLLES GGGGLVQPGGSLRLSCAASGFTFSSYDMKWVRQAPGKGLEWVSTISASGVFTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKREHAGQPPFDYWGQGTLVTVSS
(SEQ ID NO: 126)

5 BMS3h-149

EVQLLES GGGGLVQPGGSLRLSCAASGFTFNGYAMSWVRQAPGKGLEWVSTINANGKYTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKKLTLASNYFDYWGQGTLVTVSS
(SEQ ID NO: 127)

BMS3h-150

10 EVQLLES GGGGLVQPGGSLRLSCAASGFTFMDYDMKWVRQAPGKGLEWVSSITALGKKTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDSVKYPLNLFDYWGQGTLVTVSS
(SEQ ID NO: 128)

BMS3h-151

EVQLLES GGGGLVQPGGSLRLSCAASGFTFPHYTMAWVRQAPGKGLEWVSSIQSPGWRTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKYGDGLPLTFDYWGQGTLVTVSS
(SEQ ID NO: 129)

BMS3h-167

EVQLLES GGGGLVQPGGSLRLSCAASGFTFSGTPMSWVRQAPGKGLEWVSRIGDEGQETYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGVTPDLTFDYWGQGTLVTVSS
20 (SEQ ID NO: 130)

BMS3h-168

EVQLLES GGGGLVQPGGSLRLSCAASGFTFSSSSMSWVRQAPGKGLEWVSAIGSDGPSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGRIPTLHFDYWGQGTLVTVSS
(SEQ ID NO: 131)

BMS3h-169

EVQLLESGGGLVQPGGSLRLSCAASGFTFNPGEMTWVRQAPGKGLEWVSSIDGSGSSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRADDTAVYYCAKGRIPTLHFDYWGQGTLVTVSS
(SEQ ID NO: 132)

5 BMS3h-170

EVQLLESGGGLVQPGGSLRLSCAASGFTFPESMMGWVRQAPGKGLEWVSSIGYPGATYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGSRDDNFDYWGQGTLVTVSS
(SEQ ID NO: 133)

BMS3h-171

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFGQHSMDWVRQAPGKGLEWVSSISVPGPKTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKSLRDLRPGDSKSFYWGQGTLVTV
SS (SEQ ID NO: 134)

BMS3h-197

EVQLLESGGGLVQPGGSLRLSCAASGFTFGSAAMDWVRQAPGKGLEWVSSINDMGSNTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKQGGRFYWGQGTLVTVSS (SEQ
ID NO: 135)

BMS3h-199

EVQLLESGGGLVQPGGSLRLSCAASGFTFGYDRMAWVRQAPGKGLEWVSSIDGPGGATYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAEGRRVPDFDYWGQGTLVTVSS
20 (SEQ ID NO: 136)

BMS3h-200

EVQLLESGGGLVQPGGSLRLSCAASGFTFGYEMTWVRQAPGKGLEWVSRIDPFGSETYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAEGVVPDLNFDYWGQGTLVTVSS
(SEQ ID NO: 137)

BMS3h-201

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFDKYVMGWVRQAPGKGLEWVSTIGSYGGATYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKRLTLSATKFDYWGQGTLVTVSS
(SEQ ID NO: 138)

5 BMS3h-203

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFEDYVMGWVRQAPGKGLEWVSTIAHRGDITYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKRRRLSDYRFDYWGQGTLVTVSS
(SEQ ID NO: 139)

BMS3h-204

10 EVQLLES GGGGLVQP GGSRLRLSCAASGFTFGQFDYVMGWVRQAPGKGLEWVSAISPAGTGITYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKAGDRSSLFDYRGQGTLVTVSS
(SEQ ID NO: 140)

BMS3h-205

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFKDTGMTWVRQAPGKGLEWVSSISSYGRDITYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDA AVYYCAKLNAALGFDYWGQGTLVTVSS
(SEQ ID NO: 141)

BMS3h-206

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFGPYPMWVRQAPGKGLEWVSGINAPGTRITYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAQQMSSGVFDYWGQGTLVTVSS
20 (SEQ ID NO: 142)

BMS3h-207

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFSNQDMTWVRQAPGKGLEWVSSIDSSGQLITYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKVKSLARFDYWGQGTLVTVSS
(SEQ ID NO: 143)

BMS3h-208

EVQLLESGGGLVQPGGSLRLSCAASGFTTFPESDMKWVRQAPGKGLEWVSSISPNGWDTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKPAQVLFDYWGQGTLVTVSS (SEQ
ID NO: 144)

5 BMS3h-209

EVQLLESGGGLVQPGGSLRLSCAASGFTTFEQYVMGWVRQAPGKGLEWVSTIGTSGKYTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAQRRSLTRVHFDYWGQGTLVTVSS
(SEQ ID NO: 145)

BMS3h-210

10 EVQLLESGGGLVQPGGSLRLSCAASGFTTFGVEHMSWVRQAPGKGLEWVSAITGDGDRTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKTVSWNGRFDYWGQGTLVTVSS
(SEQ ID NO: 146)

BMS3h-211

EVQLLESGGGLVQPGGSLRLSCAASGFTFAWYNMGWVRQAPGKGLEWVSRIAPSGIITYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGLRGKFDYWGQGTLVTVSS (SEQ
ID NO: 147)

BMS3h-212

EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYEMRWVRQAPGKGLEWVSSISSAGTDITYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKQSLNFDYWGQGTLVTVSS (SEQ
20 ID NO: 148)

BMS3h-213

EVQLLESGGGLVQPGGSLRLSCVASGFTFDEEPMTWVRQAPGKGLEWVSIIDPGGGATYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKSNSMFDYWGQGTLVTVSS (SEQ
ID NO: 149)

BMS3h-214

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFSAYPMHWVRQAPGKGLEWVSSIASSGITTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKFTRLHFPAQFDYWGQGTLVTVSS
(SEQ ID NO: 150)

5 BMS3h-215

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFADYAMGWVRQAPGKGLEWVSRISPEGSRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLRPYASKFDYWGQGTLVTVSS
(SEQ ID NO: 151)

BMS3h-230

10 EVQLLES GGGGLVQP GGSRLRLSCAASGFTFRPYDMGWVRQAPGKGLEWVSTISHQGNRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKVSHHFDYWGQGTLVTVSS (SEQ
ID NO: 152)

BMS3h-231

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFSAYNMWWARQAPGKGLEWVSWINSTGSRTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKNWHRGRFDYWGQGTLVTVSS
(SEQ ID NO: 153)

BMS3h-232

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFDYRMGWVRQAPGKGLEWVSTINRLGQSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKVKKHKFDYWGQGTLVTVSS (SEQ
20 ID NO: 154)

BMS3h-233

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFAHYNMRWVRQAPGKGLEWVSTITKTGFRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKAGQFDFDYWGQGTLVTVSS (SEQ
ID NO: 155)

BMS3h-234

EVQLLESGGGLVQPGGSLRLSCAASGFTFYPYSMHWVRQAPGKGLEWVSTIDGSGMFTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAEDSLKASFDYWGQGLTVTVSS
(SEQ ID NO: 156)

5 BMS3h-235

EVQLLESGGGLVQPGGSLRLSCAASGFTFPLYGMWWVRQAPGKGLEWVSYIGPYGHTTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKKRKKKFDYWGQGLTVTVSS (SEQ
ID NO: 157)

BMS3h-236

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFPRYRMSWVRQAPGKGLEWVSSITPYGAHTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKYGKWYFDYWGQGLTVTVSS (SEQ
ID NO: 158)

BMS3h-237

EVQLLESGGGLVQPGGSLRLSCAASGFTFNEYAMRWVRQAPGKGLEWVSTIDRLGLHTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKSGPFTFDYWGQGLTVTVSS (SEQ
ID NO: 159)

BMS3h-238

EVQLLESGGGLVQPGGSLRLSCAASGFTFERYNMRWVRQAPGKGLEWVSTIDRLGLATYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKAGSWSFDYWGQGLTVTVSS (SEQ
20 ID NO: 160)

BMS3h-239

EVQLLESGGGLVQPGGSLRLSCAASGFTFGIYDMKWVRQAPGKGLEWVSTISSSGHTTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKYPQYPFDYWGQGLTVTVSS
(SEQ ID NO: 161)

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BMS3h-240

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFWVYDMRWVRQAPGKGLEWVSTISATGVHTYYA
 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKYPPAGRFDYWGQGTLVTVSS
 (SEQ ID NO: 162)

5 BMS3h-241

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFSTYDMIWVRQAPGKGLEWVSAISPNGTGTYA
 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKPPQVNTTEFDYRGQGTLVTVSS
 (SEQ ID NO: 163)

BMS3h-243

10 EVQLLES GGGGLVQP GGSRLRLSCAASGFTFEKEDMGWVRQAPGKGLEWVSHISPNGYATYYA
 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKSWSSFYWGQGTLVTVSS (SEQ
 ID NO: 164)

BMS3h-244

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFSATPMEWARQAPGKGLEWVSTISESGYSTYYA
 15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKWNSTTGFDYWGQGTLVTVSS
 (SEQ ID NO: 165)

BMS3h-245

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFNTVDMEWVRQAPGKGLEWVSSISPNGWDTYYA
 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAEAPHRAFDYWGQGTLVTVSS (SEQ
 20 ID NO: 166)

BMS3h-246

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFEDKEMSWVRQAPGKGLEWVSRIDALGDSTYYA
 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAEGMVPRLKFDYWGQGTLVTVSS
 (SEQ ID NO: 167)

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BMS3h-247

EVQLLESGGGLVQPGGSLRLSCAASGFTFSDHSMWVRQAPGKGLEWVSDIEPHGVHTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCANPTFDYWGQGTLVTVSS (SEQ ID
NO: 168)

5 BMS3h-248

EVQLLESGGGLVQPGGSLRLSCAASGFTFSPHTMHWVRQAPGKGLEWVSGIGPDGTTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKRSYSWDRGWTFDYWGQGTLVTVSS
(SEQ ID NO: 169)

BMS3h-249

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFYASDMKWVRQAPGKGLEWVSSISPNGWDTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKADYTYHSFDYWGQGTLVTVSS
(SEQ ID NO: 170)

BMS3h-250

EVQLLESGGGLVQPGGSLRLSCAASGFTFAHYNMRWVRQAPGKGLEWVSTITKTGFRTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKAGQFDFDYWGQGTLVTVSS (SEQ
ID NO: 171)

BMS3h-251

EVQLLESGGGLVQPGGSLRLSCAASGFTFSHYHMGWARQAPGKGLEWVSVIGPRGISTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKSPSRHRFDYWGQGTLVTVSS
20 (SEQ ID NO: 172)

BMS3h-252

EVQLLESGGGLVQPGGSLRLSCAASGFTFNEYAMRWVRQAPGKGLEWVSTIDRLGLHTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKSGPFTFDYWGQGTLVTVSS (SEQ
ID NO: 173)

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BMS3h-253

EVQLLESGGGLVQPGGSLRLSCAASGFTFGNYSMKWARQAPGKGLEWVSTITPDGWYTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKVGDAVWGWIGGFDYWGQGTLVTVS
S (SEQ ID NO: 174)

5 BMS3h-254

EVQLLESGGGLVQPGGSLRLSCAASGFTFGDYGMKWVRQAPGKGLEWVSAITSNGDFTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKSLYKFDYWGQGTLVTVSS (SEQ
ID NO: 175)

BMS3h-255

10 EVQLLESGGGLVQPGGSLRLSCAGSGFTFPTYKMGWVRQAPGKGLEWVSFIDYWGWRYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKSPYSWTHDSPHFDYWGQGTLVTVS
S (SEQ ID NO: 176)

BMS3h-256

EVQLLESGGGLVQPGGSLRLSCAASGFTFRPYTMCWARQAPGKGLEWVSCISDAGSFTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKRMSSFYWGQGTLVTVSS (SEQ
ID NO: 177)

BMS3h-257

EVQLLESGGGLVQPGGSLRLSCAASGFTFQNYQMAWVRQAPGKGLEWVSTISGTGKNTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKTPQNYFSVRRFDYWGQGTLVTVSS
20 (SEQ ID NO: 178)

BMS3h-258

EVQLLESGGGLVQPGGSLRLSCAASGFTFGAYTMGWVRQAPGKGLEWVSKISTSGGQTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKPLNWWAFDYWGQGTLVTVSS
(SEQ ID NO: 179)

25

BMS3h-272

EVQLLESGGGLVQPGGSLRLSCAASGFTFNAYPMTWVRQAPGKGLEWVSRIDGYGRHTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGIIPNFDYWGQGLTVTVSS (SEQ
ID NO: 180)

5 BMS3h-273

EVQLLESGGGLVQPGGSLRLSCAASGFTFGAVDMTWVRQAPGKGLEWVSAISPSGSATYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGRVPDLGFDYWGQGLTVTVSS
(SEQ ID NO: 181)

BMS3h-274

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFDSYAMGWARQAPGKGLEWVSAIGAKGLSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKAARGKFDYWGQGLTVTVSS (SEQ
ID NO: 182)

BMS3h-275

EVQLLESGGGLVQPGGSLRLSCAASGFTFTRYQMGWVRQAPGKGLEWVSVINVWGSSTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKMSGKFAYWGQGLTVTVSS (SEQ
ID NO: 183)

BMS3h-276

EVQLLESGGGLVQPGGSLRLSCAASGFTFGNYSMMWVRQAPGKGLEWVSTIIPAGTSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKPSIRLFDYWGQGLTVTVSS (SEQ
20 ID NO: 184)

BMS3h-279

EVQLLESGGGLVQPGGSLRLSCAASGFTFGAYDMGWVRQAPGKGLEWVSWISPNGYDYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGGVKFDYWGQGLTVTVSS (SEQ
ID NO: 185)

25

BMS3h-282

EVQLLES GGGGLVQP GGS LRLSCAASGFTFVWYEMAWVRQAPGKGLEWVSTIQADGEQTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKASYALVYPPEEFDYWGQGTLVTVS
S (SEQ ID NO: 186)

5 BMS3h-287

EVQLLES GGGGLVQP GGS LRLSCAASGFTFTNYRMSWVRQAPGKGLEWVSAIDDLGVSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKWRLKNSQPTDFDYWGQGTLVTVSS
(SEQ ID NO: 187)

BMS3h-292

10 EVQLLES GGGGLVQP GGS LRLSCAASGFTFDQAHMWWVRQAPGKGLEWVSFINPSGYITYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKPSLSPSSFYWGQGTLVTVSS
(SEQ ID NO: 188)

BMS3h-293

EVQLLES GGGGLVQP GGS LRLSCAASGFTFETGQMGWARQAPGKGLEWVSNIDGSGTYITYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKSTQNYRFDYWGQGTLVTVSS
(SEQ ID NO: 189)

BMS3h-296

EVQLLES GGGGLVQP GGS LRLSCAASGFTFGAYPMYWVRQAPGKGLEWVSSIHKDGRITYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKQGTPVDGFDYWGQGTLVTVSS
20 (SEQ ID NO: 190)

BMS3h-297

EVQLLES GGGGLVQP GGS LRLSCAASGFTFPDEGMTWVRQAPGKGLEWVSTIETGGTVITYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKMDGSGTWQTFDYWGQGTLVTVSS
(SEQ ID NO: 191)

BMS3h-298

EVQLLESGGGLVQPGGSLRLSCAASGFTFDSLGMGWARQAPGKGLEWVSYIRAEGAYTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKYLADSDYWGQGTLVTVSS (SEQ
ID NO: 192)

5 BMS3h-299

EVQLLESGGGLVQPGGSLRLSCAASGFTFSESYMEWVRQAPGKGLEWVSGIDHIGGGTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDDGRGGSMFDYWGQGTLVTVSS
(SEQ ID NO: 193)

BMS3h-300

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFSGGYMWWVRQAPGKGLEWVSSIGASGAYTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKTGGRLDYWGQGTLVTVSS (SEQ
ID NO: 194)

BMS3h-301

EVQLLESGGGLVQPGGSLRLSCAASGFTFDEGHMGWVRQAPGKDLEWVSYIGSLGLHTTYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKREFSNGGFDYWGQGTLVTVSS
(SEQ ID NO: 195)

BMS3h-302

EVQLLESGGGLVQPGGSLRLSCAASGFTFKTSPMYWVRQAPGKGLEWVSSIDRTGGHTTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKQALLTDAKRFDYWGQGTLVTVSS
20 (SEQ ID NO: 196)

BMS3h-303

EVQLLESGGGLVQPGGSLRLSCAASGFTFDGRDMWVRQAPGKGLEWVSAISPSGLDITYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAERPQMLVTNFDYWGQGTLVTVSS
(SEQ ID NO: 197)

BMS3h-304

EVQLLESGGGLVQPGGSLRLSCAASGFTFGNDPMSWVRQAPGKGLEWVSGIGREGDSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDSMRHQPFQDYWGQGTLVTVSS
(SEQ ID NO: 198)

5 BMS3h-305

EVQLLESGGGLVQPGGSLRLSCAASGFTFDETYMKWVRQAPGKGLEWVSAIGASGADTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKFTHLNGRFDYWGQGTLVTVSS
(SEQ ID NO: 199)

BMS3h-306

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFGGWPMGWVRQAPGKGLEWVSGIDIDGAPTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEEAGSWSFDYWGQGTLVTVSS
(SEQ ID NO: 200)

BMS3h-307

EVQLLESGGGLVQPGGSLRLSCAASGFTFSDQAMWWARQAPGKGLEWVSFIQGDGGFTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKPSKPFQDYWGQGTLVTVSS (SEQ
ID NO: 201)

BMS3h-308

EVQLLESGGGLVQPGGSLRLSCAASGFTFETGQMGWARQAPGKGLEWVSNIDGSGTYTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKAVRNFAFDYWGQGTLVTVSS
20 (SEQ ID NO: 202)

BMS3h-309

EVQLLESGGGLVQPGGSLRLSCAASGFTFSGHMSWVRQAPGKGLEWVSAISPHGHTHTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGIRGWIGHDTQPFQDYWGQGTLVTV
SS (SEQ ID NO: 203)

BMS3h-310

EVQLLESGGGLVQPGGSLRLSCAASGFTTFESKDMLWVRQAPGKGLEWVSSISSDGTHTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAQELGGSWQFDYWGQGTLVTVSS
(SEQ ID NO: 204)

5 BMS3h-311

EVQLLESGGGLVQPGGSLRLSCAASGFTTFADRDMLWVRQAPGKGLEWVSGIGASGTSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDAAVYYCAKGGTGPTDLWDFDYWGQGTLVTVSS
(SEQ ID NO: 205)

BMS3h-312

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFDDEKMLWVRQAPGKGLEWVSSISVSGLHTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEEAGSWSFDYWGQGTLVTVSS
(SEQ ID NO: 206)

BMS3h-313

EVQLLESGGGLVQPGGSLRLSCAASGFTFGQERMIWVRQAPGKGLEWVSDISASGGTTYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEEAGSWSFDYWGQGTLVTVSS
(SEQ ID NO: 207)

BMS3h-37-1

EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYA
DSVKGRFTISRDN SMNTLYLQMNSLRAEDTAVYYCAKELGYFDYRGRGTLVTVSS (SEQ
20 ID NO: 208)

BMS3h-37-2

EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRRAPGKGLEWVSAISGDGYRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKELGYFDYWGRGTLVTVSS (SEQ
ID NO: 209)

BMS3h-37-3

EVQLLES GGGGLVQPGGSLRLSCAASGFTFEWYEMQWRRAPGKGLEWVSAISGDGYRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKELGYFDYRVQGTLTVSS (SEQ
ID NO: 210)

5 BMS3h-37-4

EVQLLES GGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRKAPGKGLEWVSAISGDGYRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKELGYFDYWGRGTLTVSS (SEQ
ID NO: 211)

BMS3h-37-5

10 EVQLLES GGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWISAISGDGYRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKELGYFDYRVQGTLTVSS (SEQ
ID NO: 212)

BMS3h-37-6

EVQLLES GGGGLVQPGGSLRLSCAASGFTFEWYEMQWRRAPGKGLEWVSAISGDGYRTYYA
15 DSVKGRFTISRDN SENTLYLQMNSLRAEDTAVYYCAKELGYFDYWGRGTLTVSS (SEQ
ID NO: 213)

BMS3h-37-7

EVQLLETGGGLVQPGGSLRLSCAASGFTFEWYEMQWRRAPGKGLEWVSAISGDGYRTYYA
DSVKGRFTISRDN SKNTLYLQMDSLRAEDTAVYYCAKELGYFDYWGRGTLTVTS (SEQ
20 ID NO: 214)

BMS3h-37-8

EVQLLES GGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRQAPGKGLEWVSAISGDGYRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKELGYFHYWGRGTLTVSS (SEQ
ID NO: 215)

BMS3h-37-9

EVQLLES GGGGLVQP GGS LRLSCV ASGFTFEWYEMQWVRQAPGNGL EWISAISGDGYRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKELGYFDYWGRGTLTVSS (SEQ
ID NO: 216)

5 BMS3h-37-10

EVQLLES GGGGLVQP GGS LRLSCAASGFTFEWYEMQWVRRAPGKGLEWVSAISGDGYRTYYA
DSVKGRFTISRDN SKNTLYLLMNSLRAEDTAVYYCAKELGYFDYWGRGTLTVSS (SEQ
ID NO: 217)

BMS3h-37-11

10 EVQLLES GGGGLVQP GGS LRLSCAASGFTFEWYEMQWVRKAPGKGLEWVSAISGDGYRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKELGYFDYRGRGTLTVSS (SEQ
ID NO: 218)

BMS3h-37-12

EVQLLES GGGGLVQP GGS MRLSCAASGFTFEWYEMQWVRRAPGKGLEWVSAISGDGYRTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKELGYFDYRGRGTLTVSS (SEQ
ID NO: 219)

BMS3h-37-201

EVQLLES GGGGLVQP GGS LRLSCAASGFTFEWYEMQWVRRAPGKGLEWVSMISGDGYRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKELGYFDYWGRGTLTVSS (SEQ
20 ID NO: 220)

BMS3h-37-202

EVQLLES GGGGLVQP GGS LRLSCAASGFTFEWYEMQWVRRAPGKGLEWVSAISGDGWRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKELGYFDYWGRGTLTVSS (SEQ
ID NO: 221)

25

BMS3h-37-203

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFGWYEMQWRRAPGKGLEWVSAISGDGYRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKELLYFDYWGRGTLTVSS (SEQ
ID NO: 222)

5 BMS3h-37-204

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFEWYEMQWRRAPGKGLEWVSAISGDGYRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKELGFFDYWGRGTLTVSS (SEQ
ID NO: 223)

BMS3h-37-205

10 EVQLLES GGGGLVQP GGSRLRLSCAASGFTFEWYEMQWRRAPGKGLEWVSAISGDGYRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKELEYFDYWGRGTLTVSS (SEQ
ID NO: 224)

BMS3h-37-206

15 EVQLLES GGGGLVQP GGSRLRLSCAASGFTFEWYEMQWRRAPGKGLEWVSAISGDGYRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKGLEIFYDYWGRGTLTVSS (SEQ
ID NO: 225)

BMS3h-37-207

20 EVQLLES GGGGLVQP GGSRLRLSCAASGFTFEWYEMQWRRAPGKGLEWVSAISGDGYRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKELAFFDYWGRGTLTVSS (SEQ
ID NO: 226)

BMS3h-37-208

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFEWYEMQWRRAPGKGLEWVSAISGDGYRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKELLYFDYWGRGTLTVSS (SEQ
ID NO: 227)

BMS3h-37-209

EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWRRAPGKGLEWVSAISGDGYRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKELEFFDYWGRGTLTVSS (SEQ
ID NO: 228)

5 BMS3h-37-210

EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWRRAPGKGLEWVSAISGDGYRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKELQFFDYWGRGTLTVSS (SEQ
ID NO: 229)

BMS3h-37-211

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWRRAPGKGLEWVSAISGDGYRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKELLFFDYWGRGTLTVSS (SEQ
ID NO: 230)

BMS3h-37-212

EVQLLESGGGLVLRPGGSLRLSCAASGFTFEWYEMQWRRAPGKGLEWVSAISGDGYRTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKELEFFDYWGRGTLTVSS (SEQ
ID NO: 231)

BMS3h-37-213

EVQLLESGGGLVQPGGSLRLSCAASGFTFEWYEMQWRRAPGKGLEWVSAISGDGYRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKELLFFDYRGRGTLTVSS (SEQ
20 ID NO: 232)

BMS3h-37-214

EVQLLESGGGLVQPGGSLRLSCAASGFIFEWYEMQWRRAPGKGLEWVSAISGDGYRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKNLEYFDYWGRGTLTVSS (SEQ
ID NO: 233)

BMS3h-37-215

EVRLLES GGGGLVQPGGSLRLSCAASGFTFEWYEMQWVRAPGKGLEWVSAISGDGYRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKELQFFDYWGRGTLTVSS (SEQ
ID NO: 234)

5 BMS3h-38-1

EVQLLGSGGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISGSGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCSKEPFRFDYWGQGT LTVSS (SEQ
ID NO: 235)

BMS3h-38-2

10 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISGSGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRFDYWGQGT LTVSS (SEQ
ID NO: 236)

BMS3h-38-3

EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWISAISGSGGSTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRFDYWGQGT LTVSS (SEQ
ID NO: 237)

BMS3h-38-4

EVQLLDPGGGGLVQPGGSLRLSCAASGFTFGKEEMIWVRQAPGKGLEWVSSISGSGGSTYYA
DSVKGRFTISRDN SRNTLYLQMNSLRAEDTAVYYCGKEPFRFDYWGQGT LTVSS (SEQ
20 ID NO: 238)

BMS3h-38-5

EVQLLGSGGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISGSGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRFDYWGQGT LTVSS (SEQ
ID NO: 239)

BMS3h-38-6

EVQLLEPGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISGSGGSTYYA
DSVKGRFTISRDN SKNTLYLLMNSLRAEDTAVYYCSKEPFRFDYWGQ GALTVTVSS (SEQ
ID NO: 240)

5 BMS3h-38-7

EVQLLDPGGGLVQPGGSLRLSCAASGFTFGKEEMIWVRQAPGKGLEWVSSISGSGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPLRFDYWGQ GTLTVTVSS (SEQ
ID NO: 241)

BMS3h-38-8

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWISAISGSGGSTYYA
DSVKGRFTIHRDN SKNTLYLQMNSLRAEDTAVYYCSKEPFRFDYRGLGTLTVTVSS (SEQ
ID NO: 242)

BMS3h-38-9

EVQLLDPGGGLVQPGGSLRLSCAASGFTFGKEEMIWVRQAPGKGLEWVSSISGSGGSTYYA
15 DSVKGRFTISRDN SRNTLYLQMNSLRAEDTAVYYCAKEPLRFDYWGQ GTLTVTVSS (SEQ
ID NO: 243)

BMS3h-38-10

EVQLLD SGGGFVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWISAISGSGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPFRFDYWGQ GTLTVTVSS (SEQ
20 ID NO: 244)

BMS3h-38-11

EVQLLDPGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWISAISGSGGSTYYA
DSVKGRFTISRDN SNNTLYLQMNSLRAEDTAVYYCGREPFRFDYWGQ GTLTVTVSS (SEQ
ID NO: 245)

BMS3h-38-12

EVRLLESGEGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISGSGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRFDYWGQGTLTVSS (SEQ
ID NO: 246)

5 BMS3h-38-13

EVQQLES GGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISGSGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRFDYWGQGTLTVSS (SEQ
ID NO: 247)

BMS3h-38-201

10 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISGSGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFYDYWGQGTLTVSS (SEQ
ID NO: 248)

BMS3h-38-202

EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISGSGGSTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFYDYWGQGTLTVSS (SEQ
ID NO: 249)

BMS3h-38-203

EVQLLASGGGLVQPGGSLRLSCAASGFTFEEKEMIWVRQAPGKGLEWVSAISGSGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFYDYWGQGTLTVSS (SEQ
20 ID NO: 250)

BMS3h-38-204

EVQLLASGGGLVQPGGSLRLSCAASGFTFPQEEMIWVRQAPGKGLEWVSAISGSGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFYDYWGQGTLTVSS (SEQ
ID NO: 251)

BMS3h-38-205

EVQLLASGGGLVQPGGSLRLSCAASGFTFFAAEMIWVRQAPGKGLEWVSAISGSGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
ID NO: 252)

5 BMS3h-38-206

EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWVSAISRPGTSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
ID NO: 253)

BMS3h-38-207

10 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWVSAISRMGFSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
ID NO: 254)

BMS3h-38-208

EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWVSAISRWGHSTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
ID NO: 255)

BMS3h-38-209

EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWVSAISRLGWSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
20 ID NO: 256)

BMS3h-38-210

EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWVSAISRWGASTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
ID NO: 257)

BMS3h-38-211

EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEEMIWVRQAPGKGLEWVSAISRQGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
ID NO: 258)

5 BMS3h-38-212

EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEEMIWVRQAPGKGLEWVSAISVSGWSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
ID NO: 259)

BMS3h-38-213

10 EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEEMIWVRQAPGKGLEWVSAISRNGWSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
ID NO: 260)

BMS3h-38-214

EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEEMIWVRQAPGKGLEWVSAISRNLSTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
ID NO: 261)

BMS3h-38-215

EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEEMIWVRQAPGKGLEWVSAISGLGWSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
20 ID NO: 262)

BMS3h-38-216

EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEEMIWVRQAPGKGLEWVSAISALGWSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
ID NO: 263)

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BMS3h-38-217

EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEEMIWVRQAPGKGLEWVSAISRGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
ID NO: 264)

5 BMS3h-38-218

EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEEMIWVRQAPGKGLEWVSAISRHWSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
ID NO: 265)

BMS3h-38-219

10 EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEEMIWVRQAPGKGLEWVSSISRSGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
ID NO: 266)

BMS3h-38-220

15 EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEEMIWVRQAPGKGLEWVSAISRIGNSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
ID NO: 267)

BMS3h-38-221

20 EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEEMIWVRQAPGKGLEWVSAISGHGWSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
ID NO: 268)

BMS3h-38-222

EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEEMIWVRQAPGKGLEWVSAISRWGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
ID NO: 269)

BMS3h-38-223

EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISGSGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFMYDYWGQGTLVTVSS (SEQ
ID NO: 270)

5 BMS3h-38-224

EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISGSGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFYDYWGQGTLVTVSS (SEQ
ID NO: 271)

BMS3h-38-225

10 EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISGSGGGTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFYDYWGQGTLVTVSS (SEQ
ID NO: 272)

BMS3h-38-226

EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISGSGGSTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPLYDYWGQGTLVTVSS (SEQ
ID NO: 273)

BMS3h-38-227

EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISGSGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPMYYDYWGQGTLVTVSS (SEQ
20 ID NO: 274)

BMS3h-38-228

EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRNGFSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFYDYWGQGTLVTVSS (SEQ
ID NO: 275)

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BMS3h-38-229

EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRTGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
ID NO: 276)

5 BMS3h-38-230

EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISREGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
ID NO: 277)

BMS3h-38-231

10 EVQLLASGGGLVQPGGSLRLSCAASGFPFEEEEMIWVRQAPGKGLEWVSAISRQGWSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
ID NO: 278)

BMS3h-38-232

EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRGGGSTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
ID NO: 279)

BMS3h-38-233

EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRTGYSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
20 ID NO: 280)

BMS3h-38-234

EVQLLASGGGLVQPGGSLRLSCAASGFTFEEEEMIWVRQAPGKGLEWVSAISRNGRSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
ID NO: 281)

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BMS3h-38-235

EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEEMIWVRQAPGKGLEWVSAISRNGYSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
ID NO: 282)

5 BMS3h-38-236

EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEEMIWVRQAPGKGLEWVSAISRKGSSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
ID NO: 283)

BMS3h-38-237

10 EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEEMIWVRQAPGKGLEWVSAISRGGWSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
ID NO: 284)

BMS3h-38-238

EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEEMIWVRQAPGKGLEWVSAISRSGYSTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
ID NO: 285)

BMS3h-38-239

EVQLLASGGGLVQPGGSLRLSCAASGFTFEDEEEMIWVRQAPGKGLEWVSAISRNGMSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
20 ID NO: 286)

BMS3h-38-240

EVQLLES GGGLVQPGGSLRLSCAASGFTFEDEEEMIWVRQAPGKGLEWVSAISRNGYSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ
ID NO: 287)

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BMS3h-41-1

EVQLLES~~G~~EGGLVQPGGSLRLSCAASGFTTFTEHEMIWVRQAPGKGLEWVSSISGNGANTYYA
DSVKGRFTISRDN~~S~~KNTLYLQMNSLRPEDTAVYYCAKEPLRFDYWGQGTLVTVSS (SEQ
ID NO: 288)

5 BMS3h-41-2

EVQLLES~~G~~GGGLVQPGGSLRLSCAASGSTFTEYEMIWVRQAPGKGLEWISSISGNGANTYYA
DSVKGRFTISRDN~~S~~KNTLYLQMNSLRAEDTAVYFCAKEPLRFDYRGQGTLVTVSS (SEQ
ID NO: 289)

BMS3h-41-3

10 EVQLLEP~~G~~GGGLVQPGGSLRLSCAASGFTTFTEYEMIWVRKAPGKGMEWVSSISGNGANTYYA
DSVKGRFTISRDN~~S~~KNMLYLQMNSLRAEDTAVYYCAKEPLRFGYWGQGTLVTVSS (SEQ
ID NO: 290)

BMS3h-41-4

EVQLLD~~S~~GGGLVQPGGSLRLSCAASGFTTFTEYEMIWVRQAPGKGLEWVSSISGNGANTYYA
15 DSVKGRFTISRDN~~S~~KNTLYLQMNSLRAEDTAVYYCAKEPLRFDYWGRGTLVTVSS (SEQ
ID NO: 291)

BMS3h-41-5

EVQLLG~~S~~GGGLVQPGGSLRLSCAASGFTTFTEYEMIWVRQAPGKSLEWVSSISGNGANTYYA
DSVKGRFTISRDN~~S~~KNTLYLQMNSLRAEDTAVYYCAKEPLRYDDWGQGTLVTVSS (SEQ
20 ID NO: 292)

BMS3h-41-6

EVQPLE~~S~~GGGLVQPGGSLRLSCSASGFTTFNEYEMIWVRQAPGKGLEWVSSISGNGANTYYA
DSVKGRFTISRDN~~S~~KNTLYLQMNSLRAEDTAVYYCAKEPLRFDYWGQGTLVTVSS (SEQ
ID NO: 293)

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BMS3h-41-7

EVQLLESGEGLVQPGGSLRLSCAASGFTFAEYEMIWVRQAPGKGLEWVSSISGNGANTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPLRFDYWGQGTLVTVSS (SEQ
ID NO: 294)

5 BMS3h-41-8

EVQLLDPPGGGLVQPGGSLRLSCAASGFTFTESEMIWVRQAPGKGLEWVSSISGNGANTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPLRFDYWGQGTLVTVSS (SEQ
ID NO: 295)

BMS3h-41-9

10 EVQLLEPPGGGLVQPGGSLRLSCAASGFTFTEYEMIWVRKAPGKGMEWVSSISGNGANTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRPEDTAVYYCAKEPLRFDDWGQGTLVTVSS (SEQ
ID NO: 296)

BMS3h-41-10

15 EVQLLESGLVGLVQPGGSLRLSCAASGFTFTEYEMIWVRKAPGKGLEWVSSISGNGANTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPLRFDNWGQGTLVTVSS (SEQ
ID NO: 297)

BMS3h-41-11

20 EVQLLESRGGLVQPGGSLRLSCAASGFTFTEHEMIWVRQAPGKGLEWVSSISGNGANTYYA
DSVKGRFSVSRDN SKNTLYLQMNSLRAEDTAVYYCAKEPLRFDYWGQGTLVTVSS (SEQ
ID NO: 298)

BMS3h-41-12

EVQPLESGGGGLVQPGGSLRLSCAASGFTFTEYEMIWVRQAPGKGLEWVSSISGNGANTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPLRFDYWGQGTLVTVSS (SEQ
ID NO: 299)

BMS3h-41-13

EVQLLESAGGLVQPGGSLRLSCAASGFTFAEYEMIWVRQAPGKGLEWVSSISGNGANTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPLRFDYWGQ GALVTVSS (SEQ
ID NO: 300)

5 BMS3h-41-14

EVQLLEPGGGLVQPGGSLRLSCAASGFTFTEYEMIWVRQAPGKGLEWVSSISGNGANTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPLRFDNWGQGTLVTVSS (SEQ
ID NO: 301)

BMS3h-43-1

10 EVQLLESGGGLVQPGGSLRLSCTASGFTFNMYEMSWVRQAPGKGLEWVSGISR RGFTTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPITYDLRYARFDYSGQGTLVTVS
S (SEQ ID NO: 302)

BMS3h-43-2

EEQLLESGGGLVQPGGSLRLSCTASGFTFNMYEMSWVRQAPGKGLEWVSGISR RGFTTYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPITYATRYARFDYWGQGTLVTVS
S (SEQ ID NO: 303)

BMS3h-43-3

EVQLLESGGGLVQPGGSLRLSCTASGFTFNMYEMSWVRQAPGKGLEWVSGISR RGFTTYA
DSVKGRFTISRDNFKNTLYLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYGGQGTLVTVS
20 S (SEQ ID NO: 304)

BMS3h-43-4

EVQLLESGGGLVQPGGSLRLSCTASGFTFNMYEMSWVRQAPGKGLEWVSGISR RGFTTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPITYDMRYARFDNWGQGTLVTVS
N (SEQ ID NO: 305)

BMS3h-43-5

EVQLLESGGGLVQPGGSLRLSCTASGFTFNTYEMSWVRQAPGKGLEWVSGIGRRGFTTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPITYDLRYARFDYSGQGTLVTVS
S (SEQ ID NO: 306)

5 BMS3h-43-6

EVQLMESGGGLVQPGGSLRLSCTASGFSFNMYEMSWVRQAPGKGLEWVSGISRRGYTTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYWGRGTLVTVS
S (SEQ ID NO: 307)

BMS3h-43-7

10 EVQLLESGGGLVQPGGSLRLSCTASGFAFNMYEMSWVRQAPGKGLEWVSGISRHGFTTYA
DSVKGRFTVSRDN SKNTLYLQMNSLRAEDTAVYYCAKEPITYDMRYARSDYWQGTLVTVS
S (SEQ ID NO: 308)

BMS3h-43-8

15 EVQLLESGGGLVQPGGSLRLSCTASGFTFNTYEMSWVRQAPGKGLEWVSGISRRGFTTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYFCAKEPITYDMRYARSDYWQGTLVTVS
S (SEQ ID NO: 309)

BMS3h-43-9

20 EVQLLESGGGLVQPGGSLRLSCTASGFTFNTYEMSWVRQAPGKGLEWVSGISRRGFTTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPITYSMRYARFDYSGLGTMVTVS
S (SEQ ID NO: 310)

BMS3h-43-10

EVQLLESGGGLVQPGGSLRLSCTASGFTFNTYEMSWVRQAPGKGLEWVSGISRRGFTTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYSGQGTLVTVS
S (SEQ ID NO: 311)

BMS3h-43-11

EVQLLES GGGGLVQP GGS LRLSCTASGFTFNMYEMSWVRKAPGKGLEWVSGISRHGFTTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYWQGQGLTVTS
S (SEQ ID NO: 312)

5 BMS3h-43-12

EVQLFES GGGGLVQP GGS LRLSCTASGFTFNMYEMSWVRQAPGKGLEWVSGISRRGFTTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYWGRGTLTVTS
S (SEQ ID NO: 313)

BMS3h-43-13

10 EVQLLES GGGGLVQP GGS LRLSCTASGFTFNMYEMSWVRQAPGKGLEWVSGISRRGFTTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYWGRGTLTVTS
S (SEQ ID NO: 314)

BMS3h-43-14

EVQLLES GGGGSVQP GGS LRLSCTASGFSFNMYEMSWVRQAPGKGLEWVSGISRRGFTTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYWQGQGLTVTS
G (SEQ ID NO: 315)

BMS3h-43-15

EVQLLES GGGGLVQP GGS LRLSCTASGFTFNMYEMSWVRKAPGKGLEWVSGISRRGFTTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPITYDMRYARFDYWQGQGLTVTS
20 S (SEQ ID NO: 316)

BMS3h-56-1

EVQLLES GGGGLVQP GGS LRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGLTVTVSS (SEQ
ID NO: 317)

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BMS3h-56-2

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS (SEQ
ID NO: 318)

5 BMS3h-56-3

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTKLPFIFEYWGQGTLVTVSS (SEQ
ID NO: 319)

BMS3h-56-4

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFMFDDRQGQGTLVTVSS (SEQ
ID NO: 320)

BMS3h-56-5

15 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVMGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS (SEQ
ID NO: 321)

BMS3h-56-6

20 EVQLLESGGGLVQPGGSLRLSCAASGFSFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFIFDNRQGQGTLVTVSS (SEQ
ID NO: 322)

BMS3h-56-7

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTSVYHCAKPPFIFGDWGPGLVTVSS (SEQ
ID NO: 323)

BMS3h-56-8

EVQLLESGGGLVQPGGSRRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLTVSS (SEQ
ID NO: 324)

5 BMS3h-56-9

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVMGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PFMFDDRGGQTLTVSS (SEQ
ID NO: 325)

BMS3h-56-10

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKVLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNMLYLQMNSLRAEDTAVYYCAKL PFMFDDRGGQTLTVSS (SEQ
ID NO: 326)

BMS3h-56-11

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PFMFDDRGGQTLTVSS (SEQ
ID NO: 327)

BMS3h-56-12

EVQLLESGGGLIQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCLKLPFIFDYWGQGTLTVSS (SEQ
20 ID NO: 328)

BMS3h-56-13

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRADDTAVYHCKLPFIFDYWGQGTLTVSS (SEQ
ID NO: 329)

BMS3h-56-14

EVQLLES GGGGLVQP GGS LRLSCAASGFTFRDYEMWWVRQAPGMVLERSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFFFDSRGQGTLTVSS (SEQ
ID NO: 330)

5 BMS3h-56-15

EVQLLES GGGGLVQP GGS LRLSCAASGFTFRDYEMWWVRRAPGKGLERSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLTVSS (SEQ
ID NO: 331)

BMS3h-56-16

10 EVQLLES GGGGLVQP GGS LRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPQGTRTYYA
DSVMGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLTVSS (SEQ
ID NO: 332)

BMS3h-56-17

EVQLLES GGGGLVQP GGS LRLSCAASGFSFRDYEMWWYRQAPGKGLERSAINPQGTRTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLTVSS (SEQ
ID NO: 333)

BMS3h-56-18

EVQLLES GGGGLVQP GGS LRLSCAASGFTFRDYEMWWVRQAPGKVLERSAINPQGTRTYYA
DSVKGRFTISRDN SKNMLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLTVSS (SEQ
20 ID NO: 334)

BMS3h-56-19

EVQLLES GGGGLVQP GGS LRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYHCAKLPFTFEDWGQGTLTVSS (SEQ
ID NO: 335)

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BMS3h-56-20

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTKLPFTFEDWGQGTLVTVSS (SEQ
ID NO: 336)

5 BMS3h-56-21

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCLKLPFTFEDWGQGTLVTVSS (SEQ
ID NO: 337)

BMS3h-56-22

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRADDTAVYHCTKLPFIFEYWGQGTLVTVSS (SEQ
ID NO: 338)

BMS3h-56-23

15 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVMGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKEPYSFDSWGQGTLVTVSS (SEQ
ID NO: 339)

BMS3h-56-24

20 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVMGRFTISRDN SKNTLYLQMNSLRAEDTAVYHCAKEPYSYDYWGQGTLVTVSS (SEQ
ID NO: 340)

BMS3h-56-25

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRRAPGKGLERVSAINPQGTRTYYA
DSVMGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS (SEQ
ID NO: 341)

BMS3h-56-26

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRRAPGKGLERVSAINPQGTRTYYA
DSVMGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PFMFDDR GQGTLVTVSS (SEQ
ID NO: 342)

5 BMS3h-56-27

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVMGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PFMFDDW GQGTLVTVSS (SEQ
ID NO: 343)

BMS3h-56-28

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYELWWVRQAPGKGLERVSAINPQGTRTYYA
DSVMGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PFTFDDW GQGTLVTVSS (SEQ
ID NO: 344)

BMS3h-56-29

EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYELWWVRQAPGKGLERVSAINPQGTRTYYA
15 DSVMGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PFMFDDR GQGTLVTVSS (SEQ
ID NO: 345)

BMS3h-56-30

EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMWWFRQAPGKGLERVSAINPQGTRTYYA
DSVMGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PFTFDDW GQGTLVTVSS (SEQ
20 ID NO: 346)

BMS3h-56-31

EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMWWFRQAPGKGLERVSAINPQGTRTYYA
DSVMGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PFMFDDR GQGTLVTVSS (SEQ
ID NO: 347)

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BMS3h-56-32

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLEWVSAINPQGTRTYYA
DSVMGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS (SEQ
ID NO: 348)

5 BMS3h-56-33

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLEWVSAINPQGTRTYYA
DSVMGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPMFDDRGGQTLVTVSS (SEQ
ID NO: 349)

BMS3h-56-202

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPTYFSDRGQGTLVTVSS (SEQ
ID NO: 350)

BMS3h-56-203

15 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PFFFEWGGQTLVTVSS (SEQ
ID NO: 351)

BMS3h-56-204

20 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPTYFKDWGGQTLVTVSS (SEQ
ID NO: 352)

BMS3h-56-205

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PFFYFSEWGGQTLVTVSS (SEQ
ID NO: 353)

BMS3h-56-206

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYHCAKLPFFEDWGQGTLTVSN (SEQ
ID NO: 354)

5 BMS3h-56-207

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFPFSEWGQGTLTVSS (SEQ
ID NO: 355)

BMS3h-56-208

10 EVQLLES GGGGLVQP GGSRLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMDSLRAEDTAVYYCAKLPFYFSEWGQGTLTVSS (SEQ
ID NO: 356)

BMS3h-56-209

15 EVQLLES GGGGLVQP GGSRLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPYGNLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLTVSS (SEQ
ID NO: 357)

BMS3h-56-210

20 EVQLLES GGGGLVQP GGSRLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPPGTLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDRGQGTLTVSS (SEQ
ID NO: 358)

BMS3h-56-211

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLTVSS (SEQ
ID NO: 359)

BMS3h-56-212

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPMGGFTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLTVSS (SEQ
ID NO: 360)

5 BMS3h-56-213

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGSHTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLTVSS (SEQ
ID NO: 361)

BMS3h-56-214

10 EVQLLES GGGGLVQP GGSRLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPSGGLTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDRQGTLTVSS (SEQ
ID NO: 362)

BMS3h-56-215

15 EVQLLES GGGGLVQP GGSRLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPHGSLTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLTVSS (SEQ
ID NO: 363)

BMS3h-56-216

20 EVQLLES GGGGLVQP GGSRLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPAGRLTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLTVSS (SEQ
ID NO: 364)

BMS3h-56-217

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGSLTYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLTVSS (SEQ
ID NO: 365)

BMS3h-56-218

EVQLLESGGGLVQPGGSLRLSCAASGFTFPDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYHCAKLPFTFDDWGQGTLVTVSS (SEQ
ID NO: 366)

5 BMS3h-56-219

EVQLLESGGGLVQPGGSLRLSCADSGFTFPVEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLVTVSS (SEQ
ID NO: 367)

BMS3h-56-220

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPYGGLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS (SEQ
ID NO: 368)

BMS3h-56-221

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGNHTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLVTVSS (SEQ
ID NO: 369)

BMS3h-56-222

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPHGGYTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLVTVSS (SEQ
20 ID NO: 370)

BMS3h-56-223

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGRGLERVSAINPPGMLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS (SEQ
ID NO: 371)

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BMS3h-56-224

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGQLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLTVSS (SEQ
ID NO: 372)

5 BMS3h-56-225

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGYTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLTVSS (SEQ
ID NO: 373)

BMS3h-56-226

10 EVQLLES GGGGLVQP GGSRLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPSGGLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLTVSS (SEQ
ID NO: 374)

BMS3h-56-227

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPSGGLTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLTVSS (SEQ
ID NO: 375)

BMS3h-56-228

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPSGTLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLTVSS (SEQ
20 ID NO: 376)

BMS3h-56-229

EVQLLES GGGGLVQP GGSRLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPYGSLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLTVSS (SEQ
ID NO: 377)

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BMS3h-56-230

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGYTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLVTVSS (SEQ
ID NO: 378)

5 BMS3h-56-231

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGGLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLVTVSS (SEQ
ID NO: 379)

BMS3h-56-232

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGSHTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS (SEQ
ID NO: 380)

BMS3h-56-233

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGTLTYYA
15 DSVKGRFTISRDN SRNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS (SEQ
ID NO: 381)

BMS3h-56-234

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPNGRLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFADWGQGTLVTVSS (SEQ
20 ID NO: 382)

BMS3h-56-235

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGQLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS (SEQ
ID NO: 383)

BMS3h-56-236

EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPHGGLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS (SEQ
ID NO: 384)

5 BMS3h-56-237

EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPAGMLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS (SEQ
ID NO: 385)

BMS3h-56-238

10 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPHGTLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS (SEQ
ID NO: 386)

BMS3h-56-239

EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGSLTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS (SEQ
ID NO: 387)

BMS3h-56-240

EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPYGGLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS (SEQ
20 ID NO: 388)

BMS3h-56-241

EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPAGFLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS (SEQ
ID NO: 389)

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BMS3h-56-242

EVQLLES GGGGLV R PGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPYGGLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLTVSS (SEQ
ID NO: 390)

5 BMS3h-56-243

EVQLLES GGGGLV Q PGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGFTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLTVSS (SEQ
ID NO: 391)

BMS3h-56-244

10 EVQLLES GGGGLV Q PGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLTVSS (SEQ
ID NO: 392)

BMS3h-56-245

15 EVQLLES GGGGLV Q PGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPYGGLTYYA
DSVKGRFTISRDN SKNTLYLQMDSLRAEDTAVYYCAKLPFTFEDWGQGTLTVSS (SEQ
ID NO: 393)

BMS3h-56-246

20 EVQLLES GGGGLV Q PGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGTLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLTVSS (SEQ
ID NO: 394)

BMS3h-56-247

EVQLLES GGGGLV Q PGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGYTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGRGTLTVSS (SEQ
ID NO: 395)

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BMS3h-56-248

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPYGNLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS (SEQ
ID NO: 396)

5 BMS3h-56-249

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPHGGFTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLVTVSS (SEQ
ID NO: 397)

BMS3h-56-250

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPAGFYTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS (SEQ
ID NO: 398)

BMS3h-56-251

15 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPAGGLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFDDWGQGTLVTVSS (SEQ
ID NO: 399)

BMS3h-56-252

20 EVQLLESGGGLVQPGGSLRLSCAASGFAFRDYEMWWVRQAPGKGLERVSAINPHGSLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFTFEDWGQGTLVTVSS (SEQ
ID NO: 400)

BMS3h-56-253

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPAGGYTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYHCAKLPFTFEDWGQGTLVTVSS (SEQ
ID NO: 401)

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BMS3h-56-254

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PFWFTEWGQGTLVTVSS (SEQ
ID NO: 402)

5 BMS3h-56-255

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PFMFSDRGQGTLVTVSS (SEQ
ID NO: 403)

BMS3h-56-256

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PFLFQEWGQGTLVTVSS (SEQ
ID NO: 404)

BMS3h-56-257

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PTRFEDWGQGTLVTVSS (SEQ
ID NO: 405)

BMS3h-56-258

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PFYFHEWGQGTLVTVSS (SEQ
20 ID NO: 406)

BMS3h-56-259

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFYDYWGQGTLVTVSS (SEQ
ID NO: 407)

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BMS3h-56-260

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPTFFKDWGQGTLTVSS (SEQ
ID NO: 408)

5 BMS3h-56-261

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PFFFQEWGQGTLTVSS (SEQ
ID NO: 409)

BMS3h-56-262

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PQLFHDRGQGTLTVSS (SEQ
ID NO: 410)

BMS3h-56-263

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PQLFEDWGQGTLTVSS (SEQ
ID NO: 411)

BMS3h-56-264

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYHCAKL PFGFSEWGQGTLTVSS (SEQ
20 ID NO: 412)

BMS3h-56-265

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PQLFQDWGQGTLTVSS (SEQ
ID NO: 413)

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BMS3h-56-266

EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PFFFHEWGQGTLVTVSS (SEQ
ID NO: 414)

5 BMS3h-56-267

EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PHYFKDWGQGTLVTVSS (SEQ
ID NO: 415)

BMS3h-56-268

10 EVQLLES GGGGLVQSGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PFYFEWGQGTLVTVSS (SEQ
ID NO: 416)

BMS3h-56-269

15 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PFRFSDRGQGTLVTVSS (SEQ
ID NO: 417)

BMS3h-56-270

20 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PTLFQDWGQGTLVTVSS (SEQ
ID NO: 418)

BMS3h-56-271

EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PFYFSEWGQGTLVTVSN (SEQ
ID NO: 419)

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BMS3h-56-272

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PFWFQEWGQGTLTVSS (SEQ
ID NO: 420)

5 BMS3h-56-273

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGSLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PFFYFQEWGQGTLTVSS (SEQ
ID NO: 421)

BMS3h-56-274

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGSLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYHCAKL PMFFEDWGQGTLTVSN (SEQ
ID NO: 422)

BMS3h-56-275

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGSLTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PFFYFHEWGQGTLTVSS (SEQ
ID NO: 423)

BMS3h-56-276

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGSLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PFFFQEWGQGTLTVSS (SEQ
20 ID NO: 424)

BMS3h-56-277

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGSLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PFFFHEWGQGTLTVSS (SEQ
ID NO: 425)

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BMS3h-56-278

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGFTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFQEWGQGTLTVSS (SEQ
ID NO: 426)

5 BMS3h-56-279

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGFTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYHCAKLPMFFEDWGQGTLTVSN (SEQ
ID NO: 427)

BMS3h-56-280

10 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGFTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGTLTVSS (SEQ
ID NO: 428)

BMS3h-56-281

15 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGFTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PFFFQEWGQGTLTVSS (SEQ
ID NO: 429)

BMS3h-56-282

20 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGFTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKL PFFFHEWGQGTLTVSS (SEQ
ID NO: 430)

BMS3h-56-283

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGFTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFQEWGQGTLTVSS (SEQ
ID NO: 431)

BMS3h-56-284

EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYHCAKLP MFFEDWGQGTLTVSN (SEQ
ID NO: 432)

5 BMS3h-56-285

EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGTLTVSS (SEQ
ID NO: 433)

BMS3h-56-286

10 EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGLTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFFFQEWGQGTLTVSS (SEQ
ID NO: 434)

BMS3h-56-287

EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPWGGLTYYA
15 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFFFHEWGQGTLTVSS (SEQ
ID NO: 435)

BMS3h-56-288

EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYHCAKLP MFFEDWGQGTLTVSS (SEQ
20 ID NO: 436)

BMS3h-106-1

EVQLLETGGGLVQPGGSLRLSCAASGFTFSTYHMQWVRRAPGKGLEWVSMIDADGLGTYYA
DPVKGRFTISRDN SKNTLYLQMNSLRAKDTAVYYCARPGPQFGQFDYLGQGTLTVSS
(SEQ ID NO: 437)

25

BMS3h-106-2

EVQLFESGGGLVQTGGSLRLSCAASGFTFSTYHMQWVRQAPGKGLEWVSMIDADGLGKYIA
DPVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCVKPGPQFGQYDYWGQGTLVTVSS
(SEQ ID NO: 438)

5 BMS3h-107-1

EVQLLES GGGLVQPGGSLRLSCSASGFTFSGYDMQWVRQAPGKGLEWVSTISASGVYTYIA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKYPNRFALNSFDYRGRGTLVTVSS
(SEQ ID NO: 439)

BMS3h-107-2

10 EVQLLES GGGLVQPGGSLRLSCAASGFTFSGYDMQWVRQAPGRGLEWVSTISASGVYTYIT
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCTKYPNRFARNNFDYWGQGTLVTVSS
(SEQ ID NO: 440)

BMS3h-131-1

DILMTQSPSSLSASVGDRV TITCRANSSILWALAWYQQKPGEAPKLLIESSSGLQSGVPSR
15 FSGSGSGTDFTLTIS SLQPEDFATYYCVQNAVWPGTFSQGTKVEIKR (SEQ ID NO:
441)

BMS3h-131-2

DIQMTQSPSSLSASVGDRV TITCRADSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSR
FSGSGSGTDFTLTIS SLQPEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO:
20 442)

BMS3h-131-3

DIQMTVSPSSLSASVGDRV TITCRADSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSRFSGSG
SGTDFTLTIS SLQPEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO: 443)

BMS3h-131-4

25 DIQMTQSPSSLSASVGDRV TITCRANSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSR

FSGSGSGTDFTLTISLQPEDFATYYCVQNAVWPGTFDQGTKVEIKR (SEQ ID NO:
444)

BMS3h-131-5

DIQMTQSPSSLSASVGDRVITTCRANSSILWALAWYQQKPGKAPKLLIESSTGLQSGVPSR

5 FSGSGSGTDFTLTISLQPEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO:
445)

BMS3h-131-6

DIQMTVSPSSLSASVGDRVITTCRANSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSR

10 FSGSGSGTDFTLTISLQPEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO:
446)

BMS3h-131-7

DIQMTQSPSSLSASVGDRVITTCRADSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSR

FSGSGSGTDFTLTISLQPEDFATYYCVQNAVWPGTFDQGTKVEIKR (SEQ ID NO:
447)

15 BMS3h-131-8

DIQMTQSPSSLSASVGDRVITTCRANSSILWALAWYQQKPGKAPELLIESSSGLQSGVPSR

FSGSGSGTDFTLTISLQPEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO:
448)

BMS3h-131-9

20 DIQMTQSPSSLSASVGDRVITTCRANSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSR

FSGSGSGTDFTLTISLQPEDFATYYCVQNAVWPGTFGQGTKVENKR (SEQ ID NO:
449)

BMS3h-131-10

DIQMTQSPSSLSASVGDRVITTCRANSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSR

25 FSGSGSGTDFTLTISLQPEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO:

450)

BMS3h-131-11

DIQMTQSPSSLSASVGDRVTITCRANSSILWALAWYQQKPGKAPKLLIESSSGLQSGIPSR
FSGSGSGTDFTLTISLQPEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO:

5 451)

BMS3h-131-12

DIQMTQSPSSLSASVGDRVTITCRANSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO:

452)

10 BMS3h-131-13

DILLTQSPSSLSASVGDRVTITCRANSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO:

453)

BMS3h-131-14

15 DIQMTQSPSSLSASVGDRVTITCRANSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSR
FSGSGTGTDFTLTISGLQPEDFATYYCVQNAVWPGTFDQGTKVEIKR (SEQ ID NO:

454)

BMS3h-131-15

DIQMTQSPSSLSASVGDRVTIPCRANSSILWALAWYQQKPGKAPKLLIESSSGLQSGVPSR
20 FSGSASGTDFTLTISLQPEDFATYYCVQNAVWPGTFGQGTKVEIKR (SEQ ID NO:

455)

BMS3h-193-1

DIQMAQSPSSLSASVGDRVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCHQYASPLTLGQGTKVEIKR (SEQ ID NO:

25 456)

BMS3h-193-2

DIQMTQSPSSLSASVGDSVTITCRASQTIERRLNWYQQKPGEAPKLLIYLASRLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCHQYASPPPLTFGQGTNVEIKR (SEQ ID NO:
457)

5 BMS3h-193-3

DIQMTQSPSSLSASVGDRVITITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSR
FSGSGSGTDFTLTISLQPEDFAAYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:
458)

BMS3h-193-4

10 DIQMTQSPSSLSASVGDRVITITCRASRTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:
459)

BMS3h-193-5

DIQMTQSPSSLSASVGERVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSR
15 FSGSGSGTDFTLTISNLQPEDSATYYCHQYASPPPLTLGQGTKVEIKR (SEQ ID NO:
460)

BMS3h-193-6

DIQMTQSPSSLSASVGDRVITITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCHQYASPPPLTLGQGTKVEIKR (SEQ ID NO:
20 461)

BMS3h-193-7

DIQITQSPSSLSASVGDRVITITCRASQTIERRLNWYQQKPGKDPKLLIYLASRLQSGVPSRFSGS
GSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 462)

BMS3h-193-8

25 DIQMTQSPSSLSASVGDRVITITCRASQTIERRLNWYQQKPGEAPKLLIYLASRLQSGVPSR

FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKW (SEQ ID NO:
463)

BMS3h-193-9

DIQLTQSPSSLSASVGDRVITICRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSR

5 FSGSGSGTEFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:
464)

BMS3h-193-10

DIQMSQSPSTLSASVGDRVITICRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSR

10 FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLMFGQGTKVEIKR (SEQ ID NO:
465)

BMS3h-193-11

DIQMTQSPSSLSASVGDRVITICRASQTIERRLNWYQQKPGKDPKLLIYLASRLQSGVPSR

FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:
466)

15 BMS3h-193-12

DIQMTQSPSSLSASVGDRVITICRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSR

FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:
467)

BMS3h-193-13

20 DIQMTQSPSSLFASVGDRVITICRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSR

FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:
468)

BMS3h-193-14

DIQMTQYPSSLSASVGDRVITICRASQSIERRLNWYQQKPGEAPKLLIYLASRLQSGVPSR

25 FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:

469)

BMS3h-193-15

DIQMTQSPSSLSASVGDRVITITCRASRTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCHPYESPPLTFGQGTKVEIKR (SEQ ID NO:

5 470)

BMS3h-193-16

DIQMTQSPSSLSASVGDRVITITCRASQAIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCHQYASPLTLGQGTKVEIKR (SEQ ID NO:

471)

10 BMS3h-193-17

NIQMTQSPSSLSASVGDRVITITCRASQAIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:

472)

BMS3h-193-18

15 DIQMTQSPSSLSASVGDRVITITCRASQTIGRRLNWYQQKPGKAPKLLIYLASRLQSGVPSR
FSGSGSGSDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:

473)

BMS3h-193-19

DIQMTQSPSSLSASVGDRVITITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSR
FSGSGSGTEFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:

20 474)

BMS3h-193-20

DIQMTQTPSSLSASVGDRVITITCRASQTIERRLNWYQQKPGEAPKLLIYLASRLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVKIKR (SEQ ID NO:

25 475)

BMS3h-193-21

DIQMTQSPSSLSASVGDSVTITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:
476)

5 BMS3h-193-22

HIQMTQSPSSLSASVGDRVITITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:
477)

BMS3h-193-23

10 DVQMTQSPSSLSASVGDRVITITCRASQTIERRLNWYQQKPGKAPKLLIYLSRLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCHQYASPPPLTFGQGTKVEIKR (SEQ ID NO:
478)

BMS3h-193-24

DIQMTQSPSSLSASVGDRVITITCRASQTIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSR
15 FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVVIKR (SEQ ID NO:
479)

BMS3h-193-25

DIQMTQSPSSLSASVGDRVITITCRASQTIERRLNWYQQKPGKAPRLLIYLATRLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:
20 480)

BMS3h-193-26

DIQMTQSPSSLSASVGDRVITITCRASQPIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSRFSG
SGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 481)

BMS3h-193-27

25 DIQMTQSPSSLSASVGDRVITITCRASQTIGRRLNWYQQKPGKAPKLLIYLASRLQSGVPSR

FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:
482)

BMS3h-193-28

DIQMTQSPSSLSASVGDRVITICRASQSIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSR

5 FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIIR (SEQ ID NO:
483)

BMS3h-193-29

DIQMTQSPSSLSASVGDRVITICRASQTIERRLNWYQQKPGKAPKLLIYLATRLQSGVPSR

FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:
10 484)

BMS3h-193-30

DIQMTQSPSSLSASVGDRVITICRASQSIERRLNWYQQKPGKAPKLLIYLASRLQSGVPSR

FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:
485)

15 BMS3h-193-2501

DIQMTQSPSSLSASVGDRVITICRASQTIERRLNWYQQKPGKAPRLLIYLATRLQSGVPSR

FSGSGSGTDFTLTISLQPEDFATYYCHQFEHPPLTFGQGTKVEIKR (SEQ ID NO:
486)

BMS3h-193-2502

20 DIQMTQSPSSLSASVGDRVITICRASFPIDRRLNWYQQKPGKAPRLLIYLATRLQSGVPSR

FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:
487)

BMS3h-193-2503

DIQMTQSPSSLSASVGDRVITICRASSTIGRRLNWYQQKPGKAPRLLIYLATRLQSGVPSR

25 FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:

488)

BMS3h-193-2504

DIQMTQSPSSLSASVGDRVITITCRASSQIGRRLNWWYQQKPGKAPRLLIYLATRLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:

5 489)

BMS3h-193-2505

DIQMTQSPSSLSASVGDRVITITCRASERIGRRLNWWYQQKPGKAPRLLIYLATRLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:

490)

10 BMS3h-193-2506

DIQMTQSPSSLSASVGDRVITITCRASQQIGRRLNWWYQQKPGKAPRLLIYLATRLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:

491)

BMS3h-193-2507

15 DIQMTQSPSSLSASVGDRVITITCRASQPIARRLNWWYQQKPGKAPRLLIYLATRLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:

492)

BMS3h-193-2508

DIQMTQSPSSLSASVGDRVITITCRASGNIGRRLNWWYQQKPGKAPRLLIYLATRLQSGVPSR
20 FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:

493)

BMS3h-193-2509

DIQMTQSPSSLSASVGDRVITITCRASRNIDRRLNWWYQQKPGKAPRLLIYLATRLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:

25 494)

BMS3h-193-2510

DIQMTQSPSSLSASVGDRVITITCRASQSIGRRLNWWYQQKPGKAPRLLIYLAIRLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:
495)

5 BMS3h-193-2511

DIQMTQSPSSLSASVGDRVITITCRASQNIQTRLNWWYQQKPGKAPRLLIYLAIRLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:
496)

BMS3h-193-2512

10 DIQMTQSPSSLSASVGDRVITITCRASEVIGRRLNWWYQQKPGKAPRLLIYLAIRLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:
497)

BMS3h-193-2513

DIQMTQSPSSLSASVGDRVITITCRASEAIGRRLNWWYQQKPGKAPRLLIYLAIRLQSGVPSR
15 FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:
498)

BMS3h-193-2514

DIQMTQSPSSLSASVGDRVITITCRASISIRRLNWWYQQKPGKAPRLLIYLAIRLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:
20 499)

BMS3h-193-2515

DIQMTQSPSSLSASVGDRVITITCRASLNIGRRLNWWYQQKPGKAPRLLIYLAIRLQSGVPSRFSG
SGSGTDFTLTISLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO: 500)

BMS3h-193-2516

25 DIQMTQSPSSLSASVGDRVITITCRASQTIERRLNWWYQQKPGKAPRLLIYLSKLQSGVPSR

FSGSGSGTDFTLTISSLQPEDFATYYCHQYESPPLTFGQGTKVEIKR (SEQ ID NO:
501)

BMS3h-198-1

EVQLLESGGGLVQPGGSLRLSCAASGSTIAGYEMWWVRQAPGKGLERVSAISGSGGSTYYA

5 DSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCARDPYSFDYWGQGTLLTVSS (SEQ
ID NO: 502)

BMS3h-198-2

EVQPLESGGGGLVQPGGSLRLSCAASGFTFAGYEMWWVRQAPGKGLERISAIISGSGGSTYYA

DSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCARDPYSFDYWGQGTLLTVSS (SEQ
10 ID NO: 503)

BMS3h-198-3

EVQLLESGGGSVQPGGSLRLSCAATGSTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYYA

DSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCARDPYSYDYWGQGTLLVSVSS (SEQ
ID NO: 504)

15 BMS3h-198-4

EVQLLESGGGLVQPGGSLRLSCAASGLTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYYA

DSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYHCARDPYSFDYWGQGTLLTVSS (SEQ
ID NO: 505)

BMS3h-198-5

20 EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYYA

DSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYHCAKEPYSYDYWGQGTLLTVSS (SEQ
ID NO: 506)

BMS3h-198-6

EVQLLESGGGLVQPGGSLRLSCAASGSTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYYA

25 DSVKGRFTISRDDSKNTLYLQMNSLRPEDTAVYYCVKDPYSFDYWGQGTLLTVSS (SEQ

ID NO: 507)

BMS3h-198-7

EVQLLES GGGGLVQPGGSLRLSCAASGSTIAGYEMWWVRQAPGKGLERVSAISGSGGSTYYA

DSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCARDPYSFDYWGQGTPVTVSS (SEQ

5 ID NO: 508)

BMS3h-198-8

EVQLMES GGGGLVQPGGSLRLSCAASGSTFAGYEMWWYRQAPGKGLERVSAISGSGRSTYYA

DSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCAKDPYSFDYWGQGTLTVVSS (SEQ

ID NO: 509)

10 BMS3h-198-9

EVQLLES GGGGLVQPGGSLRLSCAASGFTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYYA

DSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCAKEPYSFDYWGQGTLTVVSS (SEQ

ID NO: 510)

BMS3h-198-10

15 EVQLLES GGGGLVQPGGSLRLSCAASGSTIAGYEMWWVRQAPGKGLERVSAISGSGGSTYYA

DSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCAKDPYSFDYWGQGTLTVVSS (SEQ

ID NO: 511)

BMS3h-198-11

EVQLLES GGGGLVQPGGSLRLSCAASGFTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYYA

20 DSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCARDPYSFDYWGQGLTVSVSS (SEQ

ID NO: 512)

BMS3h-198-12

EVQLLES GGGGLVQPGGSLRLSCAASGFTIAGYEMWWVRQAPGKGLERVSAISGSGGSTYYA

DSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCAKDPYSFDYWGQGTLTVVSS (SEQ

25 ID NO: 513)

BMS3h-198-13

EVQLLESGGGLVQPGGSLRLSCAASGFTTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYYA
DSVKGRFTITRDDSKNTLYLQMNSLRAEDTAVYYCAKEPYSFDYWGQGTLVTVSS (SEQ
ID NO: 514)

5 BMS3h-198-14

EVQLLESGGGLVQPGGSLRLSCAASGFTTFAGYEMWWFRQAPGKGLERVSAISGSGGSTYYA
DSVKGRFTISRDDTKNTLYLQMNSLRAEDTAVYYCAKDPYSFDYWRQGTLVTVSS (SEQ
ID NO: 515)

BMS3h-198-15

10 EVQLLESGGGLVQPGGSLRLSCAASGSTFAGYEVWWVRQAPGKGLERVSAISGSGGSTYYA
DSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCARDPYSFDYWGQGTLVTVSS (SEQ
ID NO: 516)

BMS3h-198-16

EVQLLESGGGLVQPGGSLRLSCAASGSTFAGYEMWWVRQAPGKGLERISAIISGSGGSTYYA
15 DSVKGRFTISRDDSKNTLYLKMNSLRAEDTAVYYCAKDPYSFDYWGQGTLVTVSS (SEQ
ID NO: 517)

BMS3h-198-17

EVQLLESGGGLVQPGGSLRLSCAASGFTTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYYA
DSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCARDPYSFDYWGQGTLVTVSS (SEQ
20 ID NO: 518)

BMS3h-198-18

EVQLLESGGGLVQPGGSLRLSCAASGLTFAGYEMWWVRRAPGKGLERVAAISGSGGSTYYADSVKGR
FTISRDDSKNTLYLQMNSLRAEDTAVYYCARDPYSFDYWGQGTLVTVSS (SEQ ID NO: 519)

BMS3h-198-19

25 EVQLLESGGGLVQPGGSLRLSCAASGFTTFAGYELWWVRQAPGKGLERVSAISGSGGSTYYA

DSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCARDPYSFDYRGQGTLVTVSS (SEQ
ID NO: 520)

BMS3h-198-20

EVQLLESGGGLVQPGGSLRLSCAAPGFTLAGYEMWWVRQAPGKGLERVSAISGSGGSTYYA

5 DSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCAKEPYSFDYWQGQTLVTVSS (SEQ
ID NO: 521)

BMS3h-198-21

EVQLLESGGGLVQPGGSLRLSCAASGLTFAGYEMWWVRAPGKGLERVSAISGSGGSTYYA

DSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCARDPYSFDYWGRGTLVTVSS (SEQ
10 ID NO: 522)

BMS3h-198-22

EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYYA

DSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCAKEPYSYDYWGHGTLVTVSS (SEQ
ID NO: 523)

15 BMS3h-198-23

EVQPLESGGGGLVQPGGSLRLSCAASGFTFAGYEMWWVRQAPGKGLERVSAISGSGGNTYYA

DSVKGRFTISRDDSKNTLYLQMNSLRAEDTGVYYCARDPYSFDYWQGQTLVTVSS (SEQ
ID NO: 524)

BMS3h-198-24

20 EVQLLESGGGLVQPGGSLRLSCAASGFTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYYA

DSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCAKEPYSFDSWGQTLVTVSS (SEQ
ID NO: 525)

BMS3h-198-25

EAQLLESGGGLVQPGGSLRLSCAASGLTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYYA

25 DSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCARDPYSFDYWQGQTLVTVSS (SEQ

ID NO: 526)

BMS3h-198-26

EVQLLES GGGGLVQPGGSLRLSCAASGSTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYYA
DSVKGRFSISRDDSKNTLYLQMNSLRAEDTAVYYCAKEPYSFDHWGQGTLVTVSS (SEQ

5 ID NO: 527)

BMS3h-198-27

EVQLLES GGGGLVQPGGSLRLSCAASGSTFAGYEMWWVRAPGKGLERVSAISGSGGSTYYA
DSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCARDPYSFDYWGQGTLVTVSS (SEQ

ID NO: 528)

10 BMS3h-198-28

EVQLLES GGGGLVQPGGSLRLSCAASGFTFAGYEMWWFRQAPGKGLERVSAISGSGGSTYYA
DSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCAKDPYSFDNWGQGTLVTVSS (SEQ

ID NO: 529)

BMS3h-198-29

15 EVQLLES GGGGLVEPPGGSLRLSCAASGFTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYYA
DSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCAKEPYSFDHRGQGTLVTVSS (SEQ

ID NO: 530)

BMS3h-198-30

EVQLLES GGGGLVQPGGSLRLSCAASGYTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYYA
20 DSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCAKEPYSFDHRGQGTLVTVSS (SEQ

ID NO: 531)

BMS3h-198-31

EVQLLES GGGGLVQPGGSLRLSCAASGFTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYHCAKEPYSYDYWGQGTLVTVSS (SEQ

25 ID NO: 532)

BMS3h-198-32

EVQLLESGGGLVQPGGSLRLSCAASGFTTFAGYEMWWFRQAPGKGLERVSAISGSGGSTYYA
DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKDPYSFDNWGQGTLTVSS (SEQ
ID NO: 533)

5 BMS3h-198-33

EVQLLESGGGLVQPGGSLRLSCAASGFTTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYYA
DSVKGRFTISRDD SKNTLYLQMNSLRAEDTAVYYCAKEPYSYDYWGQGTLTVSS (SEQ
ID NO: 534)

BMS3h-198-34

10 EVQLLESGGGLVQPGGSLRLSCAASGFTTFAGYEMWWVRQAPGKGLERVSAISGSGGSTYYA
DSVKGRFTISRDD SKNTLYLQMNSLRAEDTAVYYCAKDPYSFDNWGQGTLTVSS (SEQ
ID NO: 535)

BMS3h-198-35

EVQLLESGGGLVQPGGSLRLSCAASGFTTFAGYEMWWVRQAPGKGLEWVSAISGSGGSTYYA
15 DSVKGRFTISRDD SKNTLYLQMNSLRAEDTAVYHCAKEPYSYDYWGQGTLTVSS (SEQ
ID NO: 536)

BMS3h-198-36

EVQLLESGGGLVQPGGSLRLSCAASGFTTFAGYEMWWFRQAPGKGLEWVSAISGSGGSTYYA
DSVKGRFTISRDD SKNTLYLQMNSLRAEDTAVYYCAKDPYSFDNWGQGTLTVSS (SEQ
20 ID NO: 537)

BMS3h-198-37

EVQLLESGGGLVQPGGSLRLSCAASGFTTFAGYELWWVRQAPGKGLERVSAISGSGGSTYYADSVKGRFTIS
RDD SKNTLYLQMNSLRAEDTAVYYCAKDPYSFDYRGQGTLTVSS (SEQ ID NO: 538)

BMS3h-198-38

25 EVQLLESGGGLVQPGGSLRLSCAASGFTTFAGYELWWVRQAPGKGLERVSAISGSGGSTYYA

DSVKGRFTISRDDSKNTLYLQMNSLRAEDTAVYYCARDPYSFDYWGQGTTLVTVSS (SEQ
ID NO: 539)

BMS3h-202-1

EVQLLESGGGLVQPGGSLRLSCAASGFTFPTAEMLWVRKAPGKGLEWVSSISASGGSTYYA

5 DSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKEPVSYVATFDYWGQGTTLVTVSS
(SEQ ID NO: 540)

BMS3h-202-2

EVQLLVSGGGLVQPGGSLRLSCAASGFTFPTAEMLWVRQAPGKGPEWVSSISASGGSTYYA

DSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKEPVSYVATFDYWGQGTTLVTVSS

10 (SEQ ID NO: 541)

BMS3h-202-3

EVQLLESGGGLVQPGGSLRLSCAASGFTFPTAEMVWVRKAPGMGLEWVSSISASGGYTYA

DSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKEPVSYVATFDYWGQALVTVTS

(SEQ ID NO: 542)

15 BMS3h-202-4

EVQLLVSGGGLVQPGGSLRLSCAASGFTFPTAEMVWVRQAPGKGLEWVSSISASGGSTYYA

DSVKGRFSISRDDSKNTLYLQMNSLRAEDTAVYYCAKEPVSYVATFDYWGHALVTVSS

(SEQ ID NO: 543)

BMS3h-202-5

20 EVQLLESGGGLVQPGGSLRLSCAASGFTFPTAEMLWVRQAPGKGLEWVSSISASGGSTYYA

DSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKEPVSYVATFDYWGQGTTLVTVSS

(SEQ ID NO: 544)

BMS3h-202-6

EAQLLESGGGLVQPGGSLRLSCAASGFTFPTAEMVWVRQAPGKGLEWISSISASGGSTYYA

25 DSVKGRFTISRDNKNTLYLQLNSLRAEDTAVYYCAKEPVSYVATFDYWGRGTLVTVSS

(SEQ ID NO: 545)

BMS3h-202-7

EVQLLESGGGLVQPGGSLRLSCAASGFTFPTAEMLWVRQAPGKGLEWVSSISASGGSTYYA
DSVKGRFTISRDNKSTLYLQMNSLRAEDTAVYYCAKEPVSYVATFDYWGPALVTVSS

5 (SEQ ID NO: 546)

BMS3h-202-8

EVQLLESGGGLVQPGGSLRLSCAASGFTFPTAEMLWVRKAPGKGLEWVSSISASGGSTYYA
DSVKGRFTISRDNKNTLFLQMNSLRAEDTAVYYCAKEPVSYVATFDYWQGTLVTVSS

(SEQ ID NO: 547)

10 BMS3h-202-9

EVQLLESGGGLVQPGGSLRLSCAASGFTFPTAEMLWVRQAPGKGLEWVSSISASGGSTYYA
DSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKEPVSYVATFDYWGPALVTVSS

(SEQ ID NO: 548)

BMS3h-202-10

15 EVQLLESGGGLVQPGGSLRLSCAASGFTFPTAEMLWVRQAPGKGLEWVSSISASGGSTYYA
DSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKEPVYYVATFDYWQGTLVTVSS

(SEQ ID NO: 549)

BMS3h-202-11

EVQLLESGGGLVQPGGSLRLSCAASGFTFPTAEMLWVRKAPGKGLEWVSSISASGGSTYYA
20 DSVKGRFTISRDNKNTLYLQMNSLRAEDAAVYYCAKEPVSYVATFDYWQGTLVTVSS

(SEQ ID NO: 550)

BMS3h-217-1

NIQMTQSPSSLSASVGDRVITITCRASHFIGTLLTWYQHKPGKAPKLLITYGSLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO:

25 551)

BMS3h-217-2

DIQMTQSPSSLSASVGDRVITITCRASHFIGTLLSWYQQKPRKAPKLLITYGSLQSGVPSR
FSGSGSGTDFTLTISLHPEDFATYYCGQGVLPPTFGQGTKVEIKR (SEQ ID NO:
552)

5 BMS3h-217-3

DIQMTQSPSSLTASVGDRVITITCRASHFIGTLLSWYQQKPGKAPKLLVITYGSLQSGVPSR
FSGSGSGTDFTLTISNLQPEDFATYYCGQGVLPPTFGQGTKVENIR (SEQ ID NO:
553)

BMS3h-217-4

10 DIQMTQSPSSLSASVGDRVITITCRASHFIATLLSWYQQKPGKAPKLLITYGSLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPPTFGQGTKVEIKR (SEQ ID NO:
554)

BMS3h-217-5

DIQMTQSPSFLSASVGDRVITITCRASHFIATLLSWYQQKPGKAPKLLITYGSLQSGVPSR
15 FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPPTFGQGTKVEIKR (SEQ ID NO:
555)

BMS3h-217-6

DIQMTQSPSSLSASVGDRVITITCRASHFIGTLLSWYQQKPGKATKLLITYGSLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPPTFGQGTKVEIKR (SEQ ID NO:
20 556)

BMS3h-217-7

DIQMTQSPSSLSASVGDRVITITCRASHFIGSLLSWYQHKPGKAPKLLITYGSLQSGVPSRFSGS
GSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO: 557)

BMS3h-217-8

25 DIQMTQSPSSLSASVGDRVITITCRASHFIGTLLSWYQHKPGKAPKLLITYGSLQSGVPSR

FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO:
558)

BMS3h-217-9

DIQMTQSPSSLSASVGDRVITICRASHFIGTLLSWYQHKPGKAPKLLITYGSMLQSGVPSR

5 FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO:
559)

BMS3h-217-10

DIQMTQSPSSLSASVGDRVITICRASHFIGTLLSWYQHKPGKAPKLLITYGSLLQSGVPSR

FSGSGSGTEFTLTISLQPEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO:
10 560)

BMS3h-217-11

DIQMTQSPSSLTASVGDRVITICRASHFIGTLLSWYQHKPGKAPKLLITYGSLLQSGVPSR

FSGSGSGTEFTLTISLQPEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO:
561)

15 BMS3h-217-12

NIQMTQSPSSLSASVGDRVITICRASHFIGTLLSWYQHKPGKAPKLLITYGSLLQSGVPSR

FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO:
562)

BMS3h-217-13

20 DIQMTQSPSSLSASVGDRVITINCRASHFIGTLLSWYQHKPGKAPKLLITYGSLLQSGVPSR

FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO:
563)

BMS3h-217-14

DIQLTQSPSSLSASVGDRVITICRASHFIGTLLSWYQQKPGKATKLLITYGSLLQSGVPSR

25 FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPPTFGQGTKVEIKR (SEQ ID NO:

564)

BMS3h-217-15

DIQMTQSPSSLYASVGDRVITITCRVSHFIGTLLSWYQQKPGKAPKLLITYGSLQSGVPSR
FSGSGSGTDFTLSISSLQPEDFATYYCGQGVLPPTFGQGTKVEIKQ (SEQ ID NO:

5 565)

BMS3h-217-16

DIQMTQSPSSLSASVGDRVITITCRASHFIGTLLSWYQQKPRKAPKLLITYGSLQSGVPSR
FSGSGSGTDFTLTISSLQPEDFATYYCGQGVLPPTFGQGTKVEIKR (SEQ ID NO:

566)

10 BMS3h-217-17

DIQIIQSPSSLSASVGDRVITITCRASHFIGTLLSWYQQKPGKAPKLLITYGSLQSGVPSR
FSGSGSGTDFTLTISSLQPEDFATYYCGQGVLPPTFGQGTKVEIKR (SEQ ID NO:

567)

BMS3h-217-18

15 DIQMTQSPSSLSASVGDRVITITCRASHFIGTLLSWYQLKPGKAPKLLITYGSLQSGVPSR
FSGSGSGTDFTLTISSLQPEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO:

568)

BMS3h-217-19

DIQMTQSPSSLSASVGDRVITITCRASHFIGTLLSWYQLKPGKAPKLLITYGSLQSGVPSR
20 FSGSGSGTDFTLTISSLQPEDFATYYCGQGVLPATFGQGTKVENKR (SEQ ID NO:

569)

BMS3h-217-20

DIQMTQSPSSLSASVGDRVITITCRASHFIGTLLSWYQLKPGKAPKLLITYGSLQSGVPSR
FSGSGSGTDFTLTISSLQPEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO:

25 570)

BMS3h-217-21

DIQMTQAPSSLSASVGDRVTITCRASHFIGTLLSWYQLKPGKAPKLLITYGSLLQSGVPSR
FSGSGSGTDFTLTISSLQPEDFATYYCGQGVLPATFGQGTKVENKR (SEQ ID NO:
571)

5 BMS3h-217-22

DIQMTQSPSSLSASVGDRVTITCRASHFIGSLLSWYQQKPGKAPKLLITYGSLLQSGVPSR
FSGSGSGTDFALTISLQPEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO:
572)

BMS3h-217-23

10 DIQMTQSPSSLSASVGDRVTITCRASHFIGSLLSWYQVKPGKAPKLLITYGSLLQSGVPSR
FSGSGSGTDFTLTISSLQPEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO:
573)

BMS3h-217-24

DILMTQSPSSLSASVGDRVTITCRASHFIGSLLSWYQQKPGKAPKLLITYGSLLQSGVPSR
15 FSGSGSGTDFTLTISSLQPEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO:
574)

BMS3h-217-25

DIQMTQSPSSLSASVGDRVTITCRASHFIGTLVSWYQQKPGKAPKLLITYGSLLQSGVPSR
FSGSGSGTDFTLTISSLQPEDFATYYCGQGVLPATYGQGTKVEIKR (SEQ ID NO:
20 575)

BMS3h-217-26

DIQMTQSPSSLSASVGDRVTITCRASHFIGTLVSWYQQKPGKAPKLLITYGSLLQSGVPSRFSGS
GSGTDFTLTISSLQPEDFATYYCGQGVLPATFGQGTKVENKR (SEQ ID NO: 576)

BMS3h-217-27

25 DIKMTQSPSSLSASVGDRVTITCRASHFIGTLVSWYQQKPGKAPKLLITYGSMLQSGVPSR

FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO:
577)

BMS3h-217-28

DIQMTQSPSSLSASVGDRVITTCQASHFIGTLVSWYQQKPGKAPKLLITYGSLLQSGVPSR

5 FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO:
578)

BMS3h-217-29

DIQMTQSPSSLSASVGDRVITTCRASHFIGTLLSWYQQKPGKAPKLLITYGSWLQSGVPSR

FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO:
10 579)

BMS3h-217-30

DIQMTQSPSSLSASVGDRVITTCRASHFIGTLLSWYQLKPGKAPKLLITYGSWLQSGVPSR

FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO:
580)

15 BMS3h-217-31

DIQMTQSPSSLSASVGDRVITTCRASHFIGTLLSWYQQKPGKAPKLLITYGSLLQSGVPSR

FSGSGFGTDFTLTISLQPEDFATYYCGQEVLPATFGQGTKVEIKR (SEQ ID NO:
581)

BMS3h-217-32

20 DIQMTQSPSSLSASVGDRVSITCRASHFIGTLLSWYQQKPGKAPKLLITYGSLLQSGVPSR

FSGSGFGTDFTLTISLQPEDLATYYCGQEVLPATFGQGTKVEIKR (SEQ ID NO:
582)

BMS3h-217-33

DIQMTQSPSSLSASVGDRVITTCQASHFIGTLLSWYQQKPGKAPKLLITYGSLLQSGVPSR

25 FSGSGFGTDFTLTISLQPEDFATYYCGQEVLPATFGQGTKVEIKR (SEQ ID NO:

583)

BMS3h-217-34

DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQQKPGKAPKLLITYGSLQSGVPSR
FSGSGFGTEFTLTIGSLQPEDFATYYCGQGVLPATFGQGTKVEIKR (SEQ ID NO:

5 584)

BMS3h-217-35

DIQMTQSPSSLSASVGDRVTITCRASHFIGTLLSWYQQKPGKATKLLITYGSLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPPTFGQGTKVEIKR (SEQ ID NO:

585)

10 BMS3h-217-2301

DIQMTQSPSSLSASVGDRVTITCRASHFIASLLSWYQVKPGKAPKLLITYGSLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO:

586)

BMS3h-217-2302

15 DIQMTQSPSSLSASVGDRVTITCRASHFIAQLLSWYQVKPGKAPKLLITYGSLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO:

587)

BMS3h-217-2303

DIQMTQSPSSLSASVGDRVTITCRASHFIAQLLSWYQVKPGKAPKLLITYGSLQSGVPSR
20 FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTVEIRR (SEQ ID NO:

588)

BMS3h-217-2304

DIQMTQSPSSLSASVGDRVTITCRASHYIASLLSWYQVKPGKAPKLLITYGSLQSGAPSR
FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO:

25 589)

BMS3h-217-2305

DIQMTQSPSSLSASVGDRVITITCRASHFIGSLLSWYQVKPGKAPKLLITWASYLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO:
590)

5 BMS3h-217-2306

DIQMTQSPSSLSASVGDRVITITCRASHFIGSLLSWYQVKPGKAPKLLITWTSYLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO:
591)

BMS3h-217-2307

10 DIQMTQSPSSLSASVGDRVITITCRASHFIGSLLSWYQVKPGKAPKLLITWSSYLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO:
592)

BMS3h-217-2308

DIQMTQSPSSLSASVGDRVITITCRASHFIGSLLSWYQVKPGKAPKLLITWGSWLQSGVPSR
15 FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO:
593)

BMS3h-217-2309

DIQMTQSPSSLSASVGDRVITITCRASHFIGSLLSWYQVKPGKAPKLLITWASWLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO:
20 594)

BMS3h-217-2310

DIQMTQSPSSLSASVGDRVITITCRASHFIGSLLSWYQVKPGKAPKLLITWSSWLQSGVPSRFSGS
GSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 595)

BMS3h-217-2311

25 DIQMTQSPSSLSASVGDRVITITCRASHWIAQLLSWYQVKPGKAPKLLITYGSLQSGVPSR

FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO:
596)

BMS3h-217-2312

DIQMTQSPSSLSASVGDRVITICRASHFIGSLLRWYQVKPGKAPKLLITYGSLLQSGVPSR

5 FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO:
597)

BMS3h-217-2313

DIQMTQSPSSLSASVGDRVITICRASHRIAQLLSWYQVKPGKAPKLLITYGSLLQSGVPSR

FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO:
10 598)

BMS3h-217-2314

DIQMTQSPSSLSASVGDRVITICRASHYIASLLSWYQVKPGKAPKLLITYGSLLQSGVPSR

FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO:
599)

15 BMS3h-217-2315

DIQMTQSPSSLSASVGDRVITICRASHFIGSLLSWYQVKPGKAPKLLIRFGSLLQSGVPSR

FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO:
600)

BMS3h-217-2316

20 DIQMTQSPSSLSASVGDRVITICRASHFIGSLLSWYQVKPGKAPKLLITYKSYLQSGVPSR

FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO:
601)

BMS3h-217-2317

DIQMTQSPSSLSASVGDRVITICRASHFIGSLLSWYQVKPGKAPKLLITWGSYLQSGVPSR

25 FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO:

602)

BMS3h-217-2318

DIQMTQSPSSLSASVGDRVITITCRASHFIWGPLSWYQVKPGKAPKLLITYGSLQSGVPSR
FSGSGSGTDFTLTISLQPEDSATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO:

5 603)

BMS3h-217-2319

DIQMTQSPSSLSASVGDRVITITCRASHWIATLLSWYQVKPGKAPKLLITYGSLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO:

604)

10 BMS3h-217-2320

DIQMTQSPSSLSASVGDRVITITCRASHFIWGPLSWYQVKPGKAPKLLITYGSLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO:

605)

BMS3h-217-2321

15 DIQMTQSPSSLSASVGDRVITITCRASHFIGSLLNWKYQVKPGKAPKLLITYGSLQSGVPSR
FSGSGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO:

606)

BMS3h-217-2322

GIQMTQSPSSLSASVGDRVITITCRASHFIGSLLSWYQVKPGKAPKLLITYGSLQSGVPSRFSG

20 SGSGTDFTLTISLQPEDFATYYCGQGVLPATFGQGTVEIKR (SEQ ID NO: 607)

TABLA 4

Secuencias Nucleotídicas que Codifican para el Dominio

Variable Anti-CD40 Humano

BMS3h-56-201

25 GAGGTGCAGCTGTTGGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT

CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTA
 5 CTTTCAGGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 608)
 BMS3h-56-258
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 10 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTA
 CTTTCACGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 609)
 BMS3h-37
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 15 CCTGTGCAGCCTCCGGATTACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCGATTTCTGGTGATGGTTATCGTACATACTACGCA
 GACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTA
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 610)
 20 BMS3h-38
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 25 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCCGTTTCG

TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 611)

BMS3h-41

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT

CCTGTGCAGCCTCCGGATTCACCTTTACTGAGTATGAGATGATTTGGGTCCGCCAGGCTCC

5 AGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCCGGTAATGGTGCTAATACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC

AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTTAG

GTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 612)

BMS3h-43

10 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT

CCTGTACAGCCTCCGGATTCACCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCC

AGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTAGGCGTGGTTTTACTACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC

AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCCGATTAC

15 GTATGCTATGAGGTATGCGCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG

AGC (SEQ ID NO: 613)

BMS3h-56

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT

CCTGTGCAGCCTCCGGATTCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC

20 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC

AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAT

TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 614)

BMS3h-106

25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT

CCTGTGCAGCCTCCGGATTACCTTTTCGACTTATCATATGCAGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTGGAGTGGGTCTCAATGATTGATGCGGATGGTCTTGGGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGGGTCCGCA
 5 GTTTGGTCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 615)

BMS3h-107

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCTTCCGGATTACCTTTTCGGGGTATGATATGCAGTGGGTCCGCCAGGCTCC
 10 AGGGAAGGGTCTAGAGTGGGTCTCAACGATTAGTGCGTCGGGTGTTTTTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCACCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATCCTAATCG
 TTTTGCGCTTAATAATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
 (SEQ ID NO: 616)

15 BMS3h-131

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCA
 TCACTTGCCGGGCAAATAGTTCTATTTTGTGGGCGTTAGCTTGGTACCAGCAGAAACCAGG
 GAAAGCCCCTAAGCTCCTGATCGAGAGTTCTTCCGGTTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 20 ATTTTGCTACGTACTACTGTGTTTCAAGATGCGGGTTGGCCTGGTACGTTTCGGCCAAGGGAC
 CAAGGTGGAAATCAAACGG (SEQ ID NO: 617)

BMS3h-193

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCA
 TCACTTGCCGGGCAAAGTCAGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGG
 25 GAAAGCCCCTAAGCTCCTGATCTATCTTGCTTCCCGTTTGCAAAGTGGGGTCCCATCACGT

TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTCATCAGTATGCGAGTCCACCTTTGACGTTTCGGCCAAGGGAC
 CAAAGTGGAATCAAACGG (SEQ ID NO: 618)

BMS3h-198

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATCCTTATAG
 10 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 619)

BMS3h-202

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTCCGACTGCTGAGATGGTGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCCGGCTAGTGGTGGTTCTACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGGTGAG
 TTATGTGGCGACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ
 ID NO: 620)

BMS3h-217

20 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCA
 TCACTTGCCGGGCAAGTCATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACCAGG
 GAAAGCCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTTTCGGCCAAGGGAC
 25 CAAGGTGGAATCAAACGG (SEQ ID NO: 621)

BMS3h-1

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCCGAAGAATGAGATGACGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCGATTGAGTCGGATGGTCAGGCTACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGCGAAAAATCGGATTCC
 TGATCTTGTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 622)

BMS3h-2

10 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGATGCTGGGGCTATGACGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCATCTATTGATAAGGAGGGTCTGTCTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGGTAGGATTCC
 15 TGGGCTGGTTTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 623)

BMS3h-3

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCT
 GTGCAGCCTCCGGATTACCTTTGGTGATGCGGCGATGACTTGGGTCCGCCAGGCTCCAGGGAA
 20 GGGTCTAGAGTGGGTCTCAGCGATTACGCTATGGGTGATGGTACATACTACGCAGACTCCGTG
 AAGGGCCGGTTCACCGTCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCC
 TCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCGTATTCCTACTCTTCAGTTTGA
 CTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 624)

BMS3h-4

25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT

CCTGTGCAGCCTCCGGATTCACCTTTGAGGATTCGCCTATGACTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTACTTCGAATGGTTATGAGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCGTATTCC
 5 TACTCTTCATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 625)

BMS3h-5

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTGATGAGCATGATATGAGTTGGGTCCGCCAGGCTCC
 10 AGGGAAGGGTCTAGAGTGGGTCTCACGTATTGGTCCGGATGGTTTTTCATACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCGTATTCC
 TACTCTTCATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 626)

15 BMS3h-6

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTGGTGAGTATCATATGTCTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAAGGATTACTCCTCTTGGTACGCTTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCGTATTCC
 TTCGCTTACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 627)

BMS3h-7

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 25 CCTGTGCAGCCTCCGGATTCACCTTTGGTACGAATGCGATGAGTTGGGTCCGCCAGGCTCC

AGGGAAGGGTCTGGAGTGGGTCTCAAGGATTTGCCCGGGTGGTGATTATACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTGTATTACTGTGCGAAAGGGCGTGTTC
 GGATCTGCTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID

5 NO: 628)

BMS3h-8

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCCGTCTGAGGAGATGTCTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAAGGATTTCCGCTGATGGTGCTAATACATACTACGCA
 10 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACGCCGCGGTATATTACTGTGCGAAAGGGCGTGTTC
 GGATCTGCTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID

NO: 629)

BMS3h-9

15 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGCTGAGGATGATATGACTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCACGTATTGCGGTTGATGGTGATCGGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTAAGGTTCC

20 GTCTCTTCATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 630)

BMS3h-10

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGATCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTAGGACGATGGATATGTCTTGGGTCCGCCAGGCTCC
 25 AGGGAAGGGTCTAGAGTGGGTCTCACGTATTACGGGTGATGGTATGAATACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGGGGACACCGCGGTATATTACTGTGCGAAAGGGGTGACTCC
 GGATTTGACTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 631)

5 BMS3h-11

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTGAGCGTGATGATATGACGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCACGTATTAATGCTGGGGGTGTGCATACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 10 AAATGAACAGCCTGCGTGCCGAGGATAACCGCGGTATATTACTGTGCGAAAGGGGTGACTCC
 GGATTTGACTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 632)

BMS3h-12

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 15 CCTGTGCAGCCTCCGGATTCACCTTTGATGATGATTCTATGACGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCACGGATTTTCGAGTGATGGTGCGAGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGTGACTCC
 GGATTTGACTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 20 NO: 633)

BMS3h-13

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTACTGAGGAGGATATGACGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCACGTATTGATAGTGTTGGTGAGGGGACATACTACGCA
 25 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC

AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGTGACTCC
GGATTTGACTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
NO: 634)

BMS3h-14

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTCACCTTTTCTGATTCGGCGATGAGTTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCACGGATTGATAATCCTGGTCAGCATACTACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGGTACTGTTCC
10 TACGCTGGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
NO: 635)

BMS3h-15

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTCACCTTTGGGCAGCATAGTATGACTTGGGTCCGCCAGGCTCC
15 AGGGAAGGGTCTAGAGTGGGTCTCACGTATTGATGGTGGGGTTATAATACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGAGGTTCC
TCGTCTTCATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
NO: 636)

20 BMS3h-16

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTCACCTTTGGTCAGGAGCCTATGACTTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCACGGATTGCGTATAATGGTGGTGATACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
25 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATTACTCC

TAATTTGACTTTTGGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
NO: 637)

BMS3h-17

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
5 CCTGTGCAGCCTCCGGATTCACCTTTGAGAATTATCCGATGTCTTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCACGTATTAATGCTACGGGTTCTATTACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGTATTTC
TCATTTGATGTTTGGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
10 NO: 638)

BMS3h-18

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTCACCTTTCGTGATTATGATATGAGTTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCACGTATTACTGGTACTGGTAATAGTACATACTACGCA
15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAAGGGGTGGTGCC
GTATCTTGCTTTTGGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
NO: 639)

BMS3h-19

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
20 CCTGTGCAGCCTCCGGATTCACCTTTGAGGCTGATGCGATGACGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAAGGATTAATGTGGATGGTGATCGGACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTACTGTTCC
25 TACGCTGGAGTTTGGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID

NO: 640)

BMS3h-21

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGATCGGGCGGATATGACGTGGGTCCGCCAGGCTCC
 5 AGGGAAGGGTCTAGAGTGGGTCTCAAGGATTTCTGGGGGAGGGTAAGTGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATGGTTCC
 TAATTTGGTTTTTTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 641)

10 BMS3h-22

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCATTGGGAGCCGATGTCTTGGGTCCGCCAGGCTCC
 GGGGAAGGGTCTAGAGTGGGTCTCACGTATTAATTCTTCTGGTTGGGATACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 15 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATGGTTCC
 TAATTTGGTTTTTTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 642)

BMS3h-24

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 20 CCTGTGCAGCCTCCGGATTACCTTTGCTGATGAGCCGATGACTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCACGTATTCCTCCTGAGGGTGCTCCGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATTACTCC
 TAATTTGACTTTTTGACTACTGGGGTCAGGGAACCCCTGGTCACCGTCTCGAGC (SEQ ID
 25 NO: 643)

BMS3h-26

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCATAATCATGATATGTCTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCACGTATTAGTCGGGGTGGTCTTCAGACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATTGTGCC
 GGATCTGCATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 644)

BMS3h-27

10 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTAATGAGTATCCTATGTCGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCACGTATTAATGGGGATGGTGCTAATACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATTATTCC
 15 GGCTATGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 645)

BMS3h-28

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTG
 TGCAGCCTCCGGATTACCTTTGGGGATGTGCCTATGTCGTGGGTCCGCCAGGCTCCAGGGAAGG
 20 GTCTAGAGTGGGTCTCAAGGATTGATCCTTATGGTTCTAATACATACTACGCAGACTCCGTGAAG
 GGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGCG
 TGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTATTATGCCTAGTCTTACTTTTGACTACT
 GGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 646)

BMS3h-29

25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT

CCTGTGCAGCCTCCGGATTCACCTTTGCGGATTATGATATGTCTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCACGTATTTTCGGCGCTTGGTGCTACTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTCAGCTTCC
 5 GCGCTTGGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 647)

BMS3h-30

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTAAGCGTTATTATATGACTTGGGTCCGCCAGGCTCC
 10 AGGGAAGGATCTAGAGTGGGTCTCAGGTATTGTTTCCTTCTGGTAATAGGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTAGGATTCC
 GGATCTGCATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 648)

15 BMS3h-31

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTGCTGATTATGATATGACTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAAGGATTTCTCCGACGGGTGGGCAGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTGTTATTCC
 GTATTTGTCTTTTTTCTCCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
 (SEQ ID NO: 649)

BMS3h-32

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 25 CCTGTGCAGCCTCCGGATTCACCTTTTCTAAGTATTGGATGGGTTGGGCCCGCCAGGCTCC

AGGGAAGGGTCTAGAGTGGGTCTCATCGATTGATTTCGCATGGTGCTGGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGTCGAGGACACCGCGGTATATTACTGTGCGAAAGGTGCTCCTAA
 GTTTATGACTACGTATACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

5 (SEQ ID NO: 650)

BMS3h-33

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTTTGTCTTATCCGATGCATTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCATCGATTGATTTCGAGGGGTTTCGGTTACATACTACGCA
 10 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTCATAGTTG
 GACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:

651)

BMS3h-34

15 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGCGAATAGTAATATGACTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCACGTATTAATCCGGATGGTGGGTCTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGGGCGTATTCC
 20 TACTCTTCATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID

NO: 652)

BMS3h-35

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGGGCCGAGGAGGATGGGTTGGGTCCGCCAGGCTCC
 25 AGGGAAGGGTCTAGAGTGGGTCTCATCGATTGATGATATTGGTCGTAGGACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGGGGCGCAGGG
TGTGTTGTTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
NO: 653)

5 BMS3h-36

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTCACCTTTGAGGATTATAGGATGGTTTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCATCGATTTCTACTTCTGGTGAGCTGACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
10 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAACGGCGGGTCA
GTTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
654)

BMS3h-39

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
15 CCTGTGCAGCCTCCGGATTCACCTTTCCGGAGTATGAGATGGTTTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTGGAGTGGGTCTCAGCGATTTTCGCGTGAGGGTCGGGCTACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAACCTGCGTGCCGAGGATAACCGCGGTATATTACTGTGCGAAAGAGCCTGTTTCG
TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 655)

20 BMS3h-40

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTCACCTTTTCGACTTATGAGATGCTTTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCTTCTTCTGGTAATTATACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
25 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTGAT

GTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 656)

BMS3h-42

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT

CCTGTGCAGCCTCCGGATTACCTTTGATACTGAGGAGATGAGTTGGGTCCGCCAGGCTCC

5 AGGGAAGGGTCTAGAGTGGGTCTCAGCGATTAGTCCTAATGGTGCTTTTACATTCTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC

AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCTATTCT

GTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 657)

BMS3h-44

10 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT

CCTGTGCAGCCTCCGGATTACCTTTGGTCATTATGATATGGTTTGGGTCCGCCAGGCTCC

AGGGAGGGGTCTAGAGTGGGTCTCAACTATTAATGGTGCTGGTCTGAATACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC

AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAAAGTGCTAGTCG

15 TATTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
658)

BMS3h-45

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTG

TGCAGCCTCCGGATTACCTTTAGGAGTTATGAGATGGCGTGGGTCCGCCAGGCTCCAGGGAAGG

20 GTCTAGAGTGGGTCTCATCTATTAGTACTCTGGGTACGAAGACATACTACGCAGACTCCGTGAAG

GGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGCG

TGCCGAGGACACCGCGGTATATTACTGTGCGCAATCTTCTACTCATATTTTTGACTACTGGGGTC

AGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 659)

BMS3h-46

25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT

CCTGTGCAGCCTCCGGATTCACCTTTATTAGGTATGAGATGGCTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAAGTATTTTCGTCGTCTGGTTGGACGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAAGTGATGCTCA
 5 TATTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
 660)

BMS3h-47

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTTATGCTTATGAGATGGCTTGGGTCCGCCAGGCTCC
 10 AGGGAAGGGTCTAGAGTGGGTCTCATCTATTTTCGGATGATGGTACGCGGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATCTGGGGCA
 GGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
 661)

15 BMS3h-48

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTGCTGATCATGGGATGACGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGGGATTGGTCCGTCTGGTGAGGCGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATCGTATTCC
 TAATCTTGTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 662)

BMS3h-49

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 25 CCTGTGCAGCCTCCGGATTCACCTTTGAGTCTCAGGATATGTCTTGGGTCCGCCAGGCTCC

AGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTCCGAATGGTTGGGATACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATAGGTCTGA
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 663)

5 BMS3h-50

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGGGGATTATGATATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAAGGATTCGTCATCCGGGTGGTGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 10 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTGTTCTTAA
 GGGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
 664)

BMS3h-51

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 15 CCTGTGCAGCCTCCGGATTACCTTTCGGGTTTATTGGATGACTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCATCTATTGATCCGCAGGGTGGGATGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCTCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGCGCGTATTCC
 TAATTTGGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 20 NO: 665)

BMS3h-52

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGAGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTAGTGCTTATGATATGACGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTTGAGTGGGTCTCACGTATTAATCCGACGGGTTCCTATACATACTACGCA
 25 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC

AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGCTAAGATTCC
GAATTTGGTTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
NO: 666)

BMS3h-53

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTGCGGATAGTGAGATGATGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGCGCATAATGGTGGGCATACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTGGTCATCC
10 TCAGCAGACTGAGGCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
(SEQ ID NO: 667)

BMS3h-54

GAGATGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTGCTACTTATGATATGTATTGGGTCCGCCAGGCTCC
15 AGGGAAGGGTCTAGAGTGGGTCTCAAAGATTTCTCCGAATGGTTGGAGTACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATCAGACGCA
TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 668)

BMS3h-55

20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTAGTGTTTATGATATGAGGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCTTCTTCGGGTACGTATACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATCCTAAGAA
25 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 669)

BMS3h-57

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTTCTCATGAGGATATGACTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTCCGAATGGTTGGGATACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACGTACTAGGAG
 TAAGTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
 670)

BMS3h-58

10 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGAGAAGTATATTATGGGTGGGCCCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAACGATTGATTATTGGGGTCAGCATACTACTACGCA
 GACTCCGTGAAGGGCCGGTTCATCTCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACGTAGTCATCT
 15 TATTCCTCTGCAGTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ
 ID NO: 671)

BMS3h-59

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTG
 CAGCCTCCGGATTACCTTTTCTGATTATGCGATGGGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCT
 20 GGAGTGGGTCTCAACGATTTTCGTATGTGGGTATTATACATACTACGCAGACTCCGTGAAGGGCCGG
 TTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGG
 ACACCGCGGTATATTACTGTGCGAAAAAGGCTCTGCGGGGGGAGGCGTTTACGGAGCGTTTTGACTA
 CTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 672)

BMS3h-60

25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT

CCTGTGCAGCCTCCGGATTCACCTTTGGTCCGTATATGATGCATTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAACGATTGAGGTTAATGGTAATAGGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGGTGGTTC
 5 GAAGACGTCGTCGGATAAGAGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
 AGC (SEQ ID NO: 673)

BMS3h-61

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTGGTACGACGGAGATGGCTTGGGTCCGCCAGGCTCC
 10 AGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGGTAGTGCTGGTGCTTGGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAATTGGTGGGCA
 TCCTCAGGGTCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ
 ID NO: 674)

15 BMS3h-62

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGCCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTCCTAGGGAGTGGATGGCTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAAGTATTCAGCCTATGGGTCAGACTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATATTCTCGGAA
 TAAGGGGTTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 675)

BMS3h-63

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 25 CCTGTGCAGCCTCCGGATTCACCTTTACGAGTGAGTATATGGGGTGGGTCCGCCAGGCTCC

AGGGAAGGGTCTAGAGTGGGTCTCATCTATTCAGAGGTATGGTAGTACGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACATGAGTCTAA
 TTGGGAGACTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID

5 NO: 676)

BMS3h-70

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTTCGGTGTATAGTATGCAGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCGATTACTCCTAATGGTACTCGGACATACTACGCA
 10 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTCTTGGTCG
 GGGTTCTTATCCTGGTGTGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
 AGC (SEQ ID NO: 677)

BMS3h-71

15 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCCGAGTTATGCTATGACGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTGGAGTGGGTCTCACGTATTACGGCGGATGGTACTGTTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTTCTATTCC
 20 GATGCTTACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 678)

BMS3h-72

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTTCGACTTATGATATGATTTGGGTCCGCCAGGCTCC
 25 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTTCTCCTAATGGTACTGGTATATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAATCAGAGTGT
 TCATCATGCTGTTTTTGGTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ
 ID NO: 679)

5 BMS3h-73

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGAGAATTATGAGATGACGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCACGTATTGCGCCGCATGGTCGGCTTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 10 AAATGAACAGCCTGCGTGCCGAGGATAACCGCGGTATATTACTGTGCGAAAGGTCAGATTCC
 GATGCTTGATTTTGGTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 680)

BMS3h-74

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 15 CCTGTGCAGCCTCCGGATTACCTTTTCGATTATATGATGATGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCTCATTTTGGTGATATTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACCGCGGTATATTACTGTGCGAAAAATGATATGGT
 GATGAAGAATGGGGGGTTTGGTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
 20 (SEQ ID NO: 681)

BMS3h-75

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGAGAGGTATGATATGAGTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCACGTATTGATTCGCGGGGTTGGTCTACATACTACGCA
 25 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC

AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGTTGGTGCC
GCATCTGAGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
NO: 682)

BMS3h-76

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTGCGAATGCGCAGATGACTTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAAGGATTGATGCTATGGGTGATGCTACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTAAGGTTCC
10 GAGTATTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
683)

BMS3h-77

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTGCGAATGCGCAGATGACTTGGGTCCGCCAGGCTCC
15 AGGGAAGGGTCTAGAGTGGGTCTCAAGGATTGATGCTATGGGTGATGCTACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGGTGTTATTCC
GGCGTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
684)

20 BMS3h-78

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTGAGAATGATCGGATGCATTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCATCGATTTCTGCTACTGGTGGTGATACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
25 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACAGACGGGTAC

GAATCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
685)

BMS3h-79

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
5 CCTGTGCAGCCTCCGGATTCACCTTTAATCAGCCTTATATGTCGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTGGAGTGGGTCTCATCTATTGATGCTTCGGGTGGTACTACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACGCCGCGGTATATTACTGTGCGAAAGATCGTATTCC
TAATCTTGTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
10 NO: 686)

BMS3h-80

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTCACCTTTGATAATGAGAATATGACTTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCACGTATTGATGGTGGGGGTTATAATACATACTACGCA
15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCAGGTTCC
TGAGCTGCTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
NO: 687)

BMS3h-81

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
20 CCTGTGCAGCCTCCGGATTCACCTTTGTTTCGTGGAATATGACTTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTATGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTCGGATTCC
25 TACGTTGGTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID

NO: 688)

BMS3h-82

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGTTTCGTCTGAATATGACTTGGGTCCGCCAGGCTCC
 5 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTATGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATCGTATTCC
 TAATCTTGTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 689)

10 BMS3h-83

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTTCTGATGATTCGATGAGTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCACGTATTAATGATGCTGGTAGTTCTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 15 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTACTATTCC
 TCTTCTGGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 690)

BMS3h-84

GAGATGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 20 CCTGTGCAGCCTCCGGATTACCTTTGTTTCGGATACTATGAGTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCACGTATTGATGGGACTGGTGGTGATACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGGGGACACCGCGGTATATTACTGTGCGAAAGGGCTTATTCC
 TGATCTTCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 25 NO: 691)

BMS3h-85

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGATGAGGAGGAGATGACGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCACGTATTATTGGTGGTGGTCATGAGACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTACTATTCC
 TCTTCTGGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 692)

BMS3h-86

10 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGATAATGAGAATATGACTTGGGTCCGCCAGGCTCC
 AGGGAAGGATCTAGAGTGGGTCTCACGGATTACTGAGAGGGGTGATGTGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTACTGTTCC
 15 TACGCTGGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 693)

BMS3h-87

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTG
 TGCAGCCTCCGGATTACCTTTGATGAGGAGGAGATGACGTGGGTCCGCCAGGCTCCAGGGAAGG
 20 GTCTAGAGTGGGTCTCACGTATTATTGGTGGTGGTCATGAGACATACTACGCAGACTCCGTGAAG
 GGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGCG
 TGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTACTGTTCTACGCTGGAGTTTGACTACT
 GGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 694)

BMS3h-88

25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT

CCTGTGCAGCCTCCGGATTCACCTTTCATGAGACGGAGATGACGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAATCGGCTGGGTGAGGATACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTAGGATTCC
 5 TGGGCTGGTTTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 695)

BMS3h-89

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTTCTGATGATTCGATGAGTTGGGTCCGCCAGGCTCC
 10 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAATGATGCTGGTAGTTCTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTACTGTTCC
 TACGCTGGAGTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 696)

15 BMS3h-90

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTGATAATGAGAATATGACTTGGGTCCGCCAGGCTCC
 AGGGAAGGATCTAGAGTGGGTCTCAGGATTACTGAGAGGGGTGATGTGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTCGGATTCC
 TACGTTGGTGTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 697)

BMS3h-91

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 25 CCTGTGCAGCCTCCGGATTCACCTTTTCTGATGATTCGATGAGTTGGGTCCGCCAGGCTCC

AGGGAAGGGTCTAGAGTGGGTCTCACGTATTAATGATGCTGGTAGTTCTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATTACTCC
 TAATTTGACTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID

5 NO: 698)

BMS3h-92

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGCTGATGAGCCGATGACTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCACGTATTCCTCCTGAGGGTGCTCCGACATACTACGCA
 10 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCTTATTCC
 TGATCTTCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID

NO: 699)

BMS3h-93

15 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCAGGATAGTGATATGACGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTGCTGCGCCTGGTGGTAGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATCGTATTCC
 20 TAATCTTAGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID

NO: 700)

BMS3h-94

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGTTTCGGATACTATGAGTTGGGTCCGCCAGGCTCC
 25 AGGGAAGGGTCTAGAGTGGGTCTCACGTATTGATGGGACTGGTGGTGATACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCAGGTTCC
 TGAGCTGCTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 701)

5 BMS3h-95

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCAGGATAGTGATATGACGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTGCTGCGCCTGGTGGTAGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 10 AAATGAACAGCCTGCGTGCCGAGGATAACCGCGGTATATTACTGTGCGAAAGATCGTATTCC
 TAATCTTGTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 702)

BMS3h-96

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 15 CCTGTGCAGCCGCCGGATTACCTTTGATCTGGCGGAGATGACTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCACGTATTGATGAGGATGGTGCTTCTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACGCCGCGGTATATTACTGTGCGGAAGGTGTTATTCC
 GTCTCTGACTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 20 NO: 703)

BMS3h-97

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTACTGATAAGCATATGAGTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCACGGATTTGCCTGATGGTACGTATACATACTACGCA
 25 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC

AAATGAACAGCCTGCGTGCCGAGGACGCCGCGGTATATTACTGTGCGGAAGGTGTTATTCC
 GTCTCTGACTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 704)

BMS3h-98

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGCTGAGGATGATATGACTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCACGTATTGCGGTTGATGGTGATCGGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTACCGAGGACACCGCGGTATATTACTGTGCGAAAGGGAAGACGCC
 10 GCATCTTGTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 705)

BMS3h-99

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCGCCGGATTACCTTTGATCTGGCGGAGATGACTTGGGTCCGCCAGGCTCC
 15 AGGGAAGGGTCTAGAGTGGGTCTCACGTATTGATGAGGATGGTGCTTCTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTCAGGTTCC
 TGCTTTGGTTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 706)

20 BMS3h-100

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGAGGATTGATGATGTCGTGGGTCCGCCAGGCGCC
 AGGGAAGGGTCTAGAGTGGGTCTCACGGATTGATCCTGGGGGTGCTCAGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 25 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGTGACTCC

GGATTTGACTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
NO: 707)

BMS3h-101

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
5 CCTGTGCAGCCTCCGGATTCACCTTTGAGCATGCGGATATGAGTTGGGTCCGCCAGGCTTC
AGGGAAGGGTCTAGAGTGGGTCTCACGTATTGATAATAGTGGTCAGTCTACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGTGACTCC
GGATTTGACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
10 NO: 708)

BMS3h-102

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTCACCTTTAGTGAGGCGGAGATGAATTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCACGTATTACGACGGATGGTGATTCTACATACTACGCA
15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCGTATTCC
TACTCTTCATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
NO: 709)

BMS3h-103

20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCAGGATTCACCTTTGATGATAGTGATATGACTTGGGTCCGCCAGGCTCC
AGGGAAGAGTCTAGAGTGGGTCTCATATATTCGGGGTGATGATGATGAGACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAATCGGATTCC
25 TGATCTTGTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID

NO: 710)

BMS3h-108

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTAATGTGGCGGATATGCAGTGGGTCCGCCAGGCTCC
5 AGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTCCGAATGGTTGGGATACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACATGCTTCTAC
GGAGGGGCCGACTGCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

(SEQ ID NO: 711)

10 BMS3h-109

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTGGGCCGTATGATATGGGGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTGGAGTGGGTCTCATGGATTTCTGCTCATGGTTTCGTTTACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
15 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATGGCCTTATAA
GTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 712)

BMS3h-110

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGT
GCAGCCTCCGGATTACCTTTGGGAGTGGGTCTATGAGTTGGGTCCGCCAGGCTCCAGGGAAGGGT
20 CTAGAGTGGGTCTCACGGATTGGTAGTAATGGTGCGGATACATACTACGCAGACTCCGTGAAGGGC
CGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGCGTGCC
GAGGACACCGCGGTATATTACTGTGCGAAAGGGATGGTTCCTAATTTGGTTTTTGACTACTGGGGT
CAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 713)

BMS3h-111

25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT

CCTGTGCAGCCTCCGGATTCACCTTTAATCGTTTTGATATGACGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATCGTATTCC
 5 TAATCTTGTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 714)

BMS3h-112

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTGGGGAGAGTGATATGAAGTGGGTCCGCCAGGCTCC
 10 AGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTCCGAATGGTTGGGATACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCTCCTTCTTC
 TCGTCTTAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 715)

15 BMS3h-139

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTGATAGTAGTGAGATGAGTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCATCGATTGAGAATCAGGGTGGTGCGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATCGTATTCC
 TAATCTTGTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 716)

BMS3h-140

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 25 CCTGTGCAGCCTCCGGATTCACCTTGATGCGTATCCTATGTATTGGGTCCGCCAGGCTCC

AGGGAAGGGTCTAGAGTGGGTCTCATGGATTGCTTCGGGTGGTGGTGGCGACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACGTACGAAGAA
TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 717)

5 BMS3h-141

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTATGAGTTATTCTATGGCTTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAGGGATTACTTCTAATGGTAATCGGACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
10 AAATGAACAGCCTGCGTGCCGAGGATAACCGCGGTATATTACTGTGCGAAATCGACTGGGGC
TAATAGTAGGAATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ
ID NO: 718)

BMS3h-142

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
15 CCTGTGCAGCCTCCGGATTACCTTTGAGGGGTATCTGATGTCGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGCGGCTAATGGTATGCAGACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAAGCCGAGGGG
TATTTGGGATGGGGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
20 (SEQ ID NO: 719)

BMS3h-143

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTCATGAGTCTACGATGACGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAACTATTCGGCATCCGGGTGAGTTTACATACTACGCA
25 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC

AAATGAACAGCCTGCGTGCCGGGGACACCGCGGTATATTACTGTGCGAAAGGGCTTATTCC
 TGATCTTCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 720)

BMS3h-144

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGCGATGTATAGTATGAGTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCATCGATTGCGCCGCCGGGTGGTAGGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACCGCGGTATATTACTGTGCGAAACAGTCGCTGAC
 10 GGGGTATAGTAGGTCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
 (SEQ ID NO: 721)

BMS3h-145

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTTCGAGAATCCGATGTCGTGGGTCCGCCACGCTCC
 15 AGGGAAGGGTCTAGAGTGGGTCTCAACGATTCCCTGCGAATGGTCGTCCTACATCCTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACCGCGGTATATTACTGTGCGAAATATAGTCAGCA
 GCCGGGTTCGTCGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ
 ID NO: 722)

20 BMS3h-146

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGCTAATTATCATATGACGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCATCGATTCCCTGATAGTGGTAAGCAGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTAC
 25 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGTAGGATTCC

GTCTCTTCTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
NO: 723)

BMS3h-147

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
5 CCTGTGCAGCCTCCGGATTCACCTTTGCGCAGTATCATATGCGTTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAACGATTAATGATATTGGTAGTAATACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTGGGGGGCG
GGGGAGTTTTTCTTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ
10 ID NO: 724)

BMS3h-148

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTCACCTTTTCTTCGTATGATATGAAGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAACGATTAGTGCGTCTGGTGTGTTTACATACTACGCA
15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACGGGAGCATGC
GGGTCAGCCGCCTTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ
ID NO: 725)

BMS3h-149

20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTCACCTTTAATGGTTATGCTATGAGTTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAACTATTAATGCTAATGGTAAGTATACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAAGTTGACTCT
25 TGCTTCTAATTATTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ

ID NO: 726)

BMS3h-150

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTATGGATTATGATATGAAGTGGGTCCGCCAGGCTCC
 5 AGGGAAGGGTCTAGAGTGGGTCTCAAGTATTACTGCGCTTGGTAAGAAGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATAGTGTTAA
 GTATCCTCTTAATCTTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
 (SEQ ID NO: 727)

10 BMS3h-151

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCCGCATTATACGATGGCGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTGGAGTGGGTCTCATCTATTAGTCGCCTGGTTGGCGGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 15 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATATGGGGATGG
 TCTTCCTTTGACTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ
 ID NO: 728)

BMS3h-167

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 20 CCTGTGCAGCCTCCGGATTACCTTTAGTGGTACGCCGATGTCTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCACGTATTGGGGATGAGGGTCAGGAGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGTGACTCC
 GGATTTGACTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 25 NO: 729)

BMS3h-168

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTAGTAGTAGTTCGATGTCTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCGATTGGGTCTGATGGTCCGAGTACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCGTATTCC
 TACTCTTCATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 730)

BMS3h-169

10 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTAATCCTGGTGAGATGACGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGATGGGTCTGGTTCTTCGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGATGACACCGCGGTATATTACTGTGCGAAAGGGCGTATTCC
 15 TACTCTTCATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 731)

BMS3h-170

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCT
 GTGCAGCCTCCGGATTACCTTTCCTGAGTCTATGATGGGGTGGGTCCGCCAGGCTCCAGGGAA
 20 GGGTCTAGAGTGGGTCTCATCGATTGGGTATCCTGGTGCTACTACATACTACGCAGACTCCGTG
 AAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCC
 TCGGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGGTGGTAGTCGGGATGATAATTTGA
 CTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 732)

BMS3h-171

25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGCCTCT

CCTGTGCAGCCTCCGGATTCACCTTTGGTCAGCATAGTATGCATTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTGTTCCGGGTCCGAAGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTCTTAGGGA
 5 TTTGCGTCCGGGTGATAGTAAGAGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
 TCGAGC (SEQ ID NO: 733)

BMS3h-197

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTGGTTCTGCTGCTATGGATTGGGTCCGCCAGGCTCC
 10 AGGGAAGGGTCTAGAGTGGGTCTCATCTATTAATGATATGGGTTCTAATACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACAGGGTGGTCG
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 734)

BMS3h-199

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTGGTTATGATAGGATGGCTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCATCGATTGATGGTCCTGGTGGGGCTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGGGAGGAGGGT
 20 TCCTGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
 735)

BMS3h-200

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTGGTGAGTATGAGATGACTTGGGTCCGCCAGGCTCC
 25 AGGGAAGGGTCTAGAGTGGGTCTCAAGGATTGATCCGTTTGGTTCTGAGACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGGTGTGGTTCC
 TGATTTGAATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 736)

5 BMS3h-201

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGATAAGTATGTTATGGGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAACTATTGGTAGTTATGGTGGGGCTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 10 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGGCTTACTCT
 TAGTGCGACTAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ
 ID NO: 737)

BMS3h-203

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 15 CCTGTGCAGCCTCCGGATTACCTTTGAGGATTATGTGATGGGTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAACTATTGCGCATCGGGGTGATATTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACGTAGGCGTCT
 TAGTGATTATCGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ
 20 ID NO: 738)

BMS3h-204

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGGGCAGTTTGATATGTATTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCGATTAGTCCGGCTGGTACTGGTACATACTACGCA
 25 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC

AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGGGGATCG
 GTCTAGTCTTTTTGACTACAGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 739)

BMS3h-205

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTAAGGATACGGGTATGACGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAAGTATTTCTAGTTATGGTCGTGATACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACGCCGCGGTATATTACTGTGCGAAATTGAATGCGGC
 10 GCTGGGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
 740)

BMS3h-206

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGGTCCGTATCCGATGAGTTGGGTCCGCCAGGCTCC
 15 AGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAATGCGCCGGGTACGAGGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAACAGATGTCTAG
 TGGGGTTTTTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
 741)

20 BMS3h-207

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTTGAATCAGGATATGACTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGATAGTTCTGGTCAGCTTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 25 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTTAAGTCTCT

TGCGCGGTTTGGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
742)

BMS3h-208

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
5 CCTGTGCAGCCTCCGGATTCACCTTTCCTGAGTCTGATATGAAGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTCCGAATGGTTGGGATACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACCGGCTCAGGT
TCTGTTTGGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
10 743)

BMS3h-209

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTCACCTTTGAGCAGTATGTGATGGGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAACGATTGGTACGTCGGGTAAGTATACATACTACGCA
15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAACGTAGGTCTCT
GACTCGGGTTCATTTTGGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ
ID NO: 744)

BMS3h-210

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
20 CCTGTGCAGCCTCCGGATTCACCTTTGGTGTGGAGCATATGAGTTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAGCGATTACGGGTGATGGTGATCGTACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAACGGTTTCGTG
25 GAATGGTCGTTTTGGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID

NO: 745)

BMS3h-211

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGCGTGGTATAATATGGGTGGGTCCGCCAGGCTCC
 5 AGGGAAGGGTCTGGAGTGGGTCTCAAGGATTGCTCCGTCTGGTATTATTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGTTGCGTGG
 TAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
 746)

10 BMS3h-212

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTTCGAATTATGAGATGAGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCTTCGGCTGGTACTGATACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 15 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACAGTCGCTTAA
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 747)

BMS3h-213

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGTAGCCTCCGGATTACCTTTGATGAGGAGCCGATGACTTGGGTCCGCCAGGCTCC
 20 AGGGAAGGGTCTAGAGTGGGTCTCAATTATTGATCCGGGTGGTGGGGCGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCTAATAGTAT
 GTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 748)

BMS3h-214

25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT

CCTGTGCAGCCTCCGGATTCACCTTTTCTGCGTATCCTATGCATTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCATCTATTGCTTCTTCGGGTATTACGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTTACTCGGCT
 5 GCATTTTCTGCGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

(SEQ ID NO: 749)

BMS3h-215

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTGCTGATTATGCGATGGGTGGGTCCGCCAGGCTCC
 10 AGGGAAGGGTCTAGAGTGGGTCTCAAGGATTTCTCCTGAGGGTTCTAGGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTGCGGGCCGTA
 TCGCTCGAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID

NO: 750)

15 BMS3h-230

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTAGGCCGTATGATATGGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCTCATCAGGGTAATCGGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTGTCTCATCA
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 751)

BMS3h-231

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTTCTGCGTATAATATGTGGTGGGCCCCGCCAGGCTCC
 25 AGGGAAGGGTTTAGAGTGGGTCTCATGGATTAATTCGACTGGTTCTCGTACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAAATTGGCATCG
 GGGGAGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
 752)

5 BMS3h-232

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGATAGGTATCGGATGGGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAACGATTAATCGGCTGGGTCAGAGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 10 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTGAAGAAGCA
 TAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
 753)

BMS3h-233

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 15 CCTGTGCAGCCTCCGGATTACCTTTGCGCATTATAATATGCGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAACGATTACGAAGACTGGTTTTTCGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGTGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGGGCAGTT
 TGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
 20 754)

BMS3h-234

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTAGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTTATCCTTATAGTATGCATTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTGGAGTGGGTCTCAACTATTGATGGTAGTGGTATGTTTACATACTACGCA
 25 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC

AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGATTCTCTGAA
GGCTTCTTTTGACTIONACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
755)

BMS3h-235

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTCCGCTTTATGGGATGTGGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCATATATTGGGCCTTATGGTCATACTACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGATAACCGCGGTATATTACTGTGCGAAAAAGCGGAAGAA
10 GAAGTTTGACTIONACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
756)

BMS3h-236

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTCCCTAGGTATCGGATGAGTTGGGTCCGCCAGGCTCC
15 AGGGAAGGGTCTAGAGTGGGTCTCAAGTATTACTCCGTATGGTGCTCATACTACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATGGTAAGTG
GTATTTTGACTIONACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
757)

20 BMS3h-237

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTAATGAGTATGCGATGAGGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAACGATTGATCGTCTGGGTCTTCATACTACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
25 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTGGGCCTTT

TACGTTTGGTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
758)

BMS3h-238

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
5 CCTGTGCAGCCTCCGGATTCACCTTTGAGCGGTATAATATGCGTTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAACGATTGATCGGCTGGGTCTTGCTACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGGTTCGTG
GTCTTTTGGTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
10 759)

BMS3h-239

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTCACCTTTGGTATTTATGATATGAAGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAACGATTTTCGTCGTCGGGTACTCATACTACTACGCA
15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATCCTCAGCC
TTATCCTTTTGGTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
760)

BMS3h-240

GAGGTGCAGCTATTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
20 CCTGTGCAGCCTCCGGATTCACCTTTTGGGTGTATGATATGCGTTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAACGATTTCTGCGACTGGTGTGCATACTACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATCCGCCTGC
25 TGGTCGGTTTGGTACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:

761)

BMS3h-241

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTTCGACTTATGATATGATTTGGGTCCGCCAGGCTCC
 5 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTTCTCCTAATGGTACTGGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTCCGCAGGT
 GAATACTGAGTTTGACTACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 762)

10 BMS3h-243

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGAGAAGGAGGATATGGGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCACATATTTGCGCGAATGGTTATGCGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 15 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTTGGTCTAG
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 763)

BMS3h-244

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTG
 TGCAGCCTCCGGATTACCTTTAGTGCTACTCCGATGGAGTGGGCCCCGAGGCTCCAGGGAAGG
 20 GTCTAGAGTGGGTCTCAACTATTTCTGAGAGTGGTTATAGTACATACTACGCAGACTCCGTGAAG
 GGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGCG
 TGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGAATTCGACTACTGGTTTTGACTACTGGG
 GTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 764)

BMS3h-245

25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT

CCTGTGCAGCCTCCGGATTCACCTTTAATACGGTGGATATGGAGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTCCGAATGGTTGGGATACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGCTCCGCATCG
 5 GCGCTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
 765)

BMS3h-246

GAGGTGCAGCTGTTGGAGTCTGGGGGGGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTGAGGATAAGGAGATGAGTTGGGTCCGCCAGGCTCC
 10 AGGGAAGGGTCTAGAGTGGGTCTCACGGATTGATGCTTTGGGTGATTCTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAAGGGATGGTTCC
 TCGTCTGAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 766)

15 BMS3h-247

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTAGTGATCATTCGATGATGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGATATTGAGCCGCATGGTGTTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAATCCTACTTTTGA
 CTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 767)

BMS3h-248

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTTCGCCGCATACTATGCATTGGGTCCGCCAGGCTCC
 25 AGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGGTCCGGATGGTACTACTACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACGTTTCGTATAG
 TTGGGATCGTGGGTGGACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
 (SEQ ID NO: 768)

5 BMS3h-249

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTTATGCTTCGGATATGAAGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTCCGAATGGTTGGGATACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 10 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCTGATTATAC
 TTATCATTCTTTTGACTACTGGGGTCAGGGGACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 769)

BMS3h-250

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 15 CCTGTGCAGCCTCCGGATTACCTTTGCGCATTATAATATGCGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAACGATTACGAAGACTGGTTTTTCGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGTGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGGGCAGTT
 TGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
 20 770)

BMS3h-251

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTTTCGATTATCATATGGGTGGGGCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGTTATTGGGCCGAGGGGTATTTCTACATACTACGCA
 25 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC

AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCGCCTTCGCG
TCATAGGTTTGACTIONACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
771)

BMS3h-252

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTAATGAGTATGCGATGAGGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAACGATTGATCGTCTGGGTCTTCATACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTGGGCCTTT
10 TACGTTTGACTIONACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
772)

BMS3h-253

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTGGTAATTATAGTATGAAGTGGGCCCCGCCAGGCTCC
15 AGGGAAGGGTCTAGAGTGGGTCTCAACTATTACTCCTGATGGTTGGTATACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGTGGGGGATGC
TGTTTGGGGGTGGATTGGTGGGTTTGACTIONACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC (SEQ ID NO: 773)

20 BMS3h-254

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTGGGGATTATGGTATGAAGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTACGTCTAATGGTGATTTTACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
25 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATCTTTGTATAA

GTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 774)

BMS3h-255

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGGCTCCGGATTCACCTTTCCTACTTATAAGATGGGGTGGGTCCGCCAGGCTCC
5 AGGGAAGGGTCTAGAGTGGGTCTCATTTATTGATTATTGGGGTTGGCGGACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTCCGTATT
TTGGACTCATGATAGTCCTCATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
AGC (SEQ ID NO: 775)

10 BMS3h-256

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTCACCTTTAGGCCTTATACGATGTGTTGGGCCCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCATGTATTAGTGATGCTGGTTCTTTTACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
15 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAAGGATGTCTTC
TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 776)

BMS3h-257

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGT
GCAGCCTCCGGATTCACCTTTCAGAATTATCAGATGGCTTGGGTCCGCCAGGCTCCAGGGAAGGGT
20 CTAGAGTGGGTCTCAACTATTAGTGGGACTGGTAAGAATACATACTACGCAGACTCCGTGAAGGGC
CGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGCGTGCC
GAGGACACCGCGGTATATTACTGTGCGAAAACCTCCTCAGAATTATTTTAGTGTGCGTCGGTTTGAC
TACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 777)

BMS3h-258

25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT

CCTGTGCAGCCTCCGGATTCACCTTTGGGGCGTATACTATGGGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAAAGATTTGACGTCTGGTGGGCAGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTTTGAATTG
 5 GTGGGCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
 778)

BMS3h-272

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTAATGCGTATCCTATGACTTGGGTCCGCCAGGCTCC
 10 AGGGAAGGGTCTAGAGTGGGTCTCACGGATTGATGGTTATGGTCGGCATACTACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATTATTCC
 TAATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
 779)

15 BMS3h-273

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTGGGGCGGTTGATATGACGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCGATTTGCGCTAGTGGTTCTGCTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGCGTGTGCC
 GGATCTTGGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 780)

BMS3h-274

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 25 CCTGTGCAGCCTCCGGATTCACCTTTGATAGTTATGCGATGGGGTGGGCCCGCCAGGCTCC

AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTGGGGCTAAGGGTTTGTCTACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGCTAGGGG
TAAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:

5 781)

BMS3h-275

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTACTCGGTATCAGATGGGTTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAGTTATTAATGTTTGGGGTTCGAGTACATACTACGCA
10 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATGTCTGGGAA
GTTTGCCTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 782)

BMS3h-276

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTTT
15 CCTGTGCAGCCTCCGGATTACCTTTGGGAATTATAGTATGATGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAACGATTATTCCTGCTGGTACGTCTACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCGTCGATTAG
GTTGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:

20 783)

BMS3h-279

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTGGTGCATGATATGGGGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCATGGATTTCTCCGAATGGTTATGATACATACTACGCA
25 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC

AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGGGTGTGAA
GTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 784)

BMS3h-282

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
5 CCTGTGCAGCCTCCGGATTCACCTTTGTTTGGTATGAGATGGCTTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAACGATTCAGGCTGATGGTGAGCAGACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGCTTCGTATGC
TCTTGTGTATCCTCCTGAGGAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
10 AGC (SEQ ID NO: 785)

BMS3h-287

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTCACCTTTACGAATTATAGGATGTCTTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTGATGATCTGGGTGTGTGACATACTACGCA
15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATGGAGGCTTAA
GAATAGTCAGCCGACGGATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
(SEQ ID NO: 786)

BMS3h-292

20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTCACCTTTGATCAGGCTCATATGTGGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCATTTATTAATCCTTCGGGTTATTATACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTTCGCTTAG
25 TCCGTCTTCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID

NO: 787)

BMS3h-293

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGAGACTGGTCAGATGGGTGTTGGGCCCCGCCAGGCTCC
 5 AGGGAAGGGTCTAGAGTGGGTCTCAAATATTGATGGGTCTGGTACGTATACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAAGTACGCAGAA
 TTATCGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
 788)

10 BMS3h-296

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGGTGCTTATCCGATGTATTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCATCTATTCTATAAGGATGGTAGGATTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 15 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACAGGGTACGCC
 GGTTGATGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 789)

BMS3h-297

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 20 CCTGTGCAGCCTCCGGATTACCTTTCCTGATGAGGGTATGACGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAACGATTGAGACTGGTGGTACGGTGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAATGGATGGGTC
 TGGTACATGGCAGACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
 25 (SEQ ID NO: 790)

BMS3h-298

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTGATAGTCTGGGTATGGGTGGGCCCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCATATATTCGGGCTGAGGGTGCTTATACATACTACGCA
5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAATATCTTGCGGA
TTCTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 791)

BMS3h-299

GAGGTGCAGCTGTTGGAATCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
10 CCTGTGCAGCCTCCGGATTACCTTTAGTGAGTCGTATATGGAGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGATCATATTGGTGGTGGGACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATGATGGTCG
TGGTGGGTCTATGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ
15 ID NO: 792)

BMS3h-300

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTTCTGGTGGGTATATGTGGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAAGTATTGGGGCTAGTGGTGCGTATACATACTACGCA
20 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAACGGGGGGTAG
GTTAGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 793)

BMS3h-301

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
25 CCTGTGCAGCCTCCGGATTACCTTTGATGAGGGGCATATGGGGTGGGTCCGCCAGGCTCC

AGGGAAGGATCTAGAGTGGGTCTCATATATTGGGAGTCTGGGTTTGCATACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACGGGAGTTTAG
 TAATGGGGGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID

5 NO: 794)

BMS3h-302

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTAAGACTAGTCCTATGTATTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCATCGATTGATCGGACTGGTGGGCATACATACTACGCA
 10 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACAGGCTCTGCT
 TACTGATGCGAAGCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC

(SEQ ID NO: 795)

BMS3h-303

15 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGATGGTTCGGGATATGGTTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTCCGAGTGGTCTGGATACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGGAACGTCCCTCAGAT

20 GCTGGTTACTAATTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ
 ID NO: 796)

BMS3h-304

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGGTAATGATCCGATGAGTTGGGTCCGCCAGGCTCC
 25 AGGGAAGGGTCTAGAGTGGGTCTCAGGGATTGGTCGGGAGGGTGATTCTACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGATTCTATGCG
 GCATCAGCCGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 797)

5 BMS3h-305

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGATGAGACTTATATGAAGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCGATTGGGGCGTCGGGTGCTGATACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 10 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATTTACGCATCT
 GAATGGTCGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 798)

BMS3h-306

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 15 CCTGTGCAGCCTCCGGATTACCTTTGGGGGGTGGCCTATGGGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGATATTGATGGTGCTCCGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGGAGGCGGG
 TTCTTGGTCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 20 NO: 799)

BMS3h-307

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTAGTGATCAGGCGATGTGGTGGGCCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCATTTATTCAGGGTGATGGTGGTTTTACATACTACGCA
 25 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC

AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACCTAGTAAGCC
GTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 800)

BMS3h-308

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
5 CCTGTGCAGCCTCCGGATTCACCTTTGAGACTGGTCAGATGGGTTGGGCCCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAAATATTGATGGGTCTGGTACGTATACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGCGGTGCGGAA
TTTTGCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO:
10 801)

BMS3h-309

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTCACCTTTAGTGGGCATGATATGTCTTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTCCTCATGGTACGCATACATACTACGCA
15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGGGATTAGGGG
TTGGATTGGTCATGATACGCAGCCTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
TCGAGC (SEQ ID NO: 802)

BMS3h-310

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
20 CCTGTGCAGCCTCCGGATTCACCTTTGAGAGTAAGGATATGCTTTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCATCTATTTTCGTCGGATGGTACTCATACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGCAAGAGCTGGGTGG
25 GTCTTGGCAGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID

NO: 803)

BMS3h-311

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGCGGATCGTGATATGGTTTGGGTCCGCCAGGCTCC
 5 AGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGGGGCGTCGGGTACGTCTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACGCCGCGGTATATTACTGTGCGAAAGGTGGGACGGG
 TCCTACTGATTTGTGGGATTTTGA TACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
 (SEQ ID NO: 804)

10 BMS3h-312

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGATGATGAGAAGATGCTTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAAGTATTAGTGTGAGTGGTCTGCATACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 15 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGGAGGCGGG
 TTCTTGGTCTTTTGA TACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 805)

BMS3h-313

GAGGTGCAGCTGTTGGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 20 CCTGTGCAGCCTCCGGATTACCTTTGGGCAGGAGAGGATGATTTGGGTCCGCCAGGCTCC
 TGGGAAGGGTCTAGAGTGGGTCTCAGATATTTCCGGCTTCGGGTGGGACTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGGAGGCGGG
 TTCTTGGTCTTTTGA TACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 25 NO: 806)

BMS3h-37-1

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCTCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCGATTTCTGGTGATGGTTATCGTACATACTACGCA
 5 GACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCATGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTA
 TTTTGACTACAGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 807)

BMS3h-37-2

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGTGCAGCCTCCGGATTACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCC
 AGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGGTGATGGTTATCGTACATACTACGCA
 GACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTA
 TTTTGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 808)

15 BMS3h-37-3

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCGATTTCTGGTGATGGTTATCGTACATACTACGCA
 GACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTA
 TTTTGACTACCGGGTTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 809)

BMS3h-37-4

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCAAGGCTCC
 25 AGGGAAGGGTCTAGAGTGGGTCTCAGCGATTTCTGGTGATGGTTATCGTACATACTACGCA

GACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTA
 TTTTGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 810)
 BMS3h-37-5

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGATCTCAGCGATTTCTGGTGATGGTTATCGTACATACTACGCA
 GACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTA
 10 TTTTGACTACAGGGTTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 811)
 BMS3h-37-6

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCGATTTCTGGTGATGGTTATCGTACATACTACGCA
 15 GACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCGAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTA
 TTTTGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 812)
 BMS3h-37-7

GAGGTGCAGCTGTTGGAGACTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 20 CCTGTGCAGCCTCCGGATTACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCGATTTCTGGTGATGGTTATCGTACATACTACGCA
 GACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGGACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTA
 TTTTGACTACTGGGGTCGGGGAACCCTGGTCACCGTCACGAGC (SEQ ID NO: 813)
 25 BMS3h-37-8

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAGCGATTTCTGGTGATGGTTATCGTACATACTACGCA
GACTCCGTGAAAGGCCGGTTCACCATCTCACGCGACAATTCCAAGAACACGCTGTATCTGC
5 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTA
TTTTCACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 814)
BMS3h-37-9

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGTAGCCTCCGGATTACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCAGGCTCC
10 AGGGAATGGTCTAGAGTGGATCTCAGCGATTTCTGGTGATGGTTATCGTACATACTACGCA
GACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTA
TTTTGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 815)
BMS3h-37-10

15 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCTGGATTACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAGCGATATCTGGTGATGGTTATCGTACATACTACGCA
GACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
TAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTA
20 TTTCGACTACTGGGGTCGGGGAACCCTCGTCACCGTCTCGAGC (SEQ ID NO: 816)
BMS3h-37-11

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCAAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAGCGATTTCTGGTGATGGTTATCGTACATACTACGCA
25 GACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC

AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTA
TTTTGACTACAGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 817)

BMS3h-37-12

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCATGCGTCTCT
5 CCTGTGCAGCCTCCGGATTCACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCAGCGATTTCTGGTGATGGTTATCGTACATACTACGCA
GACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTA
TTTTGACTACAGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 818)

10 BMS3h-37-201

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTCACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCC
AGGGAAGGGATTAGAGTGGGTCTCAATGATTTCCGGGGATGGTTATCGTACATACTACGCA
GACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
15 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTA
TTTTGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 819)

BMS3h-37-202

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTCACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCC
20 AGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGGTGACGGTTGGCGCACATACTACGCA
GACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTTGGGTA
TTTTGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 820)

BMS3h-37-203

25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT

CCTGTGCAGCCTCCGGATTCACCTTTGGGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCC
 AGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGGTGATGGTTATCGTACATACTACGCA
 GACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTGCTCTA
 5 CTTTGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 821)
 BMS3h-37-204
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCC
 AGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGGTGATGGTTATCGTACATACTACGCA
 10 GACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTGGGGTT
 CTTTGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 822)
 BMS3h-37-205
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 15 CCTGTGCAGCCTCCGGATTCACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCC
 AGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGGTGATGGTTATCGTACATACTACGCA
 GACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGTTGGAGTA
 TTTTGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 823)
 20 BMS3h-37-206
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCC
 AGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGGTGATGGTTATCGTACATACTACGCA
 GACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 25 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGGGTTGGAGTA

TTTTGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 824)

BMS3h-37-207

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCC

5 AGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGGTGATGGTTATCGTACATACTACGCA
GACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTGGCCTT
CTTTGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 825)

BMS3h-37-208

10 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCC
AGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGGTGATGGTTATCGTACATACTACGCA
GACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTCTTGTA

15 CTTTGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 826)

BMS3h-37-209

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCC
AGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGGTGATGGTTATCGTACATACTACGCA

20 GACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGTTGGAGTT
CTTTGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 827)

BMS3h-37-210

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
25 CCTGTGCAGCCTCCGGATTACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCC

AGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGGTGATGGTTATCGTACATACTACGCA
 GACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCTGCAGTT
 CTTTGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 828)

5 BMS3h-37-211

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCC
 AGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGGTGATGGTTATCGTACATACTACGCA
 GACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 10 AAATGAACAGCCTGCGTGCCGAGGATAACCGCGGTATATTACTGTGCGAAAGAGCTGCTCTT
 CTTTGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 829)

BMS3h-37-212

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACGGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCC
 15 AGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGGTGATGGTTATCGTACATACTACGCA
 GACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACCGCGGTATATTACTGTGCGAAAGAGTTGGAGTT
 CTTTGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 830)

BMS3h-37-213

20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCC
 AGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGGTGATGGTTATCGTACATACTACGCA
 GACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGTTGCTCTT
 25 CTTTGACTACCGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 831)

BMS3h-37-214

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCATCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCC
 AGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGGTGATGGTTATCGTACATACTACGCA
 5 GACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAACTTGGAGTA
 TTTTGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 832)

BMS3h-37-215

GAGGTGCGGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGTGCAGCCTCCGGATTCACCTTTGAGTGGTATGAGATGCAGTGGGTCCGCCGGGCTCC
 AGGGAAGGGACTAGAGTGGGTCTCAGCGATTTCTGGTGATGGTTATCGTACATACTACGCA
 GACTCCGTGAAAGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGTTGCAGTT
 CTTTGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 833)

15 BMS3h-38-1

GAGGTGCAGCTGTTGGGGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTTGCGAAAGAGCCGTTTCG
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 834)

BMS3h-38-2

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGTCAGGCTCC
 25 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 835)
 BMS3h-38-3

5 GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGATCTCAGCTATTAGTGGAAGTGGTGGTAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 10 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 836)
 BMS3h-38-4

GAGGTGCAGCTGTTGGATCCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTGGGAAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCATCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAGGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 837)
 BMS3h-38-5

GAGGTGCAGCTGTTGGGGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC
 20 TCTCCTGTGCAGCCTCCGGATTCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCA
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACA
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACA
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGG
 GAAAGAGCCGTTTTCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
 25 (SEQ ID NO: 838)

BMS3h-38-6

GAGGTGCAGCTGTTGGAGCCTGGGGGAGGCTTGGTACAGCCTGGGGGCTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 TAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTTGCGAAAGAGCCGTTTCG
 TTTTGACTACTGGGGTCAGGGAGCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 839)

BMS3h-38-7

GAGGTGCAGCTGTTGGATCCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGTGCAGCCTCCGGATTACCTTTGGGAAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCATCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 GACTCCGTTAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGCGAAAGAGCCGTTACG
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 840)

15 BMS3h-38-8

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATCTGGGTCCGCCAGGCTCC
 TGGGAAGGGTCTAGAGTGGATCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCCACCGCGACAATTCTAAGAACACTCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTTGCGAAAGAGCCGTTTCG
 TTTTGACTACAGGGGTCTGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 841)

BMS3h-38-9

GAGGTGCAGCTGTTGGATCCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGGGAAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 25 AGGGAAGGGTCTAGAGTGGGTCTCATCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAGGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCCGTTACG
 TTTTGACTACTGGGGTCAGGGGACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 842)
 BMS3h-38-10

5 GAGGTGCAGCTGTTGGATTCTGGGGGAGGCTTTGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGATCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTGTATTACTGTGCGAAAGAGCCGTTTCG
 10 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 843)
 BMS3h-38-11

GAGGTGCAGCTGTTGGATCCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGATCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAATAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAGAGAGCCGTTTCG
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 844)
 BMS3h-38-12

GAGGTGCGGCTGTTGGAGTCTGGGGAAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC
 20 TCTCCTGTGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCA
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACA
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCACGCGACAATTCCAAGAACA
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGG
 GAAAGAGCCGTTTCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
 25 (SEQ ID NO: 845)

BMS3h-38-13

GAGGTGCAGCAGTTGGAGTCTGGGGGAGGCCTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 846)

BMS3h-38-201

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCCTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGTCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGGGAAAGAGCCGTTCTA
 CTACGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 847)

15 BMS3h-38-202

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCCTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGTCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGGGAAAGAGCCGTTCTA
 CTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 848)

BMS3h-38-203

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCCTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGAAGGAGATGATTTGGGTCCGTCAGGCTCC
 25 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTCTT
 CTACGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 849)
 BMS3h-38-204

5 GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTCCCCAGGAGGAGATGATTTGGGTCCGTCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 10 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 850)
 BMS3h-38-205

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTTTTCGCCGCCGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 851)
 BMS3h-38-206

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC
 20 TCTCCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCA
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAGGCCCGGTACGAGCACA
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACA
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGG
 GAAAGAGCCGTTTTCGTTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
 25 (SEQ ID NO: 852)

BMS3h-38-207

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTCGGATGGGTTTCAGCACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 853)

BMS3h-38-208

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTCGGTGGGGTCACAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 854)

15 BMS3h-38-209

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTCGCCTCGGTTGGAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 855)

BMS3h-38-210

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGTCAGGCTCC
 25 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTCGCTGGGGTGCCAGCACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 856)
 BMS3h-38-211

5 GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGTCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAGGCAGGGTGGGAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGTGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 10 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 857)
 BMS3h-38-212

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGTGTCCGGTTGGAGCACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 858)
 BMS3h-38-213

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGT
 20 CTCTCCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGC
 CAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTCGGTGGGGTTGGAGC
 ACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAG
 AACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTAC
 TGTGGGAAAGAGCCGTTTCGTTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
 25 TCGAGC (SEQ ID NO: 859)

BMS3h-38-214

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTCGGAACGGTCTGAGCACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 860)

BMS3h-38-215

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGGCTGGGTTGGAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 861)

15 BMS3h-38-216

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGC GTTGGGTTGGAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 862)

BMS3h-38-217

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 25 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTCGCAGGGGTTACAGCACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 863)
 BMS3h-38-218

5 GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGTCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAGGCACGGTTGGAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 10 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 864)
 BMS3h-38-219

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAAGCATTAGCAGGAGTGGTGGTAGCACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 865)
 BMS3h-38-220

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGT
 20 CTCTCCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGC
 CAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTCGGATCGGTAACAGC
 ACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAG
 AACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTAC
 TGTGGGAAAGAGCCGTTTCGTTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
 25 TCGAGC (SEQ ID NO: 866)

BMS3h-38-221

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGGCACGGTTGGAGCACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 867)

BMS3h-38-222

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTTGAGGTGGGGTGGTAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 868)

15 BMS3h-38-223

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGTCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGGGAAAGAGCCGTTTCAT
 GTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 869)

BMS3h-38-224

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGTCAGGCTCC
 25 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTCCC
 GTACGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 870)
 BMS3h-38-225

5 GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTGCAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGTCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTGGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 10 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 871)
 BMS3h-38-226

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGTCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTGTA
 CTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 872)
 BMS3h-38-227

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC
 20 TCTCCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGTCA
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACA
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACA
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGG
 GAAAGAGCCCATGTACTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
 25 (SEQ ID NO: 873)

BMS3h-38-228

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAGGAACGGTTTCAGCACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 874)

BMS3h-38-229

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTCGCACGGGTGGGAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 875)

15 BMS3h-38-230

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTCGGGAGGGTGGGAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 876)

BMS3h-38-231

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGGTTCCCCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 25 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTCGGCAGGGTTGGAGCACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 877)
 BMS3h-38-232

5 GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAGGGGCGGTGGGAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 10 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 878)
 BMS3h-38-233

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTCGCACGGGTTACAGCACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 879)
 BMS3h-38-234

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGT
 20 CTCTCCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGC
 CAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAGGAACGGTAGGAGC
 ACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAG
 AACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTAC
 TGTGGGAAAGAGCCGTTTCGTTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTC
 25 TCGAGC (SEQ ID NO: 880)

BMS3h-38-235

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAGGAACGGTTACAGCACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 881)

BMS3h-38-236

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAGGAAGGGTAGCAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 882)

15 BMS3h-38-237

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTCGGGGCGGTTGGAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 883)

BMS3h-38-238

GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 25 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTCGCTCGGGTTACAGCACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 884)
 BMS3h-38-239

5 GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAGGAACGGTATGAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 10 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 885)
 BMS3h-38-240

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAGGAACGGTTACAGCACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 886)
 BMS3h-41-1

GAGGTGCAGCTGTTGGAGTCTGGGGAAGGCTTGGTACAGCCTGGGGGGTCCCTGCGT
 20 CTCTCCTGTGCAGCCTCCGGATTACCTTTACTGAGCATGAGATGATTTGGGTCCGC
 CAGGCTCCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCTGGGTAATGGTGCTAAT
 ACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAG
 AACACGCTGTATCTGCAAATGAACAGCCTGCGTCCCGAGGACACCGCGGTATATTAC
 TGTGCGAAAGAGCCGCTTAGGTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTC
 25 TCGAGC (SEQ ID NO: 887)

BMS3h-41-2

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATCCACCTTTACTGAGTATGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTGGAGTGGATCTCATCTATTTCTGGGTAATGGTGCTAATACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTTCTGTGCGAAAGAGCCGCTTAG
 GTTTGACTACAGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 888)

BMS3h-41-3

GAGGTGCAGCTGTTGGAGCCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGTGCAGCCTCCGGATTACCTTTACTGAGTATGAGATGATTTGGGTCCGCAAGGCTCC
 AGGGAAGGGTATGGAGTGGGTCTCATCTATTTCTGGGTAATGGTGCTAATACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACATGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTTAG
 GTTTGGCTACTGGGGTCAGGGTACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 889)

15 BMS3h-41-4

GAGGTGCAGCTGTTGGATTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCACTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTACTGAGTATGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCTGGGTAATGGTGCTAATACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTAC
 20 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTTAG
 GTTTGACTACTGGGGTCGGGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 890)

BMS3h-41-5

GAGGTGCAGCTGTTGGGGTCAGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTACTGAGTATGAGATGATTTGGGTCCGCCAGGCTCC
 25 AGGGAAGAGTCTGGAGTGGGTCTCATCTATTTCTGGGTAATGGTGCTAATACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTTAG
 GTATGACGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 891)

BMS3h-41-6

5 GAGGTGCAGCCGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTTCAGCCTCCGGATTACCTTTAATGAGTATGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCCGGTAATGGTGCTAATACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTTAG
 10 GTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 892)

BMS3h-41-7

GAGGTGCAGCTGTTGGAGTCTGGGGAAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGCTGAGTATGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAAGGTCTGGAGTGGGTCTCATCTATTTCCGGTAATGGTGCTAATACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTTAG
 GTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 893)

BMS3h-41-8

GAGGTGCAGCTGTTGGACCCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC
 20 TCTCCTGTGCAGCCTCCGGATTACCTTTACTGAGTCTGAGATGATTTGGGTCCGCCA
 GGCTCCAGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCCGGAAATGGTGCTAATACA
 TACTACGCGGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACA
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC
 GAAAGAGCCGCTTAGGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
 25 (SEQ ID NO: 894)

BMS3h-41-9

GAGGTGCAGCTGTTGGAGCCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTACTGAGTATGAGATGATTTGGGTCCGCAAGGCTCC
 AGGGAAGGGTATGGAGTGGGTCTCATCTATTTCGGGTAATGGTGCTAATACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTCCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTTAG
 GTTTGACGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 895)

BMS3h-41-10

GAGGTGCAGCTGTTGGAGTCTGGGGTAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGTGCAGCCTCCGGATTACCTTTACTGAGTATGAGATGATTTGGGTCCGCAAGGCCCC
 AGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGGGTAATGGTGCTAATACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAACCGCTTAG
 GTTTGACAACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 896)

15 BMS3h-41-11

GAGGTGCAGTTGTTGGAGTCTCGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTACTGAGCATGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGGGTAATGGTGCTAATACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCCTCCGTCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTTAG
 GTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 897)

BMS3h-41-12

GAGGTGCAGCCGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCTGCCTCCGGATTACCTTTACTGAGTATGAGATGATTTGGGTCCGCCAGGCTCC
 25 AGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCGGGTAATGGTGCTAATACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTTAG
 GTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 898)
 BMS3h-41-13

5 GAGGTGCAGCTGTTGGAGTCTGCGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTGCTGAGTATGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTGGAGTGGGTCTCATCAATTTCCGGTAATGGTGCTAATACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTTAG
 10 GTTTGACTACTGGGGTCAGGGAGCCCTGGTCACCGTCTCGAGC (SEQ ID NO: 899)
 BMS3h-41-14

GAGGtGCAGCtGTTGGAGCCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCTGCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTACTGAGTATGAGATGATTTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTGGAGTGGGTCTCATCTATTTCCGGTAATGGTGCTAATACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGCTTAG
 GTTTGACAACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 900)
 BMS3h-43-1

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCTCTGCGTCTCT
 20 CCTGTACAGCCTCCGGATTCACCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTAGACGTGGTTTTACTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCCGATTAC
 GTATGATTTGAGGTATGCGCGTTTTGACTACTCGGGTCAGGGAACCCTGGTCACCGTCTCG
 25 AGC (SEQ ID NO: 901)

BMS3h-43-2

GAGGAGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTACAGCCTCCGGATTACCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTAGACGTGGTTTTACTACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCCGATTAC
 GTATGCTACGAGGTATGCGCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
 AGC (SEQ ID NO: 902)

BMS3h-43-3

10 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTACAGCCTCCGGATTACCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTAGGCGTGGTTTTACTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTTCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCCGATTAC
 15 GTATGATATGAGGTATGCGCGTTTTGACTACGGGGGTCAGGGAACCCTGGTCACCGTCTCG
 AGC (SEQ ID NO: 903)

BMS3h-43-4

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGT
 ACAGCCTCCGGATTACCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCCAGGGAAGGGT
 20 CTAGAGTGGGTCTCAGGTATTAGTAGGCGTGGTTTTACTACATACTACGCAGACTCCGTGAAGGGC
 CGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGCGTGCC
 GAGGATACCGCGGTATATTACTGTGCGAAAGAGCCGATTACGTATGATATGAGGTATGCGCGTTTT
 GACAACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAAC (SEQ ID NO: 904)

BMS3h-43-5

25 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT

CCTGTACAGCCTCCGGATTCACCTTTAATACGTATGAGATGTCGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGGTATTGGTAGGCGTGGTTTTACTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCCGATTAC
 5 GTATGATTTGAGGTATGCGCGTTTTGACTACTCGGGTCAGGGAACCCTGGTCACCGTCTCG
 AGC (SEQ ID NO: 905)

BMS3h-43-6

GAGGTGCAGCTGATGGAGTCAGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTACAGCCTCCGGATTCCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCC
 10 AGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTAGGCGTGGTTATACTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCCGATTAC
 GTATGATATGAGGTATGCGCGTTTTGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCG
 AGC (SEQ ID NO: 906)

15 BMS3h-43-7

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTGCAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTACAGCCTCCGGATTCGCCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCC
 AGGGAAGGGACTAGAGTGGGTCTCAGGTATTAGTAGGCATGGTTTTACTACGTACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCGTCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCCGATTAC
 GTATGATATGCGGTATGCGCGTTCTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
 AGC (SEQ ID NO: 907)

BMS3h-43-8

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 25 CCTGTACAGCCTCCGGATTCACCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCC

AGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTAGGCGTGGTTTTACTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTTCTGTGCGAAAGAGCCGATTAC
 GTATGATATGAGGTATGCGCGTTCTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG

5 AGC (SEQ ID NO: 908)

BMS3h-43-9

GAGGTGCAGCTGTTGGAGTCTGGGGGGGGCTTGGTTCAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTACAGCCTCCGGGTTCACCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTAGGCGTGGTTTTACTACATACTACGCA
 10 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCCGATTAC
 GTATTCTATGAGGTATGCGCGTTTTGACTACTCGGGTCTGGGAACCATGGTCACCGTCTCG

AGC (SEQ ID NO: 909)

BMS3h-43-10

15 GAGGTGCAGCTGCTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTTCGTCTCT
 CCTGTACAGCCTCCGGATTACCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTAGGCGTGGTTTTACTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCCGATTAC
 20 GTATGATATGAGGTATGCGCGTTTTGACTACAGTGGTCAGGGAACCCTGGTCACCGTCTCG

AGC (SEQ ID NO: 910)

BMS3h-43-11

GAGGTGCAGCTGTTGGAGTCTGGAGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTACAGCCTCCGGATTACCTTTAATATGTATGAGATGTCGTGGGTCCGCAAGGCTCC
 25 AGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTAGGCATGGTTTTACTACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGCGAAAGAGCCGATTAC
 GTATGATATGAGGTATGCGCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
 AGC (SEQ ID NO: 911)

5 BMS3h-43-12

GAGGTGCAGCTGTTGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTACAGCCTCCGGATTACCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTAGGCGTGGTTTTACTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 10 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGCGAAGGAGCCGATTAC
 GTATGATATGAGGTATGCGCGTTTTGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCG
 AGC (SEQ ID NO: 912)

BMS3h-43-13

GAGGTGCAGCTGTTGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGATCCCTGCGTCTCT
 15 CCTGTACAGCCTCCGGTTTCACCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTAGGCGTGGTTTTACTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGCGAAAGAGCCGATTAC
 GTATGATATGAGGTATGCGCGTTTTGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCG
 20 AGC (SEQ ID NO: 913)

BMS3h-43-14

GAGGTGCAGCTGTTGAGTCTGGGGGAGGCTCGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTACAGCCTCCGGATTCTCCTTTAATATGTATGAGATGTCGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTAGGCGTGGTTTTACTACATACTACGCA
 25 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC

AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCCGATTAC
 GTATGATATGAGGTATGCGCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
 GGC (SEQ ID NO: 914)

BMS3h-43-15

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAACCTGGGGGGTCCCTGCGTCTCT
 CCTGTACAGCCTCCGGATTCACCTTTAATATGTATGAGATGTCGTGGGTCCGCAAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGGTATTAGTAGGCGTGGTTTTACTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGTGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCCGATTAC
 10 GTATGATATGAGGTATGCGCGTTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCG
 AGC (SEQ ID NO: 915)

BMS3h-56-1

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 15 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 916)

BMS3h-56-2

20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 25 TTTTGACGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 917)

BMS3h-56-3

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCAGAGGATACCGCGGTATATTACTGTACGAAACTTCCGTTTAT
 TTTTGAATACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 918)

BMS3h-56-4

GAGGTGCAGCTGTTGGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAT
 GTTTGACGACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 919)

15 BMS3h-56-5

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 GACTCCGTGATGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGACGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 920)

BMS3h-56-6

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCTCCTTTCGGGATTATGAGATGTGGTGGTACCGCCAGGCTCC
 25 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATATTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAT
 TTTTGACAACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 921)
 BMS3h-56-7

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCTCGGTATATCACTGTGCGAAACTTCCGTTTAT
 10 TTTTGGCGACTGGGGTCCGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 922)
 BMS3h-56-8

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCGGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 GGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACGATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 923)
 BMS3h-56-9

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCG
 20 TCTATCCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCC
 GCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACG
 CGTACATACTACGCAGACTCCGTGATGGGCCGGTTCACCATCTCCCGCGACAATTC
 CAAGAACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGATACTGCGGTAT
 ATTACTGTGCGAAACTTCCGTTTATGTTTGACGACCGGGGTCAGGGAACCCTGGTC
 25 ACCGTCTCGAGC (SEQ ID NO: 924)

BMS3h-56-10

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGTTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACATGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACTGCGGTATATTACTGTGCGAAACTTCCGTTTAT
 GTTTGACGACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 925)

BMS3h-56-11

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGAGCCGAGGATACTGCGGTATATTACTGTGCGAAACTTCCGTTTAT
 GTTTGACGACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 926)

15 BMS3h-56-12

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGATACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTTTGAAACTTCCGTTTAT
 TTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 927)

BMS3h-56-13

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTAT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 25 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAACCCGCAGGGTACGCGTACATACTATGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGATGATACCGCGGTATATCACTGTACGAACTTCCGTTTAT
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 928)
 BMS3h-56-14

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGATGGTTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTATATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACCGCGGTATATTACTGTGCGAACTTCCGTTTTT
 10 TTTTGACTCCAGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 929)
 BMS3h-56-15

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCGGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 15 GACTCTGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACCGCGGTATATTACTGTGCGAACTTCCGTTTAC
 TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 930)
 BMS3h-56-16

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC
 20 TCTCCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCA
 GGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACA
 TACTACGCAGACTCCGTGATGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACA
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC
 GAAACTTCCGTTTACTTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
 25 (SEQ ID NO: 931)

BMS3h-56-17

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCTCCTTTCGGGATTATGAGATGTGGTGGTACCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATATTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 932)

BMS3h-56-18

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGTTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACATGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 933)

15 BMS3h-56-19

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATCACTGTGCGAAACTTCCGTTTAC
 TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 934)

BMS3h-56-20

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 25 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTACGAACTTCCGTTTAC
TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 935)
BMS3h-56-21

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTTTGAAGCTTCCGTTTAC
10 TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 936)
BMS3h-56-22

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTAT
CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAACCCGCAGGGTACGCGTACATACTATGCA
15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGATGATACCGCGGTATATCACTGTACGAACTTCCGTTTAT
TTTTGAATACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 937)
BMS3h-56-23

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGT
20 CTCTCCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGC
CAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGT
ACATACTACGCAGACTCCGTGATGGGCCGGTTCACCATCTCCCGCGACAATTCCAAG
AACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTAC
TGTGCGAAAGAACCTTATAGTTTTGACTCCTGGGGTCAGGGAACCCTGGTCACCGTC
25 TCGAGC (SEQ ID NO: 938)

BMS3h-56-24

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 5 GACTCCGTGATGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATCACTGTGCGAAAGAACCTTATAG
 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 939)

BMS3h-56-25

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCGGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 GACTCCGTGATGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGACGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 940)

15 BMS3h-56-26

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTAT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCGGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 GACTCCGTGATGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGATACTGCGGTATATTACTGTGCGAAACTTCCGTTTAT
 GTTTGACGACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 941)

BMS3h-56-27

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTAT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 25 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA

GACTCCGTGATGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACTGCGGTATATTACTGTGCGAAACTTCCGTTTAT
 GTTTGACGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 942)
 BMS3h-56-28

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGCTGGGTATGAGTTGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 GACTCCGTGATGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 10 TTTTGACGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 943)
 BMS3h-56-29

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGCTGGGTATGAGTTGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 15 GACTCCGTGATGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACTGCGGTATATTACTGTGCGAAACTTCCGTTTAT
 GTTTGACGACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 944)
 BMS3h-56-30

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGT
 20 CTCTCCTGTGCAGCCTCCGGATTACCTTTGCTGGGTATGAGATGTGGTGGTTCCGC
 CAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGT
 ACATACTACGCAGACTCCGTGATGGGCCGGTTCACCATCTCCCGCGACAATTCCAAG
 AACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTAC
 TGTGCGAAACTTCCGTTTACTTTTGACGACTGGGGTCAGGGAACCCTGGTCACCGTC
 25 TCGAGC (SEQ ID NO: 945)

BMS3h-56-31

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGCTGGGTATGAGATGTGGTGGTTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 5 GACTCCGTGATGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACTGCGGTATATTACTGTGCGAAACTTCCGTTTAT
 GTTTGACGACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 946)

BMS3h-56-32

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 GACTCCGTGATGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGACGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 947)

15 BMS3h-56-33

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTAT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 GACTCCGTGATGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGATACTGCGGTATATTACTGTGCGAAACTTCCGTTTAT
 GTTTGACGACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 948)

BMS3h-56-202

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 25 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGACCTA
 CTTTTCGACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 949)
 BMS3h-56-203

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTT
 10 CTTTGAGGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 950)
 BMS3h-56-204

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGACGTA
 CTTTAAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 951)
 BMS3h-56-205

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC
 20 TCTCCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCA
 GGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACA
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACA
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC
 GAAACTTCCGTTTTTACTTTTCCGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
 25 (SEQ ID NO: 952)

BMS3h-56-206

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATCACTGTGCGAAACTTCCGATGTT
 CTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAAC (SEQ ID NO: 953)

BMS3h-56-207

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTCC
 GTTTTCGGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 954)

15 BMS3h-56-208

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGGACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTC
 CTTTTCGGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 955)

BMS3h-56-209

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 25 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTACGGTAACCTCACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 956)
 BMS3h-56-210

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCCCCGGTACCTTGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 10 TTTTGAGGACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 957)
 BMS3h-56-211

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTGGCTTGACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 958)
 BMS3h-56-212

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCT
 20 CTCCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGG
 CTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGATGGGTGGGTTCACATAC
 TACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCT
 GTATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAC
 TTCCGTTTACTTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ
 25 ID NO: 959)

BMS3h-56-213

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTTCGCACACATACTACGCA
5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 960)

BMS3h-56-214

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
10 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTCCGGTGGGCTGACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
TTTTGACGACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 961)

15 BMS3h-56-215

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCACGGTTCGTTGACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
20 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
TTTTGACGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 962)

BMS3h-56-216

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
25 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGGCCGGTCGGTTGACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 963)
 BMS3h-56-217

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTAGCTTGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 10 TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 964)
 BMS3h-56-218

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGCGACTACGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATCACTGTGCGAAACTTCCGTTTAC
 TTTTGACGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 965)
 BMS3h-56-219

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC
 20 TCTCCTGTGCAGACTCCGGATTACCTTTCGCCCCGTGGAGATGTGGTGGGTCCGCCA
 GGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACA
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACA
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGC
 GAAACTTCCGTTTACTTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
 25 (SEQ ID NO: 966)

BMS3h-56-220

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTACGGTGGGCTGACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGACGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 967)

BMS3h-56-221

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTAACCACACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 968)

15 BMS3h-56-222

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCACGGTGGCTACACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 969)

BMS3h-56-223

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 25 AGGGAGGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCCCCGGTATGCTCACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGACGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 970)
 BMS3h-56-224

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTCAGTTGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 10 TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 971)
 BMS3h-56-225

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTGGCTACACATACTACGCA
 15 GACTCCGTGAAGGGCCGATTACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGACGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 972)
 BMS3h-56-226

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC
 20 TCTCCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCA
 GGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGCGGTGGGCTGACA
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACA
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGC
 GAAACTTCCGTTTACTTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
 25 (SEQ ID NO: 973)

BMS3h-56-227

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTCTGGGTGGGTGACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGACGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 974)

BMS3h-56-228

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTCTGGGTACGCTCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 975)

15 BMS3h-56-229

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTACGGTTCGTTGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGACGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 976)

BMS3h-56-230

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 25 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTGGCTACACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 977)
 BMS3h-56-231

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTGGGCTGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 10 TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 978)
 BMS3h-56-232

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTTCCACACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGACGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 979)
 BMS3h-56-233

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC
 20 TCTCCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCA
 GGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTACCTTGACA
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAGGAACA
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGC
 GAAACTTCCGTTTACTTTTGACGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
 25 (SEQ ID NO: 980)

BMS3h-56-234

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGAACGGTCGGCTGACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGCGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 981)

BMS3h-56-235

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTCAGCTGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGACGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 982)

15 BMS3h-56-236

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCACGGTGGCCTCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGATAACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGACGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 983)

BMS3h-56-237

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 25 AGGGAAGGGTCTGGAGCGGGTCTCAGCTATTAATCCGGCGGGTATGTTGACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGACGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 984)
 BMS3h-56-238

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCACGGTACCTTGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 10 TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 985)
 BMS3h-56-239

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTTCGTTGACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGACGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 986)
 BMS3h-56-240

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC
 20 TCTCCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCA
 GGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTACGGTGGCCTGACA
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACA
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGC
 GAAACTTCCGTTTACTTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
 25 (SEQ ID NO: 987)

BMS3h-56-241

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTCGGGATTACGAGATGTGGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGGCCGGTTTCTTGACATACTACGCA
5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGATAACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 988)

BMS3h-56-242

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACGGCCTGGGGGGTCCCTGCGTCTCT
10 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTGGAGCGGGTCTCAGCTATTAATCCGTACGGTGGCCTGACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGATAACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 989)

15 BMS3h-56-243

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTGGGTTACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
20 AAATGAACAGCCTGCGTGCCGAGGATAACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 990)

BMS3h-56-244

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
25 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTGGGTTGACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGACGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 991)
 BMS3h-56-245

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTACGGTGGGCTGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGGACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 10 TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 992)
 BMS3h-56-246

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTACGTTGACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 993)
 BMS3h-56-247

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC
 20 TCTCCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCA
 GGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTGGCTACACA
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACA
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGC
 GAAACTTCCGTTTACTTTTGAGGACTGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC
 25 (SEQ ID NO: 994)

BMS3h-56-248

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTACGGTAACCTGACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGACGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 995)

BMS3h-56-249

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCACGGTGGGTTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 996)

15 BMS3h-56-250

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGGCCGGTTTCTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGACGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 997)

BMS3h-56-251

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 25 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGGCGGGTGGCCTCACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 TTTTGACGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 998)
 BMS3h-56-252

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTTCGCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCACGGTTCCTCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAC
 10 TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 999)
 BMS3h-56-253

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTTCACCTTTCGTGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGGCCGGTGGGTACACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATCACTGTGCGAAACTTCCGTTTAC
 TTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1000)
 BMS3h-56-254

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGT
 20 CTCTCCTGTGCAGCCTCCGGATTTCACCTTTCGGGATTATGAGATGTGGTGGGTCCGC
 CAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGT
 ACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAG
 AACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTAC
 TGTGCGAAACTTCCGTTTGGTTTACGGAGTGGGGTCAGGGAACCCTGGTCACCGTC
 25 TCGAGC (SEQ ID NO: 1001)

BMS3h-56-255

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTCAT
 GTTTTCCGACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1002)

BMS3h-56-256

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTT
 GTTTCAGGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1003)

15 BMS3h-56-257

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGACGCG
 GTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1004)

BMS3h-56-258

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 25 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTA
 CTTTCACGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1005)
 BMS3h-56-259

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCG
 10 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1006)
 BMS3h-56-260

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGACGTT
 CTTTAAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1007)
 BMS3h-56-261

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGT
 20 CTCTCCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGC
 CAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACACGT
 ACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAG
 AACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGATAACCGCGGTATATTAC
 TGTGCGAAACTTCCGTTTTTCTTTCAGGAGTGGGGTCAGGGAACCCTGGTCACCGTC
 25 TCGAGC (SEQ ID NO: 1008)

BMS3h-56-262

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGCAGTT
GTTTCACGACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1009)

BMS3h-56-263

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
10 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGCAGCT
CTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1010)

15 BMS3h-56-264

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
20 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATCACTGTGCGAAACTTCCGTTTGG
GTTTTCCGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1011)

BMS3h-56-265

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
25 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGCAGTT
 GTTTCAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1012)
 BMS3h-56-266

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTT
 10 CTTTCACGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1013)
 BMS3h-56-267

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGCACTA
 CTTTAAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1014)
 BMS3h-56-268

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGTCTGGGGGGTCCCTGCGT
 20 CTCTCCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGC
 CAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGT
 ACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAG
 AACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTAC
 TGTGCGAAACTTCCGTTTTACTTTGAGGAGTGGGGTCAGGGAACCCTGGTCACCGTC
 25 TCGAGC (SEQ ID NO: 1015)

BMS3h-56-269

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTAG
 GTTTTCCGACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1016)

BMS3h-56-270

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGACGCT
 GTTTCAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1017)

15 BMS3h-56-271

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTT
 CTTTCCGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAAC (SEQ ID NO: 1018)

BMS3h-56-272

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 25 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTG
 GTTTCAGGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1019)
 BMS3h-56-273

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTTCGTTGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTA
 10 CTTTCAGGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1020)
 BMS3h-56-274

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTTCGTTGACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATCACTGTGCGAAACTTCCGATGTT
 CTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAAC (SEQ ID NO: 1021)
 BMS3h-56-275

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGT
 20 CTCTCCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGC
 CAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTTCGTTG
 ACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAG
 AACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTAC
 TGTGCGAAACTTCCGTTTTACTTTCACGAGTGGGGTCAGGGAACCCTGGTCACCGTC
 25 TCGAGC (SEQ ID NO: 1022)

BMS3h-56-276

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTTCGTTGACATACTACGCA
5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTT
CTTTCAGGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1023)

BMS3h-56-277

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
10 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTTCGTTGACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTT
CTTTCACGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1024)

15 BMS3h-56-278

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTGGGTTACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
20 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTTA
CTTTCAGGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1025)

BMS3h-56-279

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
25 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTGGGTTACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATCACTGTGCGAAACTTCCGATGTT
 CTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAAC (SEQ ID NO: 1026)
 BMS3h-56-280

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTGGGTTCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTA
 10 CTTTCACGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1027)
 BMS3h-56-281

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTGGGTTCACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTT
 CTTTCAGGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1028)
 BMS3h-56-282

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC
 20 TCTCCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCA
 GGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTGGGTTCACA
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACA
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGC
 GAAACTTCCGTTTTTCTTTACGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
 25 (SEQ ID NO: 1029)

BMS3h-56-283

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTGGGTGACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTTA
 CTTTCAGGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1030)

BMS3h-56-284

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTGGGTGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATCACTGTGCGAAACTTCCGATGTT
 CTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAAC (SEQ ID NO: 1031)

15 BMS3h-56-285

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTGGGTGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTA
 CTTTCACGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1032)

BMS3h-56-286

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 25 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTGGGTGACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTTT
 CTTTCAGGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1033)
 BMS3h-56-287

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGTGGGGTGGGTTGACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAACTTCCGTTTTT
 10 CTTTCACGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1034)
 BMS3h-56-288

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATCACTGTGCGAAACTTCCGATGTT
 CTTTGAGGACTGGGGTCAGGGAACCCTGGTCACCGTCTCCAGC (SEQ ID NO: 1035)
 BMS3h-106-1

GAGGTGCAGCTGTTGGAGACTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 20 CCTGTGCAGCCTCCGGATTACCTTTTCGACTTATCATATGCAGTGGGTCCGCCGGGCTCC
 AGGGAAGGGCCTGGAGTGGGTCTCAATGATTGATGCGGATGGTCTTGGGACATACTACGCA
 GACCCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCAAGGACACCGCGGTATATTACTGTGCGAGACCGGGTCCGCA
 GTTTGGTCAGTTTGACTACTTGGGTGAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 25 NO: 1036)

BMS3h-106-2

GAGGTGCAGCTGTTTGAGTCTGGGGGAGGCTTGGTACAGACTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTTCGACTTATCATATGCAGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTGGAGTGGGTCTCAATGATTGATGCGGATGGTCTTGGGAAATACTACGCA
 5 GACCCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGTGAAACCGGGTCCGCA
 GTTTGGTCAGTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID
 NO: 1037)

BMS3h-107-1

10 GAGGTGCAGCTGTTGGAGTCAGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGGCTCT
 CCTGTTTCAGCTTCCGGATTACCTTTTCGGGGTATGATATGCAGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAACGATTAGTGCGTCGGGTGTTTATACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAATATCCTAATCG
 15 TTTTGCCTTAATAGTTTTGACTACAGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC
 (SEQ ID NO: 1038)

BMS3h-107-2

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTG
 TGCAGCTTCCGGATTACCTTTTCGGGGTATGATATGCAGTGGGTCCGCCAGGCTCCAGGGAGGG
 20 GTCTAGAGTGGGTCTCAACGATTAGTGCGTCGGGTGTTTATACATACTACACAGACTCCGTGAAG
 GGCCGGTTCACCACCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGCG
 TGCCGAGGACACCGCGGTATATTACTGTACGAAATATCAAATCGTTTTGCGCGTAATAATTTTG
 ACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1039)

BMS3h-131-1

25 GACATCCTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA

TCACTTGCCGGGCAAATAGTTCTATTTTGTGGGCGTTAGCTTGGTACCAGCAGAAACCAGG
GGAAGCCCCTAAGCTCCTGATCGAGAGTTCTTCCGGTTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTGTTTTCAGAATGCGGTTTGGCCTGGTACGTTTCAGCCAAGGGAC

5 CAAGGTGGAAATCAAACGG (SEQ ID NO: 1040)

BMS3h-131-2

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCA
TCACTTGCCGGGCGAGACAGTTCTATTTTGTGGGCGTTAGCTTGGTACCAGCAGAAACCAGG
GAAAGCCCCTAAGCTCCTGATCGAGAGTTTCATCCGGTTTGCAAAGTGGGGTCCCATCACGT
10 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTGTTTTCAGAATGCGGTTTGGCCTGGTACGTTTCGGCCAAGGGAC
CAAGGTGGAAATCAAACGG (SEQ ID NO: 1041)

BMS3h-131-3

GACATCCAGATGACCGTGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCA
15 TCACTTGCCGGGCGAGATAGTTCTATTTTGTGGGCGTTAGCTTGGTACCAGCAGAAACCAGG
GAAAGCCCCTAAGCTCCTGATCGAGAGTTCTTCCGGATTGCAAAGCGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTGTTTTCAGAATGCGGTTTGGCCTGGTACGTTTCGGCCAAGGGAC
CAAGGTGGAAATCAAACGG (SEQ ID NO: 1042)

20 BMS3h-131-4

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCA
TCACTTGCCGGGCAAATAGTTCTATTTTGTGGGCGTTAGCTTGGTACCAGCAGAAACCAGG
GAAAGCCCCTAAGCTCCTGATCGAGAGTTCTTCCGGTTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
25 ATTTTGCTACGTACTACTGTGTTTTCAGAATGCGGTTTGGCCTGGTACGTTTCGACCAAGGGAC

CAAGGTGGAAATCAAACGG (SEQ ID NO: 1043)

BMS3h-131-5

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
TCACTTGCCGGGCAAATAGTTCTATTTTGTGGGCGTTAGCTTGGTACCAGCAGAAACCAGG
5 GAAAGCCCCTAAGCTCCTGATCGAGAGTTCTACCGGTTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTGTTTTCAGAATGCGGTTTGGCCTGGTACGTTTCGGCCAAGGGAC
CAAGGTGGAAATCAAACGG (SEQ ID NO: 1044)

BMS3h-131-6

10 GACATCCAGATGACCGTGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
TCACTTGCCGGGCAAATAGTTCTATTTTGTGGGCGTTAGCTTGGTACCAGCAGAAACCAGG
GAAAGCCCCTAAGCTCCTGATCGAGAGTTCTTCCGGATTGCAAAGCGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTGTTTTCAGAATGCGGTTTGGCCTGGTACGTTTCGGCCAAGGGAC
15 CAAGGTGGAAATCAAACGG (SEQ ID NO: 1045)

BMS3h-131-7

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
TCACTTGCCGGGCAGATAGTTCTATTTTGTGGGCGTTAGCTTGGTACCAGCAGAAACCAGG
GAAAGCCCCTAAGCTCCTGATCGAGAGTTCTTCCGGTTTGCAAAGTGGGGTCCCATCACGT
20 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTGTTTTCAGAATGCGGTTTGGCCTGGTACGTTTCGACCAAGGGAC
CAAGGTGGAAATCAAACGG (SEQ ID NO: 1046)

BMS3h-131-8

GACATCCAGATGACCCAGTCTCCATCCTCACTGTCTGCATCTGTAGGAGACCGTGTACCA
25 TCACTTGCCGGGCAAATAGTTCTATTTTGTGGGCGTTAGCTTGGTACCAGCAGAAACCAGG

GAAAGCCCCTGAGCTCCTGATCGAGAGTTCTTCCGGTCTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTGTTTCAAGATGCGGTTTGGCCTGGTACGTTTCGGCCAAGGGAC
 CAAGGTGGAAATCAAACGG (SEQ ID NO: 1047)

5 BMS3h-131-9

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
 TCACTTGCCGGGCGAATAGTTCTATATTGTGGGCGTTGGCTTGGTACCAGCAGAAACCAGG
 GAAAGCCCCTAAGCTCCTGATCGAGAGTTCTTCCGGTTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 10 ATTTTGCTACGTACTACTGTGTTTCAAGATGCGGTTTGGCCTGGTACGTTTCGGCCAAGGGAC
 CAAGGTGGAAAACAAACGG (SEQ ID NO: 1048)

BMS3h-131-10

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
 TCACTTGCCGGGCGAATAGTTCTATTTCTGTGGGCGTTAGCTTGGTACCAGCAGAAACCTGG
 15 GAAAGCCCCTAAGCTCCTGATCGAGAGTTCTTCCGGTTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCCGAAG
 ATTTTGCTACGTACTACTGTGTTTCAAGATGCGGTTTGGCCTGGTACGTTTCGGCCAAGGGAC
 CAAGGTGGAAATCAAACGG (SEQ ID NO: 1049)

BMS3h-131-11

20 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTAGGAGACCGTGTACCA
 TCACTTGCCGGGCGAATAGTTCTATTTTGTGGGCGTTAGCTTGGTACCAGCAGAAACCAGG
 GAAAGCCCCTAAGCTCCTGATCGAGAGTTCTTCCGGTTTGCAAAGTGGGATCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTGTTTCAAGATGCGGTTTGGCCTGGTACGTTTCGGCCAAGGGAC
 25 CAAGGTGGAAATCAAACGG (SEQ ID NO: 1050)

BMS3h-131-12

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTTGGAGACCGTGTCACCA
TCACTTGCCGGGCAAATAGTTCTATTTTGTGGGCGTTAGCTTGGTACCAGCAGAAACCAGG
GAAAGCCCCTAAGCTCCTGATCGAGAGTTCTTCCGGATTGCAAAGCGGGGTCCCATCACGT
5 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTGTTTTCAGAATGCGGTTTGGCCTGGTACGTTTCGGCCAAGGGAC
CAAGGTGGAAATCAAACGG (SEQ ID NO: 1051)

BMS3h-131-13

GACATCCTGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCA
10 TCACTTGCCGGGCAAATAGTTCTATTTTGTGGGCGTTAGCTTGGTACCAGCAGAAACCAGG
GAAAGCCCCTAAGCTCCTGATCGAGAGTTCTTCCGGTTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTGTTTTCAGAATGCGGTTTGGCCTGGTACGTTTCGGCCAAGGGAC
CAAGGTGGAAATCAAACGG (SEQ ID NO: 1052)

15 BMS3h-131-14

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCA
TCACTTGCCGGGCAAATAGTTCTATTTTGTGGGCGTTAGCTTGGTACCAGCAGAAACCAGG
GAAAGCCCCTAAGCTCCTGATCGAGAGTTCTTCCGGTTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGAAGTGGAAGTGGGACAGATTTCACTCTCACCATCAGCGGTCTGCAACCTGAAG
20 ATTTTGCTACGTACTACTGTGTTTTCAGAATGCGGTTTGGCCTGGTACGTTTCGACCAAGGGAC
CAAGGTGGAAATCAAACGG (SEQ ID NO: 1053)

BMS3h-131-15

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCA
TCCCTTGCCGGGCAAATAGTTCTATTTTGTGGGCGTTAGCTTGGTACCAGCAGAAACCAGG
25 GAAAGCCCCTAAGCTCCTGATCGAGAGTTCTTCCGGTTTGCAAAGTGGGGTCCCATCACGT

TTCAGTGGCAGTGCATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTGTTTCAAGATGCGGTTTGGCCTGGTACGTTTCGGCCAAGGGAC
 CAAGGTGGAGATCAAACGG (SEQ ID NO: 1054)

BMS3h-193-1

5 GACATCCAGATGGCCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
 TCACTTGCCGGGCAAGTCAGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGG
 GAAAGCCCCTAAGCTCCTGATCTATCTTGCTTCCCGTTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTCATCAGTATGCGAGTCCACCTTTGACGTTAGGCCAAGGGAC
 10 CAAAGTGGAAATCAAACGG (SEQ ID NO: 1055)

BMS3h-193-2

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGTGTACCA
 TCACTTGCCGGGCAAGTCAGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGG
 GGAAGCCCCTAAGCTCCTGATCTATCTTGCTTCCCGTTTGCAAAGTGGGGTCCCATCACGT
 15 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGCCATCAGTATGCGAGTCCACCTTTGACGTTTCGGCCAAGGGAC
 CAATGTGGAAATCAAACGG (SEQ ID NO: 1056)

BMS3h-193-3

GACATCCAGATGACCCAGTCTCCATCCTCCCTATCTGCATCTGTAGGAGACCGTG
 20 TCACCATCACTTGCCGGGCAAGTCAGACGATTGAGCGTCGTTTAAATTGGTATCA
 GCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATCTTGCTTCCCGTTTGCAA
 AGTGGGGTCCCATCACGTTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCA
 CCATCAGCAGTCTGCAACCTGAAGATTTTGCTGCGTACTACTGTCATCAGTACGA
 GAGTCCACCTTTGACGTTTGGCCAAGGGACCAAAGTGGAAATCAAACGG (SEQ
 25 ID NO: 1057)

BMS3h-193-4

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
TCACTTGCCGGGCAAGTCGGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGG
GAAAGCCCCTAAGCTCCTGATCTATCTTGCTTCGCGTTTGCAAAGTGGGGTCCCATCACGT
5 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC
CAAAGTGGAATCAAACGG (SEQ ID NO: 1058)

BMS3h-193-5

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGAACGTGTACCA
10 TCACTTGCCGGGCAAGTCAGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGG
GAAAGCCCCTAAGCTCCTGATCTATCTTGCTTCCCGTTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCTGAAG
ATTCTGCTACGTACTACTGTCATCAGTATGCGAGTCCACCTTTGACGTTAGGCCAAGGGAC
CAAAGTGGAATCAAACGG (SEQ ID NO: 1059)

15 BMS3h-193-6

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
TCACTTGCCGGGCAAGCCAGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGG
GAAGGCCCTAAGCTCCTGATCTATCTTGCTTCCCGTTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
20 ATTTTGCTACGTACTACTGTCATCAGTATGCGAGTCCACCTTTGACGTTAGGCCAAGGGAC
CAAAGTGGAATCAAACGG (SEQ ID NO: 1060)

BMS3h-193-7

GACATCCAGATAACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
TCACTTGCCGGGCAAGTCAGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGG
25 GAAAGACCCTAAGCTCCTGATCTATCTTGCTTCCCGTTTGCAAAGTGGGGTCCCATCACGT

TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCTCCTTTGACGTTTCGGCCAAGGGAC
 CAAAGTGGAAATCAAACGG (SEQ ID NO: 1061)

BMS3h-193-8

5 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
 TCACTTGCCGGGCAAGTCAGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGG
 GGAAGCCCCTAAGCTCCTGATCTATCTTGCTTCCCGTTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC
 10 CAAAGTGGAAATCAAATGG (SEQ ID NO: 1062)

BMS3h-193-9

GACATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCA
 TCACTTGCCGGGCAAGTCAGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGG
 GAAAGCCCCTAAGCTCCTGATCTATCTTGCTTCCCGTTTGCAAAGTGGGGTCCCATCACGT
 15 TTCAGTGGCAGTGGATCTGGGACAGAATTCCTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC
 CAAAGTGGAAATCAAACGG (SEQ ID NO: 1063)

BMS3h-193-10

GACATCCAGATGTCCCAGTCTCCATCCACCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCG
 20 GGCAAGTCAGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGA
 TCTATCTTGCTTCCCGCTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTT
 ACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACC
 TTTGATGTTTCGGCCAAGGGACCAAAGTGGAAATCAAACGG (SEQ ID NO: 1064)

BMS3h-193-11

25 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA

TTACTTGCCGGGCAAGTCAGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGG
 GAAAGACCCTAAGCTCCTGATCTATCTTGCTTCCCGTTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCAGAAG
 ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC

5 CAAAGTGGAAATCAAACGG (SEQ ID NO: 1065)

BMS3h-193-12

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCCGTAGGAGACCGTGTACCA
 TCACTTGCCGGGCAAGTCAGACGATTGAGCGTCGTTTAAACTGGTATCAGCAGAAACCAGG
 GAAAGCCCCTAAGCTCCTGATCTATCTTGCTTCCCGTTTGCAAAGTGGGGTCCCATCACGT
 10 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC

CAAAGTGGAAATCAAACGG (SEQ ID NO: 1066)

BMS3h-193-13

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTTTGCATCTGTAGGGGACCGTGTACCA
 15 TCACTTGCCGGGCAAGTCAGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGG
 GAAAGCCCCTAAGCTCCTGATCTATCTTGCTTCCCGTTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC

CAAAGTGGAAATCAAACGG (SEQ ID NO: 1067)

20 BMS3h-193-14

GACATCCAGATGACCCAGTATCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
 TCACTTGCCGGGCAAGTCAGTCGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGG
 GGAAGCCCCTAAGCTCCTGATCTATCTTGCTTCCCGTTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG

25 ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC

TAAAGTGGAAATCAAACGG (SEQ ID NO: 1068)

BMS3h-193-15

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
TCACTTGCCGGGCAAGTCGGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGG
5 GAAAGCCCCCTAAGCTCCTGATCTATCTTGCTTCGCGTTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTCATCCGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC
CAAAGTGGAAATCAAACGG (SEQ ID NO: 1069)

BMS3h-193-16

10 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
TCACTTGCCGGGCAAGTCAGGCGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGG
GAAAGCCCCCTAAGCTCCTGATCTATCTTGCTTCCCGTTTGCAAAGTGGGGTCCCATCTCGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAGCCAGAAG
ATTTTGCTACGTACTACTGTCATCAGTATGCGAGTCCACCTTTGACGCTCGGCCAAGGGAC
15 CAAAGTGGAAATCAAACGG (SEQ ID NO: 1070)

BMS3h-193-17

AACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
TCACTTGCCGGGCAAGTCAGGCGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGG
GAAAGCCCCCTAAGCTCCTGATCTATCTTGCTTCTCGTTTGCAAAGTGGGGTCCCATCACGT
20 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC
CAAAGTGGAAATCAAACGG (SEQ ID NO: 1071)

BMS3h-193-18

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
25 TCACTTGCCGGGCAAGTCAGACGATTGGGCGTCGTTTAAATTGGTATCAGCAGAAACCAGG

GAAAGCCCCTAAGCTCCTGATCTATCTTGCTTCCCGTTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGTGAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC
 CAAAGTGGAATCAAACGG (SEQ ID NO: 1072)

5 BMS3h-193-19

GACATCCAGATGACCCAGTCTCCATCCTCCCTTTCTGCATCTGTAGGAGACCGTGTACCA
 TCACTTGCCGAGCAAGTCAGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGG
 GAAAGCCCCTAAGCTCCTGATCTATCTTGCTTCCCGTTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGAATTTACTCTCACCATCAGCAGTCTGCAACCTGAAG
 10 ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC
 CAAAGTGGAATCAAACGG (SEQ ID NO: 1073)

BMS3h-193-20

GACATCCAGATGACCCAGACTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
 TCACTTGCCGGGCAAGTCAGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGG
 15 GGAAGCCCCTAAGCTCCTGATCTATCTTGCTTCCCGTTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCCACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC
 CAAAGTGAAAATCAAACGG (SEQ ID NO: 1074)

BMS3h-193-21

20 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGTGTACCA
 TCACTTGCCGGGCAAGTCAGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGG
 GAAAGCCCCTAAGCTCCTGATCTATCTTGCTTCCCGTTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCCGAAG
 ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC
 25 CAAAGTGGAATCAAACGG (SEQ ID NO: 1075)

BMS3h-193-22

CACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
 TCACTTGCCGGGCAAGTCAGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGG
 GAAAGCCCCTAAGCTCCTGATCTATCTTGCTTCCCGTTTGCAAAGTGGGGTCCCATCACGT
 5 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGCCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC
 CAAAGTGGAAATCAAACGG (SEQ ID NO: 1076)

BMS3h-193-23

GACGTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
 10 TCACTTGCCGGGCAAGTCAGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGG
 GGAAGCCCCTAAGCTCCTGATCTATCTTACTTCCCGTTTGCAAAGCGGGGTCCCATCACGT
 TTCAGTGGTAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGCCATCAGTATGCGAGTCCACCTTTGACGTTTCGGCCAAGGGAC
 CAAGGTGGAAATCAAACGG (SEQ ID NO: 1077)

15 BMS3h-193-24

GACATCCAGATGACCCAGTCGCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
 TCACTTGCCGGGCAAGTCAGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCAGG
 GAAAGCCCCTAAGCTCCTGATCTATCTTGCTTCCCGTTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 20 ATTTTGCTACGTACTACTGTCACCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC
 CAAAGTGGTAATCAAACGG (SEQ ID NO: 1078)

BMS3h-193-25

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCA
 TCACTTGCCGGGCAAGTCAGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCTGG
 25 GAAAGCCCCTAGGCTCCTGATCTATCTTGCTACCCGTTTGCAAAGTGGGGTCCCATCACGC

TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC
 CAAAGTGGAAATCAAACGG (SEQ ID NO: 1079)

BMS3h-193-26

5 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
 TCACTTGCCGGGCAAGTCAGCCGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAGCCAGG
 GAAAGCCCCTAAGCTCCTGATCTATCTTGCTTCCCGTTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACATACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC
 10 CAAAGTGGAAATCAAACGG (SEQ ID NO: 1080)

BMS3h-193-27

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCG
 GGCAAGTCAGACGATTGGGCGTCGTTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGA
 TCTATCTTGCTTCCCGTTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTTC
 15 ACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACC
 TTTGACGTTTCGGCCAAGGGACCAAAGTGGAAATCAAACGG (SEQ ID NO: 1081)

BMS3h-193-28

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
 TCACTTGCCGGGCAAGTCAGTCGATTGAGCGCCGTTTAAATTGGTATCAGCAGAAACCAGG
 20 GAAAGCCCCTAAGCTCCTGATCTATCTTGCTTCCCGTTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCTCCTTTGACGTTTCGGCCAAGGGAC
 CAAAGTGGAAATCATACGG (SEQ ID NO: 1082)

BMS3h-193-29

25 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCA

TCACCTGCCGGGCAAGTCAGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCTGG
 GAAAGCCCCTAAGCTCCTGATCTATCTTGCTACCCGTTTGCAAAGTGGGGTCCCATCACGC
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC

5 CAAAGTGGAAATCAAACGG (SEQ ID NO: 1083)

BMS3h-193-30

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
 TCACTTGCCGGGCAAGTCAGTCGATTGAGCGCCGTTTAAATTGGTATCAGCAGAAACCAGG
 GAAAGCCCCTAAGCTCCTGATCTATCTTGCTTCCCGTTTGCAAAGTGGGGTCCCATCACGT
 10 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCTCCTTTGACGTTTCGGCCAAGGGAC

CAAAGTGGAAATCAAACGG (SEQ ID NO: 1084)

BMS3h-193-2501

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCA
 15 TCACTTGCCGGGCAAGTCAGACGATTGAGCGTCGTTTAAATTGGTATCAGCAGAAACCTGG
 GAAAGCCCCTAGGCTCCTGATCTATCTTGCTACCCGTTTGCAAAGTGGGGTCCCATCACGC
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTCATCAGTTCGAGCACCCACCTTTGACGTTTCGGCCAAGGGAC

CAAAGTGGAAATCAAACGG (SEQ ID NO: 1085)

20 BMS3h-193-2502

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCA
 TCACTTGCCGGGCAAGTTTCCCATTGACCGTCGTTTAAATTGGTATCAGCAGAAACCTGG
 GAAAGCCCCTAGGCTCCTGATCTATCTTGCTACCCGTTTGCAAAGTGGGGTCCCATCACGC
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 25 ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC

CAAAGTGGAAATCAAACGG (SEQ ID NO: 1086)

BMS3h-193-2503

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCA

TCACTTGCCGGGCAAGTTCCACCATTGGCCGTCGTTTAAATTGGTATCAGCAGAAACCTGG

5 GAAAGCCCCTAGGCTCCTGATCTATCTTGCTACCCGTTTGCAAAGTGGGGTCCCATCACGC

TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG

ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC

CAAAGTGGAAATCAAACGG (SEQ ID NO: 1087)

BMS3h-193-2504

10 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTTACCA

TCACTTGCCGGGCAAGTTCCCAGATTGGGCGTCGTTTAAATTGGTACCAGCAGAAACCAGG

GAAAGCCCCTAGGCTCCTGATCTATCTTGCTACCCGTTTGCAAAGTGGGGTCCCATCACGC

TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG

ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC

15 CAAAGTGGAAATCAAACGG (SEQ ID NO: 1088)

BMS3h-193-2505

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCA

TCACTTGCCGGGCAAGTGAGCGGATTGGGCGTCGTTTAAATTGGTATCAGCAGAAACCAGG

GAAAGCCCCTAGGCTCCTGATCTATCTTGCTACCCGTTTGCAAAGTGGGGTCCCATCACGC

20 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG

ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC

CAAAGTGGAAATCAAACGG (SEQ ID NO: 1089)

BMS3h-193-2506

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCA

25 TCACTTGCCGGGCAAGTCAGCAGATTGGCCGCCGTTTAAATTGGTATCAGCAGAAACCTGG

GAAAGCCCCTAGGCTCCTGATCTATCTTGCTACCCGTTTGCAAAGTGGGGTCCCATCACGC
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC
 CAAAGTGGAATCAAACGG (SEQ ID NO: 1090)

5 BMS3h-193-2507

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCA
 TCACTTGCCGGGCAAGTCAGCCGATTGCCCGGCGTTTAAATTGGTACCAGCAGAAACCAGG
 GAAAGCCCCTAGGCTCCTGATCTATCTTGCTACCCGTTTGCAAAGTGGGGTCCCATCACGC
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 10 ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC
 CAAAGTGGAATCAAACGG (SEQ ID NO: 1091)

BMS3h-193-2508

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCA
 TCACTTGCCGGGCAAGTGGGAACATTGGCCGTCGTTTAAATTGGTACCAGCAGAAACCAGG
 15 GAAAGCCCCTAGGCTCCTGATCTATCTTGCTACCCGTTTGCAAAGTGGGGTCCCATCACGC
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC
 CAAAGTGGAATCAAGCGG (SEQ ID NO: 1092)

BMS3h-193-2509

20 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCA
 TCACTTGCCGGGCAAGTCGGAACATTGACCGTCGTTTAAATTGGTACCAGCAGAAACCAGG
 GAAAGCCCCTAGGCTCCTGATCTATCTTGCTACCCGTTTGCAAAGTGGGGTCCCATCACGC
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC
 25 CAAAGTGGAATCAAACGG (SEQ ID NO: 1093)

BMS3h-193-2510

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCA
 TCACTTGCCGGGCAAGTCAGAGCATTGGGCGTCGTTTAAATTGGTACCAGCAGAAACCTGG
 GAAAGCCCCTAGGCTCCTGATCTATCTTGCTACCCGTTTGCAAAGTGGGGTCCCATCACGC
 5 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC
 CAAAGTGGAATCAAACGG (SEQ ID NO: 1094)

BMS3h-193-2511

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCA
 10 TCACTTGCCGGGCAAGTCAGAACATTGGGACGCGTTTAAATTGGTACCAGCAGAAACCAGG
 GAAAGCCCCTAGGCTCCTGATCTATCTTGCTACCCGTTTGCAAAGTGGGGTCCCATCACGC
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC
 CAAAGTGGAATCAAACGG (SEQ ID NO: 1095)

15 BMS3h-193-2512

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCA
 TCACTTGCCGGGCAAGTGAGGTCATTGGGCGTCGTTTAAATTGGTACCAGCAGAAACCAGG
 GAAAGCCCCTAGGCTCCTGATCTATCTTGCTACCCGTTTGCAAAGTGGGGTCCCATCACGC
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 20 ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC
 CAAAGTGGAATCAAACGG (SEQ ID NO: 1096)

BMS3h-193-2513

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCA
 TCACTTGCCGGGCAAGTGAGGCGATTGGCCGTCGTTTAAATTGGTATCAGCAGAAACCAGG
 25 GAAAGCCCCTAGGCTCCTGATCTATCTTGCTACCCGTTTGCAAAGTGGGGTCCCATCACGC

TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC
CAAAGTGGAAATCAAACGG (SEQ ID NO: 1097)

BMS3h-193-2514

5 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCA
TCACTTGCCGGGCAAGTACCAGCATTGCGCGTCGTTTAAATTGGTATCAGCAGAAACCTGG
GAAAGCCCCTAGGCTCCTGATCTATCTTGCTACCCGTTTGCAAAGTGGGGTCCCATCACGC
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC
10 CAAAGTGGAAATCAAACGG (SEQ ID NO: 1098)

BMS3h-193-2515

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCA
TCACTTGCCGGGCAAGTTTGAACATTGGGCGTCGTTTAAATTGGTACCAGCAGAAACCAGG
GAAAGCCCCTAGGCTCCTGATCTATCTTGCTACCCGTTTGCAAAGTGGGGTCCCATCACGC
15 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTCATCAGTATGAGAGTCCACCTTTGACGTTTCGGCCAAGGGAC
CAAAGTGGAAATCAAACGG (SEQ ID NO: 1099)

BMS3h-193-2516

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGT
20 CACCATCACTTGCCGGGCAAGTCAGACGATTGAGCGTCGTTTAAATTGGTACCAGC
AGAAACCAGGGAAAGCCCCTAGGCTCCTGATCTATCTTTCGTCTGAAGTTGCAAAGT
GGGGTCCCATCACGCTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCAT
CAGCAGTCTGCAACCTGAAGATTTTGCTACGTACTACTGTCATCAGTATGAGAGTC
CACCTTTGACGTTTCGGCCAAGGGACCAAAGTGGAAATCAAACGG (SEQ ID NO:
25 1100)

BMS3h-198-1

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTTCAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATCCACCATTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGTGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGAGACGATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGCGAGAGATCCTTATAG
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1101)

BMS3h-198-2

GAGGTGCAGCCGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGTGCAGCCTCCGGATTACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGATCTCAGCTATTAGCGGTAGTGGTGGTAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGCGAGAGATCCTTATAG
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1102)

15 BMS3h-198-3

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTCGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCACCGGATCCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGCGAGAGATCCTTACAG
 TTATGACTACTGGGGTCAGGGAACCCTGGTCTCCGTCTCGAGC (SEQ ID NO: 1103)

BMS3h-198-4

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGACTCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCACC
 25 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACCGCAGTATATCACTGTGCGAGAGATCCTTATAG
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1104)
 BMS3h-198-5

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 GACTCTGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACCGCGGTATATCACTGTGCGAAAGAACCTTATAG
 10 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1105)
 BMS3h-198-6

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATCCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTCCCGAGGATAACCGCGGTATATTACTGTGTGAAAGATCCTTATAG
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1106)
 BMS3h-198-7

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC
 20 TCTCCTGTGCAGCCTCCGGATCCACCATTGCCGGGTATGAGATGTGGTGGGTCCGCCA
 GGCTCCGGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACA
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACA
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGATAACCGCGGTATATTACTGTGC
 GAGAGATCCTTATAGTTTTGACTACTGGGGTCAGGGAACCCCGGTACCGTCTCGAGC
 25 (SEQ ID NO: 1107)

BMS3h-198-8

GAGGTGCAGCTGATGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATCCACCTTTGCTGGGTATGAGATGTGGTGGTACCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGAAGTGGTAGAAGCACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACCGCGGTATATTACTGTGCGAAAGATCCTTATAG
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1108)

BMS3h-198-9

GAGGTGCAGCTGCTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGTGCAGCCTCCGGATTACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACGTACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACCGCAGTATATTACTGTGCGAAAGAACCTTATAG
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1109)

15 BMS3h-198-10

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATCCACCATTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGATAACCGCGGTATATTACTGTGCGAAAGATCCATATAG
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1110)

BMS3h-198-11

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCC
 25 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAGAGACCCTTATAG
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCTCCGTCTCGAGC (SEQ ID NO: 1111)
 BMS3h-198-12

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCATGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCCGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCG
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATCCTTATAG
 10 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTTTCGAGC (SEQ ID NO: 1112)
 BMS3h-198-13

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGTGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCACCCGCGACGATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAGCCTTATAG
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1113)
 BMS3h-198-14

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGT
 20 CTCTCCTGTGCAGCCTCCGGATTACCTTTGCTGGGTATGAGATGTGGTGGTTCCGC
 CAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGC
 ACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATACCAAG
 AACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTAC
 TGTGCGAAAGATCCTTATAGTTTTGACTACTGGCGTCAGGGAACCCTGGTCACCGTC
 25 TCGAGC (SEQ ID NO: 1114)

BMS3h-198-15

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATCCACCTTTGCTGGGTATGAGGTGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTGGAGCGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGCGAGAGATCCTTATAG
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1115)

BMS3h-198-16

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGTGCAGCCTCCGGATCCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGATCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGA
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGCGAAAGATCCTTATAG
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1116)

15 BMS3h-198-17

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGCGAGAGATCCTTATAG
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1117)

BMS3h-198-18

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGACTCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCGGGCTCC
 25 AGGGAAGGGTCTAGAGCGGGTCGCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAGAGATCCTTATAG
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1118)
 BMS3h-198-19

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGCTGGGTATGAGTTGTGGTGGGTCCGCCAGGCCCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGAAGTGGTGGTAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAGAGATCCTTATAG
 10 TTTTGACTACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1119)
 BMS3h-198-20

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCCCCGGATTACCTTAGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAACCTTATAG
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1120)
 BMS3h-198-21

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCG
 20 TCTCTCCTGTGCAGCCTCCGGACTCACCTTTGCTGGGTATGAGATGTGGTGGGTCC
 GTCGGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGTAGTGGTGGT
 AGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCACCTCCCGCGACGATTC
 CAAGAACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTAT
 ATTACTGTGCGAGAGATCCTTATAGTTTTGACTACTGGGGTCGGGGAACCCTGGTC
 25 ACCGTCTCGAGC (SEQ ID NO: 1121)

BMS3h-198-22

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCCGGGGGTCCCTGCGTCTCT
CCTGTGCCGCCTCCGGATTACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGTAGCGGTGGTAGCACATACTACGCA
5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGCGAAAGAACCTTATAG
TTATGACTACTGGGGTCATGGAACCCTGGTTACTGTCTCGAGC (SEQ ID NO: 1122)

BMS3h-198-23

GAGGTGCAGCCGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
10 CCTGTGCAGCCTCCGGATTACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGTAGTGGTGGTAACACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGATAACGGGGTATATTACTGTGCGAGAGATCCTTATAG
TTTTGACTACTGGGGTCAGGGTACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1123)

15 BMS3h-198-24

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
20 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGCGAAAGAACCTTATAG
TTTTGACTCCTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1124)

BMS3h-198-25

GAGGCGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTAACCTTCGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCC
25 AGGGAAGGGTCTAGAGCGCGTCTCAGCTATTAGTGGTAGTGGCGGTAGCACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAGAGATCCTTATAG
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1125)
 BMS3h-198-26

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATCCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAACCTTATAG
 10 TTTTGACCACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1126)
 BMS3h-198-27

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCGGGATCCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCAGGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAGAGATCCTTATAG
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1127)
 BMS3h-198-28

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCG
 20 TCTCTCCTGTGCAGCCTCCGGATTACCTTTGCTGGGTATGAGATGTGGTGGTTCC
 GCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGTAGTGGTGGT
 AGCACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTC
 CAAGAACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTAT
 ATTACTGTGCGAAAGATCCTTATAGTTTTGACAACCTGGGGTCAGGGAACCCTGGTC
 25 ACCGTCTCGAGC (SEQ ID NO: 1128)

BMS3h-198-29

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTAGAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGCGAAAGAACCTTATAG
 TTTTGACCACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1129)

BMS3h-198-30

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGTGCAGCCTCCGGATACACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGCGAAAGAACCTTATAG
 TTTTGACCACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1130)

15 BMS3h-198-31

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 GACTCTGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATCACTGTGCGAAAGAACCTTATAG
 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1131)

BMS3h-198-32

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGCTGGGTATGAGATGTGGTGGTTCCGCCAGGCTCC
 25 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATCCTTATAG
 TTTTGACAACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1132)
 BMS3h-198-33

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 GACTCTGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGAACCTTATAG
 10 TTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1133)
 BMS3h-198-34

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCAGGCTCC
 CGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGCGAAAGATCCTTATAG
 TTTTGACAACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1134)
 BMS3h-198-35

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC
 20 TCTCCTGTGCAGCCTCCGGATTCACCTTTGCTGGGTATGAGATGTGGTGGGTCCGCCA
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACA
 TACTACGCAGACTCTGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACA
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATCACTGTGC
 GAAAGAACCTTATAGTTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC
 25 (SEQ ID NO: 1135)

BMS3h-198-36

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGCTGGGTATGAGATGTGGTGGTTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCA
 5 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGCGAAAGATCCTTATAG
 TTTTGACAACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1136)

BMS3h-198-37

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 10 CCTGTGCAGCCTCCGGATTACCTTTGCTGGGTATGAGTTGTGGTGGGTCCGCCAGGCCCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGAAGTGGTGGTAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGCGAAAGATCCTTATAG
 TTTTGACTACCGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1137)

15 BMS3h-198-38

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTGCTGGGTATGAGTTGTGGTGGGTCCGCCAGGCCCC
 AGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAGTGGAAGTGGTGGTAGCACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC
 20 AAATGAACAGCCTGCGTGCCGAGGATAACGCGGTATATTACTGTGCGAGAGATCCTTATAG
 TTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ ID NO: 1138)

BMS3h-202-1

GAGGTGCAGCTGTTGGAGTCTGGGGGGGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCCGACTGCTGAGATGCTGTGGGTCCGCAAGGCTCC
 25 AGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCCGGCTAGTGGTGGTTCTACATACTACGCA

GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGGTGAG
 TTATGTGGCGACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ
 ID NO: 1139)

5 BMS3h-202-2

GAGGTGCAGCTGTTGGTGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCCGACTGCTGAGATGTTGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCCAGAGTGGGTCTCATCAATTTCCGGCTAGTGGTGGTTCTACATACTATGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 10 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGGTGAG
 TTATGTGGCGACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ
 ID NO: 1140)

BMS3h-202-3

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 15 CGTGTGCAGCCTCCGGATTACCTTTCCGACTGCCGAGATGGTGTGGGTCCGCAAGGCTCC
 AGGGATGGGTCTAGAGTGGGTCTCATCTATTTCCGGCTAGTGGTGGTTATACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACATGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGGTGAG
 TTATGTGGCGACGTTTGACTACTGGGGTCAGGGAGCCCTGGTCACCGTCACGAGC (SEQ
 20 ID NO: 1141)

BMS3h-202-4

GAGGTGCAGCTGTTGGTGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCCGACTGCTGAGATGGTGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCCGGCTAGTGGTGGTTCTACATACTACGCA
 25 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACGATTCCAAGAACACGCTGTATCTGC

AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGGTGAG
 TTATGTGGCGACGTTTGACTACTGGGGTCATGGAGCCCTGGTCACCGTCTCGAGC (SEQ
 ID NO: 1142)

BMS3h-202-5

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACATTTCCGACTGCTGAGATGTTGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCATCTATTTTCGGCTAGTGGTGGTTCTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGAGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGGTGAG
 10 TTATGTGGCAACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ
 ID NO: 1143)

BMS3h-202-6

GAGGCGCAGCTGTTGGAGTCTGGGGGTGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACCTTTCCGACTGCTGAGATGGTGTGGGTCCGCCAGGCTCC
 15 AGGGAAGGGTCTAGAGTGGATCTCATCTATTTTCGGCTAGTGGTGGTTCTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AATTGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGGTGAG
 TTATGTGGCGACGTTTGACTACTGGGGTCGGGGAACCCTGGTCACCGTCTCGAGC (SEQ
 ID NO: 1144)

20 BMS3h-202-7

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTCACATTTCCGACTGCTGAGATGTTGTGGGTCCGCCAGGCTCC
 AGGGAAGGGTCTAGAGTGGGTCTCATCTATTTTCGGCTAGTGGTGGTTCTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAGCACGCTGTATCTGC
 25 AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGGTGAG

TTATGTGGCGACGTTTGACTACTGGGGTCCAGGAGCCCTGGTCACCGTCTCGAGC (SEQ
ID NO: 1145)

BMS3h-202-8

GAGGTGCAGCTGTTGGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
5 CCTGTGCAGCCTCCGGATTCACCTTTCCGACTGCTGAGATGCTGTGGGTCCGCAAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCCGCTAGTGGTGGTTCTACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTTTCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCCAAAGAGCCGGTGAG
TTATGTGGCGACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ

10 ID NO: 1146)

BMS3h-202-9

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTCACATTTCCGACTGCTGAGATGTTGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCCGCTAGTGGTGGTTCTACATACTACGCA
15 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGGTGAG
TTATGTGGCGACGTTTGACTACTGGGGTCCAGGAGCCCTGGTCACCGTCTCGAGC (SEQ
ID NO: 1147)

BMS3h-202-10

20 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
CCTGTGCAGCCTCCGGATTCACCTTTCCGACTGCTGAGATGCTGTGGGTCCGCCAGGCTCC
AGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCCGCTAGTGGTGGTTCTACATACTACGCA
GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATTTGC
AAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAAGAGCCGGTGTA
25 TTATGTGGCGACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ

ID NO: 1148)

BMS3h-202-11

GAGGTGCAGCTGTTGGAGTCCGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCT
 CCTGTGCAGCCTCCGGATTACCTTTCCGACTGCTGAGATGCTGTGGGTCCGCAAGGCTCC
 5 AGGGAAGGGTCTAGAGTGGGTCTCATCTATTTCCGGCTAGTGGTGGTTCTACATACTACGCA
 GACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGC
 AAATGAACAGCCTGCGTGCCGAGGACGCCGCGGTATATTACTGTGCGAAAGAGCCGGTGAG
 TTATGTGGCGACGTTTGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGC (SEQ
 ID NO: 1149)

10 BMS3h-217-1

AACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
 TCACTTGCCGGGCAAGTCATTTTATTGGTACTCTGTTAACTTGGTACCAGCATAAACCAGG
 GAAAGCCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 15 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTTCCGGCCAAGGGAC
 CAAGGTGGAAATCAAACGG (SEQ ID NO: 1150)

BMS3h-217-2

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
 TCACTTGCCGGGCAAGTCATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACCACG
 20 GAAAGCCCCCTAAACTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCATCCTGAAG
 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTCCGACGTTCCGGTCAAGGGAC
 CAAGGTGGAAATCAAACGG (SEQ ID NO: 1151)

BMS3h-217-3

25 GACATCCAGATGACCCAGTCTCCGTCCTCCCTGACTGCATCTGTAGGAGACCGTGTACCA

TCACTTGCCGGGCAAGTCATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACCAGG
 GAAAGCCCCTAAGCTCCTGGTCACTTATGGTTCCTTGTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTCCTACGTTTCGGCCAAGGGAC
 5 CAAGGTGGAAAACATACGG (SEQ ID NO: 1152)

BMS3h-217-4

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
 TCACTTGCCGGGCAAGTCATTTTATTGCTACTCTGTTATCTTGGTACCAGCAGAAACCAGG
 GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTGCAAAGTGGGGTCCCATCACGT
 10 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTCCGACGTTTCGGCCAAGGGAC
 CAAGGTGGAAATCAAACGG (SEQ ID NO: 1153)

BMS3h-217-5

GACATCCAGATGACCCAGTCTCCATCCTTCCTGTCTGCATCTGTAGGAGACCGTGTACCA
 15 TCACTTGCCGGGCAAGTCATTTTATTGCTACTCTGTTATCTTGGTACCAGCAGAAACCAGG
 GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTCCGACGTTTCGGCCAAGGGAC
 CAAGGTGGAAATCAAACGG (SEQ ID NO: 1154)

20 BMS3h-217-6

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
 TCACTTGCCGGGCAAGTCATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACCAGG
 GAAAGCCACTAAGCTCCTGATCACTTATGGTTCCTTGTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 25 ACTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCCCCGACGTTTCGGCCAGGGGAC

CAAGGTGGAAATCAAACGT (SEQ ID NO: 1155)

BMS3h-217-7

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
TCACTTGCCGGGCAAGTCATTTTATTGGTTCTCTGTTATCTTGGTACCAGCATAAACCAGG
5 GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTTTCGGCCAAGGGAC
CAAGGTGGAAATCAAACGG (SEQ ID NO: 1156)

BMS3h-217-8

10 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
TCACTTGCCGGGCAAGTCATTTTATTGGTACTCTGTTATCTTGGTACCAGCATAAACCAGG
GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTTTCGGCCAAGGGAC
15 CAAGGTGGAAATCAAACGG (SEQ ID NO: 1157)

BMS3h-217-9

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
TCACTTGCCGGGCAAGTCATTTTATTGGTACTCTGTTATCTTGGTACCAGCATAAACCAGG
GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCATGTTGCAAAGTGGGGTCCCATCACGT
20 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCAACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTTTCGGCCAAGGGAC
CAAGGTGGAAATCAAACGG (SEQ ID NO: 1158)

BMS3h-217-10

GACATCCAGATGACTCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGAGTCACCA
25 TCACTTGCCGGGCAAGTCATTTTATTGGTACTCTGTTATCCTGGTACCAGCATAAACCAGG

GAAAGCCCCTAAGCTCCTGATCACCTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGAATTCCTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTGGTCAGGGAGTGCTGTGGCCTGCGACGTTTCGGCCAAGGGAC
 CAAGGTGGAAATCAAACGG (SEQ ID NO: 1159)

5 BMS3h-217-11

GACATCCAGATGACCCAGTCTCCATCCTCCCTGACTGCATCTGTAGGAGACCGTGTCACCA
 TCACTTGCCGGGCAAGTCATTTTATTGGTACTCTGTTATCTTGGTACCAGCATAAACCAGG
 GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGAATTCCTCTCACCATCAGCAGTCTGCAACCTGAAG
 10 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTTTCGGCCAAGGGAC
 CAAGGTGGAAATCAAACGG (SEQ ID NO: 1160)

BMS3h-217-12

AACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCA
 TCACTTGCCGGGCAAGTCATTTTATTGGTACTCTGTTATCTTGGTACCAGCATAAACCAGG
 15 GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTTTCGGCCAAGGGAC
 CAAGGTGGAAATCAAACGG (SEQ ID NO: 1161)

BMS3h-217-13

20 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCA
 TCAATTGCCGGGCAAGTCATTTTATTGGTACTCTGTTATCTTGGTACCAGCATAAACCAGG
 GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTTTCGGCCAAGGGAC
 25 CAAGGTGGAAATCAAACGG (SEQ ID NO: 1162)

BMS3h-217-14

GACATCCAGTTGACCCAGTCACCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
 TCACTTGCCGGGCAAGTCATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACCAGG
 GAAAGCCACTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT
 5 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTCCGACGTTTCGGCCAAGGGAC
 CAAGGTGGAAATCAAACGG (SEQ ID NO: 1163)

BMS3h-217-15

GACATCCAGATGACACAGTCTCCATCCTCCCTGTATGCATCTGTAGGAGACCGTGTACCA
 10 TCACTTGCCGGGTAAGTCATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACCAGG
 GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCAGCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCCCCGACGTTTCGGACAAGGGAC
 CAAGGTGGAAATCAAACAG (SEQ ID NO: 1164)

15 BMS3h-217-16

GACATTCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
 TCACTTGCCGGGCAAGTCATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACCAAG
 GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 20 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTCCGACGTTTCGGCCAAGGGAC
 CAAGGTGGAAATCAAACGG (SEQ ID NO: 1165)

BMS3h-217-17

GACATCCAGATTATCCAGTCTCCATCCTCCCTTTCTGCATCTGTAGGAGACCGTGTACCA
 TCACTTGCCGGGCAAGTCATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACCAGG
 25 GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT

TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTCCGACGTTCGGCCAAGGGAC
 CAAGGTGGAAATCAAACGG (SEQ ID NO: 1166)

BMS3h-217-18

5 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
 TCACTTGCCGGGCAAGTCATTTTATTGGTACTCTGTTATCTTGGTACCAGCTGAAACCAGG
 GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTTCGGCCAAGGGAC
 10 CAAGGTGGAAATCAAACGG (SEQ ID NO: 1167)

BMS3h-217-19

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCG
 GGCAAGTCATTTTATTGGTACTCTGTTATCTTGGTACCAGCTGAAACCAGGGAAAGCCCCAAAGCTCCTGA
 TCACTTATGGTTCCTGGTTGCAAAGTGGGGTCCCATCACGTTCAGTGGCAGTGGATCTGGGACAGATTTTC
 15 ACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCC
 TCGCAGGTTTCGGCCAAGGGACCAAGGTAGAAAACAAACGG (SEQ ID NO: 1168)

BMS3h-217-20

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
 TCACTTGCCGGGCAAGTCATTTTATTGGTACTCTGTTATCTTGGTACCAGCTTAAACCAGG
 20 GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAACGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTTTCGGCCAAGGGAC
 CAAGGTGGAAATCAAACGG (SEQ ID NO: 1169)

BMS3h-217-21

25 GACATCCAGATGACCCAGGCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA

TCACTTGCCGGGCAAGTCATTTTATTGGTACTCTGTTATCTTGGTACCAGCTGAAACCAGG
 GAAAGCCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTCAGAGTGGGGTCCCATCACGT
 TTCAGTGGTAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTTTCGGCCAAGGGAC

5 CAAGGTTGAAAACAAACGG (SEQ ID NO: 1170)

BMS3h-217-22

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
 TCACTTGCCGGGCAAGTCATTTTATTGGTTCCTGTTATCTTGGTACCAGCAGAAACCAGG
 GAAAGCCCCAAAGCTCCTGATCACTTATGGTTCCTTGTTCGAAAGTGGGGTCCCATCACGT
 10 TTCAGTGGCAGTGGATCTGGGACAGATTTGCTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTTTCGGCCAAGGGAC

CAAGGTGGAATCAAACGG (SEQ ID NO: 1171)

BMS3h-217-23

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
 15 TCACTTGCCGGGCAAGTCATTTTATTGGTAGTCTGTTATCTTGGTACCAGGTGAAACCAGG
 GAAAGCCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTCGAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTTTCGGCCAAGGGAC

AACGGTGGAATCAAACGG (SEQ ID NO: 1172)

20 BMS3h-217-24

GACATCCTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
 TCACTTGCCGGGCAAGTCATTTTATTGGTAGTCTGTTATCTTGGTACCAGCAGAAACCAGG
 GAAAGCCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTCGAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 25 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTTTCGGCCAAGGGAC

CAAGGTGGAAATCAAACGG (SEQ ID NO: 1173)

BMS3h-217-25

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCA

TCACTTGCCGGGCAAGTCATTTTATTGGTACTCTGGTATCTTGGTACCAGCAGAAACCGGG

5 GAAAGCCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT

TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG

ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTACGGCCAAGGGAC

CAAGGTGGAAATCAAACGG (SEQ ID NO: 1174)

BMS3h-217-26

10 GACATCCAGATGACCCAGTCTCCATCCTCTCTGTCTGCATCTGTAGGAGACCGTGTCACCA

TCACTTGCCGGGCAAGTCATTTTATTGGTACTCTGGTATCTTGGTACCAGCAGAAACCAGG

GAAAGCCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT

TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG

ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACTTTCGGCCAAGGGAC

15 CAAGGTGGAAAACAAACGG (SEQ ID NO: 1175)

BMS3h-217-27

GACATCAAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCA

TCACTTGCCGGGCGAGTCATTTTATTGGTACTCTGGTATCTTGGTACCAGCAGAAACCAGG

GAAAGCCCCAAAGCTCCTGATCACTTATGGTTCATGTTGCAAAGTGGGGTCCCATCACGT

20 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG

ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTTTCGGCCAAGGGAC

CAAGGTGGAAATCAAACGG (SEQ ID NO: 1176)

BMS3h-217-28

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCA

25 TCACTTGCCAGGCAAGTCATTTTATTGGTACTCTGGTATCCTGGTACCAGCAGAAACCAGG

GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCCGCGACGTTTCGGCCAAGGGAC
CAAGGTGGAAATCAAACGG (SEQ ID NO: 1177)

5 BMS3h-217-29

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCA
TCACTTGCCGGGCAAGTCATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACCAGG
GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTGGTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
10 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTTTCGGCCAAGGGAC
CAAGGTGGAAATCAAACGG (SEQ ID NO: 1178)

BMS3h-217-30

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTTGGAGACCGTGTCACCA
TCACTTGCCGGGCAAGTCATTTTATTGGTACTCTGTTATCTTGGTACCAGCTGAAACCAGG
15 GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTGGTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTTTCGGCCAAGGGAC
CAAGGTGGAAATCAAACGG (SEQ ID NO: 1179)

BMS3h-217-31

20 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCA
TCACTTGCCGGGCAAGTCATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACCGGG
GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATTTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTGGTCAGGAGGTGCTGTGGCCTGCGACGTTTCGGCCAAGGGAC
25 TAAGGTGGAAATCAAACGG (SEQ ID NO: 1180)

BMS3h-217-32

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCTCCA
TCACTTGCCGAGCAAGTCATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACCAGG
GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT
5 TTCAGTGGCAGTGGATTTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATCTTGCTACGTACTACTGTGGTCAGGAGGTGCTGTGGCCTGCGACGTTTCGGCCAAGGGAC
CAAGGTGGAAATCAAACGG (SEQ ID NO: 1181)

BMS3h-217-33

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
10 TCACTTGCCAGGCAAGTCATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACCAGG
GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATTTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCCGAAG
ATTTTGCTACGTACTACTGTGGTCAGGAGGTGCTGTGGCCTGCGACGTTTCGGCCAAGGGAC
CAAGGTGGAAATCAAACGG (SEQ ID NO: 1182)

15 BMS3h-217-34

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCAGTAGGAGACCGTGTACCA
TCACTTGCCGGGCAAGTCATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACCTGG
GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATTTGGGACAGAATTCCTCTCACCATCGGCAGTCTGCAACCTGAAG
20 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCCTGCGACGTTTCGGCCAAGGGAC
CAAGGTGGAAATCAAACGG (SEQ ID NO: 1183)

BMS3h-217-35

GACATCCAGATGACCCAGTCACCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
TCACTTGCCGGGCAAGTCATTTTATTGGTACTCTGTTATCTTGGTACCAGCAGAAACCAGG
25 GAAAGCCACTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT

TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTCCGACGTTCGGCCAAGGGAC
CAAGGTGGAAATCAAACGG (SEQ ID NO: 1184)

BMS3h-217-2301

5 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
TCACTTGCCGGGCAAGTCACTTCATTGCCAGTCTGTTATCTTGGTACCAGGTGAAACCAGG
GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTTCGGCCAAGGGAC
10 AACGGTGGAAATCAAACGG (SEQ ID NO: 1185)

BMS3h-217-2302

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
TCACTTGCCGGGCAAGTCATTTTCATTGCCAGCTGTTATCTTGGTACCAGGTGAAACCAGG
GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT
15 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTTCGGCCAAGGGAC
AACGGTGGAAATCAAACGG (SEQ ID NO: 1186)

BMS3h-217-2303

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCG
20 TGTACCATCACTTGCCGGGCAAGTCATTTTCATTGCCAGCTGTTATCTTGGT
ACCAGGTGAAACCAGGGAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTG
TTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTT
CACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTTGCTACGTACTACTGTG
GTCAGGGGGTGCTGTGGCCTGCGACGTTCGGCCAAGGGACAACGGTGGAAATC
25 AGACGG (SEQ ID NO: 1187)

BMS3h-217-2304

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCA
TCACTTGCCGGGCAAGTCATTACATTGCCTCCCTGTTATCTTGGTACCAGGTGAAACCAGG
GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTGTCAGAGTGGGGCCCCATCACGT
5 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCCTGCGACGTTTCGGCCAAGGGAC
AACGGTGGAAATCAAACGG (SEQ ID NO: 1188)

BMS3h-217-2305

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCA
10 TCACTTGCCGGGCAAGTCATTTTATTGGTAGTCTGTTATCTTGGTACCAGGTGAAACCAGG
GAAAGCCCCTAAGCTCCTGATCACTTGGGCCTCCTACTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCCTGCGACGTTTCGGCCAAGGGAC
AACGGTGGAAATCAAACGG (SEQ ID NO: 1189)

15 BMS3h-217-2306

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCA
TCACTTGCCGGGCAAGTCATTTTATTGGTAGTCTGTTATCTTGGTACCAGGTGAAACCAGG
GAAAGCCCCTAAGCTCCTGATCACTTGGACGTCCTACTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
20 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCCTGCGACGTTTCGGCCAAGGGAC
AACGGTGGAAATCAAACGG (SEQ ID NO: 1190)

BMS3h-217-2307

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCA
TCACTTGCCGGGCAAGTCATTTTATTGGTAGTCTGTTATCTTGGTACCAGGTGAAACCAGG
25 GAAAGCCCCTAAGCTCCTGATCACTTGGTCGTCCTACTTGCAAAGTGGGGTCCCATCACGT

TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTTCGGCCAAGGGAC
 AACGGTGGAAATCAAACGG (SEQ ID NO: 1191)

BMS3h-217-2308

5 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
 TCACTTGCCGGGCAAGTCATTTTATTGGTAGTCTGTTATCTTGGTACCAGGTGAAACCAGG
 GAAAGCCCCTAAGCTCCTGATCACTTGGGGTCCTGGTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTTCGGCCAAGGGAC
 10 AACGGTGGAAATCAAACGG (SEQ ID NO: 1192)

BMS3h-217-2309

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
 TCACTTGCCGGGCAAGTCATTTTATTGGTAGTCTGTTATCTTGGTACCAGGTGAAACCAGG
 GAAAGCCCCTAAGCTCCTGATCACTTGGGCGTCCTGGTTGCAAAGTGGGGTCCCATCACGT
 15 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTTCGGCCAAGGGAC
 AACGGTGGAAATCAAACGG (SEQ ID NO: 1193)

BMS3h-217-2310

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCG
 20 TGTACCATCACTTGCCGGGCAAGTCATTTTATTGGTAGTCTGTTATCTTGGT
 ACCAGGTGAAACCAGGGAAAGCCCCTAAGCTCCTGATCACTTGGAGCTCCTGG
 TTGCAAAGTGGGGTCCCATCACGTTCAGTGGCAGTGGATCTGGGACAGATTT
 CACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTTGCTACGTACTACTGTG
 GTCAGGGGGTGCTGTGGCCTGCGACGTTCGGCCAAGGGACAACGGTGGAAATC
 25 AAACGG (SEQ ID NO: 1194)

BMS3h-217-2311

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
TCACTTGCCGGGCAAGTCATTGGATTGCCAGCTGTTATCTTGGTACCAGGTGAAACCAGG
GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT
5 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCCTGCGACGTTTCGGCCAAGGGAC
AACGGTGGAAATCAAACGG (SEQ ID NO: 1195)

BMS3h-217-2312

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
10 TCACTTGCCGGGCAAGTCATTTTATTGGTTCGCTCTTACGCTGGTACCAGGTGAAACCAGG
GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCCTGCGACGTTTCGGCCAAGGGAC
AACGGTGGAAATCAAACGG (SEQ ID NO: 1196)

15 BMS3h-217-2313

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
TCACTTGCCGGGCAAGTCATCGGATTGCCAGCTGTTATCTTGGTACCAGGTGAAACCAGG
GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
20 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCCTGCGACGTTTCGGCCAAGGGAC
AACGGTGGAAATCAAACGG (SEQ ID NO: 1197)

BMS3h-217-2314

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
TCACTTGCCGGGCAAGTCATTACATTGCCTCCCTGTTATCTTGGTACCAGGTGAAACCAGG
25 GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT

TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTTCGGCCAAGGGAC
AACGGTGGAAATCAAACGG (SEQ ID NO: 1198)

BMS3h-217-2315

5 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
TCACTTGCCGGGCAAGTCATTTTATTGGTAGTCTGTTATCTTGGTACCAGGTGAAACCAGG
GAAAGCCCCTAAGCTCCTGATCCGGTTCGGCTCCTTGTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTTCGGCCAAGGGAC
10 AACGGTGGAAATCAAACGG (SEQ ID NO: 1199)

BMS3h-217-2316

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
TCACTTGCCGGGCAAGTCATTTTATTGGTAGTCTGTTATCTTGGTACCAGGTGAAACCAGG
GAAAGCCCCTAAGCTCCTGATCACTTACAAGTCCTACTTGCAAAGTGGGGTCCCATCACGT
15 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTTCGGCCAAGGGAC
AACGGTGGAAATCAAACGG (SEQ ID NO: 1200)

BMS3h-217-2317

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCG
20 TGTACCATCACTTGCCGGGCAAGTCATTTTATTGGTAGTCTGTTATCTTGGT
ACCAGGTGAAACCAGGGAAAGCCCCTAAGCTCCTGATCACTTGGGGCTCCTAC
TTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGACAGATTT
CACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTTGCTACGTACTACTGTG
GTCAGGGGGTGCTGTGGCCTGCGACGTTCGGCCAAGGGACAACGGTGGAAATC
25 AAACGG (SEQ ID NO: 1201)

BMS3h-217-2318

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
TCACTTGCCGGGCAAGTCATTTTATTTGGGGGCCCTTATCTTGGTACCAGGTGAAACCAGG
GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT
5 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTCTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCCTGCGACGTTTCGGCCAAGGGAC
AACGGTGGAAATCAAACGG (SEQ ID NO: 1202)

BMS3h-217-2319

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
10 TCACTTGCCGGGCAAGTCATTGGATTGCCACCCTGTTATCTTGGTACCAGGTGAAACCAGG
GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
ATTTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCCTGCGACGTTTCGGCCAAGGGAC
AACGGTGGAAATCAAACGG (SEQ ID NO: 1203)

15 BMS3h-217-2320

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
TCACTTGCCGGGCAAGTCATTTTATTTGGGGGCCCTTATCTTGGTACCAGGTGAAACCAGG
GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
20 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGTGTGGCCTGCGACGTTTCGGCCAAGGGAC
AACGGTGGAAATCAAACGG (SEQ ID NO: 1204)

BMS3h-217-2321

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
TCACTTGCCGGGCAAGTCATTTTATTGGTAGCCTCTTAAACTGGTACCAGGTGAAACCAGG
25 GAAAGCCCCTAAGCTCCTGATCACTTATGGTTCCTTGTTGCAAAGTGGGGTCCCATCACGT

TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTTCGGCCAAGGGAC
 AACGGTGGAAATCAAACGG (SEQ ID NO: 1205)

BMS3h-217-2322

5 GGCATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCA
 TCACTTGCCGGGCAAGTCATTTTATTGGTAGTCTGTTATCTTGGTACCAGGTGAAACCAGG
 GAAAGCCCCTAAGCTCCTGATCACTTACGGGTCCTGGTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG
 ATTTTGCTACGTACTACTGTGGTCAGGGGGTGCTGTGGCCTGCGACGTTCGGCCAAGGGAC
 10 AACGGTGGAAATCAAACGG (SEQ ID NO: 1206)

Ejemplo 1

Generación de Dominios Variables Humanos Anti-CD40

BMS3h-1 a BMS3h-225

El siguiente Ejemplo describe la generación de una
 15 serie de dominios variables anti-CD40 humano, designados
 BMS3h-1 a BMS3h-225. Después de la expresión recombinante de
 un repertorio de dominios variables de inmunoglobulina
 simples sobre la superficie del fago, la selección es llevada
 a cabo al poner en contacto el repertorio de fagos con el
 20 antígeno objetivo inmovilizado, lavando para remover el fago
 no enlazado, y propagando el fago enlazado. Este proceso
 denominado frecuentemente como "visualización panorámica."
 Es aplicable a la selección de los dominios variables de
 inmunoglobulina simple, así como otros fragmentos de
 25 anticuerpo que pueden ser expresados sobre una biblioteca de

visualización, por ejemplo scFv, Fab, y Fab'. Alternativamente, el fago puede ser preseleccionado para la expresión de variantes de miembros apropiadamente plegados, mediante visualización panorámica contra un ligando genérico inmovilizado (por ejemplo, la proteína A o la proteína L) que es únicamente enlazado por miembros plegados. Esto tiene la ventaja de reducir la proporción de miembros no funcionales, con lo cual se incrementa la proporción de miembros que probablemente se enlazan a un antígeno objetivo. La preselección con ligandos genéricos es enseñada en WO 99/20749, por ejemplo. La selección de las bibliotecas de anticuerpos fagos es descrita en general, por ejemplo, por Harrison et al., *Meth. Enzymol.* 267: 83-109 (1996).

La selección es comúnmente llevada a cabo utilizando el antígeno purificado inmovilizado sobre un soporte sólido, por ejemplo, tubos o pozos de plástico, o sobre una matriz de cromatografía, por ejemplo Sepharose^{MR} (Pharmacia). La selección o la clasificación puede ser realizada sobre antígenos complejos, tales como la superficie de las células (Marks et al., *BioTechnology* 11: 1145 (1993); de Kruif et al., *Proc. Natl. Acad. Sci. USA* 92: 3938 (1995)). Otra alternativa más involucra la selección por el enlace al antígeno biotinilado en solución, seguido por la captura sobre esferas recubiertas con estreptavidina.

Clones BMS3h-1 al BMS3h-69:

Se llevaron a cabo tres rondas de selecciones utilizando concentraciones cada vez menores del antígeno (100 nM en la ronda 1; 10 nM en la ronda 2; 1 nM en la ronda 3) en paralelo contra el monómero de CD40 humano biotinilado (suministrado por BMS, 1.5 moles de biotina/mol de CD40) y el CD40-Ig humano biotinilado (suministrado por BMS, 3.3 moles de biotina/mol de CD40-Ig). Los fagos provenientes de las bibliotecas de dAb intactas Domantis 4G y 6G fueron combinados como sigue antes de iniciar las selecciones:

- 1) 4G + 6G VH CDR3 longitudes entre 7 - 9 aminoácidos.
- 2) 4G + 6G VH CDR3 longitudes entre 10 - 12 aminoácidos.
- 3) 4G + 6G VH CDR3 longitudes entre 13 - 15 aminoácidos.
- 4) 4G VK
- 5) 6G VK

Cada ronda de selección involucró la adición de la concentración deseada del antígeno a una mezcla de 750 µl del fago proveniente de uno de los combinados de la biblioteca intacta o el fago de salida de producción de selección subsecuente y 750 µl de PBS+2% de Marvel (Solución Salina Amortiguada con Fosfato que contiene 2% (p/v) de Marvel [Premier Foods, Reino Unido]) e incubando a temperatura ambiente por 1 hora al mezclar extremo sobre extremo. El complejo de fago de antígeno biotinilado fue luego capturado por la adición de 100 µl de Estreptavidina Dynabeads® M-280

resuspendida [Invitrogen, Reino Unido] e incubada por 5 minutos con mezclado extremo sobre extremo a temperatura ambiente. Las Dynabeads® fueron luego recuperadas utilizando un separador magnético KingFisher [Thermo Fisher Scientific, Reino Unido] y lavadas 7 x 1 ml de PBS + 0.1% de Tween 20 (PBS que contiene 0.1% (v/v) de monolaurato de polioxietilensorbitán [Sigma-Aldrich, Reino Unido], PBST) seguido por 1 x 1 ml PBS. El fago enlazado retenido sobre las Dynabeads® lavadas fue luego eluido por incubación con 500 µl de tripsina-PBS (50 µl de tripsina a 10 mg/ml [Sigma-Aldrich, Reino Unido] disuelto en Tris-HCl 50 mM de pH 7.4, CaCl₂ 1 mM agregado a 450 µl de PBS). La solución que contiene el fago fue recuperada y se utilizaron 250 µl para infectar 1.75 ml de *E. coli* en fase de crecimiento logarítmico TG1 (a una OD₆₀₀ de 0.4) por 30 minutos a 37°C. El cultivo infectado con el fago de TG1 de *E. coli* fue centrifugado a 11,600 g en una microcentrífuga por 1 minuto. La pella celular resultante fue resuspendida en 1 ml de 2xTY (16 g Triptona, 10 g de extracto de levadura, y 5 g cloruro de sodio en 1 litro, se calentó en autoclave por 15 minutos a 121°C) y se sembró en placa sobre una caja de Petri de 9 cm que contenía TY suplementado con 15 µg/ml de tetraciclina. Las placas fueron incubadas toda la noche a 37°C. Luego se agregaron 2 ml de 2xTY suplementado con 15% de glicerol a cada placa, y las células fueron soltadas con un dispersor de

vidrio y mezcladas perfectamente. 50 ml de las bacterias raspadas fueron utilizados para inocular 50 ml de 2xTY suplementado con 15 µg/ml de tetraciclina y se desarrollaron toda la noche a 37°C con agitación a 250 rpm. El cultivo de
5 toda la noche fue centrifugado a 3,300 g por 15 minutos para concentrar las bacterias. Para precipitar el fago, 10 ml PEG/NaCl (20% de polietilenglicol 8000, NaCl 2.5 M) fueron agregados a 40 ml del sobrenadante. La solución de fago/PEG fue mezclada y dejada sobre hielo por 1 hora, luego
10 centrifugada a 3,300 g por 30 minutos a 4°C, y el sobrenadante se desechó. La pella fue resuspendida en 2 ml de PBS a 11,600 g por 10 minutos en una microcentrífuga para eliminar los desechos bacterianos remanentes. El sobrenadante resultante que contenía el fago fue luego
15 utilizado para la siguiente ronda de selección contra el antígeno CD40 biotinilado, apropiado.

Los ELISAs de fago monoclonal fueron llevados a cabo después las rondas de selección 2 y 3. Todos los lavados fueron realizados utilizando 3 lavados de 250 µl de
20 PBST seguido por tres lavados de 250 µl de PBS. Las placas fueron recubiertas toda la noche a 4°C con 50 µl/pozo de 1 µg/ml de NeutrAvidina (Thermo Scientific, Reino Unido) en amortiguador de carbonato-bicarbonato 0.2 M, pH 9.4. Las placas fueron lavadas y luego bloqueadas con 2% de MPBS (2%
25 p/v de leche en polvo descremada Marvel [Premier Foods] en

PBS) por 1 hora a temperatura ambiente. Las placas fueron luego lavadas e incubadas con 50 μ l/pozo del 0.7 μ g/ml de CD40 humano biotinilado en 2% de MPBS. Las placas fueron lavadas, y los sobrenadantes del fago fueron agregados a un volumen igual de 2% de MPBS. Las placas fueron luego incubadas por 1 hora a temperatura ambiente. Las placas fueron lavadas y el fago enlazado detectado con el conjugado anti-M13-HRP (GE Healthcare, Reino Unido) diluido 1:5000 en 2% de MPBS e incubado por 1 hora a temperatura ambiente. Las placas fueron lavadas y el ELISA fue desarrollado utilizando la solución de peroxidasa SureBlue 1-Component TMB MicroWell (KPL Inc, Estados Unidos). Los fagos específicos fueron identificados por comparación a las placas recubiertas con NeutrAvidin pero sin el CD40 biotinilado. Se utilizó un MidiPrep para aislar los V-genes de dAb a partir de los resultados de la ronda 2 y la ronda 3 de pDOM4 (Domantis) y clonados dentro de pDOM5 (Domantis). pDOM4, descrito en WO 2007/085815, es un derivado del vector de fago Fd en el cual la secuencia peptídica de señal del gen III es reemplazada con el péptido de señal de proteína superficial anclada al glucolípido de levadura (GAS por sus siglas en Inglés) (WO 2005/093074). pDOM4 también contiene una etiqueta c-myc entre la secuencia guía y el gen III, lo cual coloca al gen III nuevamente en la estructura.

Los dAbs de enlace fueron identificados como sigue.

Noventa y seis colonias individuales (en pDOM5) fueron recogidas de cada producción en 200 µL de caldo Terrific que contenía el medio de autoinducción OnEx (Novagen, Reino Unido) toda la noche a 37° C con agitación a 250 rpm en

5 Placas de Cultivo de Células de 96 pozos Costar (Corning Incorporated, Estados Unidos). Los cultivos fueron centrifugados hasta obtener una pelotilla de las células, y los sobrenadantes fueron evaluados mediante ELISA de enlace al antígeno para los dAbs que se enlazan a CD40. Las

10 inmunoplasmas de 96 pozos MaxiSorp (Nunc, Estados Unidos) fueron recubiertas toda la noche a 4°C con 50 µl/pozo de 1 µg/ml de NeutrAvidin en amortiguador carbonato-bicarbonato 0.2 M, pH 9.4. Todos los lavados fueron como se describe para el ELISA de fago. Las placas fueron bloqueadas por 1

15 hora a temperatura ambiente con 200 µl de PBS que contenía 1% de Tween 20. La placa fue luego lavada e incubada con 50 µl/pozo de CD40 biotinilada a 0.7 µg/ml en 0.1% de PBST. El sobrenadante de cultivo que contenía el dAb clarificado, fue agregado a la placa de ELISA con un volumen igual de 0.1% de

20 PBST. Las placas fueron incubadas por 1 hora a temperatura ambiente y luego lavadas. El dAb fue detectado utilizando un proceso de dos pasos: primeramente 9E10 (IgG anti-myc, Sigma-Aldrich, Reino Unido) diluido 1:2000 en 0.1 % de PBST fue agregado por 1 hora a temperatura ambiente y luego lavado,

25 seguido por el Fc-HRP anti-ratón (Sigma-Aldrich, Reino Unido)

diluido 1:2000 en 0.1% de PBST por 1 hora a temperatura ambiente. Las placas fueron lavadas, y el ELISA fue desarrollado utilizando la solución de peroxidasa SureBlue 1-Component TMB MicroWell (KPL Inc, Estados Unidos). Se dejó
5 desarrollar el color, y la reacción colorimétrica fue detenida por la adición de un volumen igual de HCl 1 M. La placa de ELISA fue leída a 450 nm. Los fagos específicos fueron identificados por comparación a las placas recubiertas con NeutrAvidin pero sin el CD40 biotinilado.

10 Los clones específicos para CD40 fueron probados ya sea en el ensayo de enlace al receptor basado en esferas o en ELISA (RBA) para evaluar la inhibición del enlace al ligando de CD40. Los anticuerpos de dominio que mostraron inhibición en el RBA fueron probados en el ensayo de proliferación de
15 células B y luego en una variedad de otros ensayos celulares *in vitro*. Estos ensayos son descritos con mayor detalle más adelante.

BMS3h-106 a -225:

Los BMS3h-106 a -225 fueron aislados a partir de
20 las selecciones contra CD40 biotinilado o CD40-Fc biotinilado, como se describe para BMS3h-1 a BMS3h-69, pero con las siguientes modificaciones. El fago proveniente de las bibliotecas 4G y 6G intactas, fue combinado como sigue antes de iniciar las selecciones:

25 6) 4G VH CDR3 longitudes entre 7 - 9 aminoácidos.

- 7) 4G VH CDR3 longitudes entre 10 - 12 aminoácidos.
- 8) 4G VH CDR3 longitudes entre 13 - 15 aminoácidos.
- 9) 6G VH CDR3 longitudes entre 7 - 9 aminoácidos.
- 10) 6G VH CDR3 longitudes entre 10 - 12 aminoácidos.
- 5 11) 6G VH CDR3 longitudes entre 13 - 15 aminoácidos.
- 12) 4G VK
- 13) 6G VK

La ronda uno fue utilizada a una concentración de antígeno de 160 nM para CD40-Fc y de 100 nM para CD40. Los
 10 títulos producidos estuvieron en el intervalo de 2.0×10^4 a 9.0×10^7 TU/ml (título viral funcional).

Para la ronda dos, los fagos enriquecidos de la ronda uno fueron combinados en pares antes de utilizarse en las selecciones:

- 15 1) 4G + 6G VH CDR3 longitudes entre 7 - 9 aminoácidos (combinados 1 + 4 de la ronda 1).
- 2) 4G + 6G VH CDR3 longitudes entre 10 - 12 aminoácidos (combinados 2 + 5 de la ronda 1).
- 3) 4G + 6G VH CDR3 longitudes entre 13 - 15 aminoácidos
- 20 (combinados 3+6 de la ronda 1).
- 4) 4G + 6G VK (combinados 7+8 de la ronda 1)

Las selecciones fueron realizadas a una concentración de antígeno de 100 nM, y los complejos antígeno-fago fueron capturados utilizando las Dynabeads®
 25 activadas con M-280 tosil (Invitrogen) que habían sido

acopladas con NeutrAvidin (Thermo Fisher Scientific, Reino Unido). Los títulos producidos estuvieron en el intervalo de 6.5×10^7 a 7.5×10^8 TU/ml.

La ronda tres fue realizada a una concentración de
5 antígeno de 20 nM, en el caso de las selecciones de CD40-Fc, en presencia de la cola Fc humana libre 6.7 μ M (BMS por sus siglas en Inglés). Los títulos producidos estuvieron en el intervalo de 4.3×10^7 a 1.6×10^9 TU/ml.

La ronda cuatro fue realizada como se describe para
10 la ronda dos, pero a una concentración de antígeno de 2 nM y en presencia y ausencia de un exceso de 500 veces de CD40-Fc no marcado. La adición de este competidor fue realizada después del periodo inicial de incubación de una hora del fago con el antígeno biotinilado, y la mezcla fue luego
15 incubada toda la noche, como se describe anteriormente. Este paso de competencia fue incluido con el objetivo de mejorar la selección de los dAbs con una velocidad de apagado más lenta. Los títulos producidos estuvieron en el intervalo de 1.8×10^7 a 4.4×10^7 sin competencia y 1.8×10^6 a 2.3×10^7 TU/ml
20 con competencia.

Para monitorizar el progreso de las selecciones, fueron llevados a cabo ELISAs de fago monoclonal después de las rondas 2 y 3. Éstos fueron realizadas como se describe para BMS3h-1 a BMS3h-69. Los dAbs de enlace fueron
25 identificados como se describe para BMS3h-1 a BMS3h-69

excepto que, en el caso de la selección de la biblioteca VK, la proteína L fue incluida a una concentración final de 0.8 µg/ml. La adición de la proteína L incrementó la fuerza de la señal por reticulación de los dAbs.

5

BMS3h-70 a -105:

BMS3h-70 a -105 fueron aislados a partir de las selecciones contra el antígeno que había sido pasivamente adsorbido a los inmuntubos. Los fagos provenientes de las bibliotecas de dAb 4G y 6G Domantis intactas, fueron
10 combinados como sigue antes de iniciar las selecciones:

- 1) 4G VH CDR3 longitudes entre 7 - 9 aminoácidos.
- 2) 4G VH CDR3 longitudes entre 10 - 12 aminoácidos.
- 3) 4G VH CDR3 longitudes entre 13 - 15 aminoácidos.
- 4) 6G VH CDR3 longitudes entre 7 - 9 aminoácidos.
- 15 5) 6G VH CDR3 longitudes entre 10 - 12 aminoácidos.
- 6) 6G VH CDR3 longitudes entre 13 - 15 aminoácidos.
- 7) 4G VK
- 8) 6G VK

Para la primera ronda de selección, 1 ml de la
20 fusión humana CD40-Fc a 10 µg/ml (BMS) en amortiguador de carbonato-bicarbonato 0.2 M, pH 9.4, fue agregado a un inmuntubo Nunc MaxiSorp y luego incubado toda la noche a 4°C con agitación giratoria. El tubo fue luego vaciado y lavado tres veces con solución salina amortiguada con fosfato (PBS).
25 El tubo fue luego bloqueado mediante relleno del borde con

MPBS e incubando por 1 hora a temperatura ambiente. El tubo fue luego vaciado y lavado tres veces con PBS. Los fagos de biblioteca en 4 ml de MPBS fueron agregados al tubo e incubados por 1 hora con rotación extremo sobre extremo a
5 temperatura ambiente.

El tubo fue vaciado y lavado diez veces con PBST (PBS con 0.1% (v/v) de Tween 20). Los fagos enlazados retenidos sobre el tubo lavado fueron eluidos por incubación con 500 μ l de tripsina-PBS (50 μ l de tripsina a 10 mg/ml
10 [Sigma-Aldrich, Reino Unido] disuelto en Tris-HCl 50 mM pH 7.4, cloruro de calcio 1 mM agregado a 450 μ l de PBS) con rotación en extremo sobre extremo por 10 minutos a temperatura ambiente. La solución que contenía el fago fue recuperada, y se utilizaron 250 μ l para infectar 1.75 ml de
15 *E. coli* TG1 en fase logarítmica de crecimiento (a una OD₆₀₀ de 0.4) por 30 minutos a 37°C. El cultivo infectado con el fago TG1 de *E. coli* fue centrifugado a 11,600 g en una microcentrífuga por 1 minuto, y la pellet celular resultante fue resuspendido en 1 ml de 2xTY (16 g Tryptone,
20 10 g de extracto de levadura, y 5 g de NaCl en 1 litro. La suspensión fue calentada en autoclave por 15 minutos a 121°C) y sembrada en placas sobre una caja de Petri de 9 cm que contenía agar LB suplementado con 15 μ g/ml tetraciclina. Las placas fueron incubadas toda la noche a 37°C. Dos mililitros
25 de 2xTY suplementado con 15% de glicerol fueron luego

agregados a cada placa, y las células fueron soltadas con un dispersor de vidrio y mezcladas perfectamente.

Cincuenta microlitros de las bacterias raspadas fueron utilizados para inocular 50 ml de 2xTY suplementado con 15 µg/ml de tetraciclina y desarrollados toda la noche a 37°C con agitación a 250 rpm. El cultivo de toda la noche fue centrifugado a 3,300 g por 15 minutos para concentrar las bacterias. Para precipitar el fago, se agregaron 10 ml de PEG/NaCl (20% de polietilenglicol 8000, NaCl 2.5 M) a 40 ml de sobrenadante. La solución de fago/PEG fue mezclada y dejada sobre hielo por 1 hora. La solución fue luego centrifugada a 3,300 g por 30 minutos a 4°C, y el sobrenadante fue desechado. La pellet fue resuspendido en 2 ml de PBS y centrifugado a 11,600 g por 10 minutos en una microcentrífuga para eliminar los desechos bacterianos remanentes. El sobrenadante resultante que contiene el fago fue luego utilizado para la siguiente ronda de selección contra el antígeno CD40-Fc. Los títulos producidos a partir de la ronda 1 estuvieron en el intervalo de 7.5×10^4 a 1.5×10^7 TU/ml (unidades de transformación por ml).

Una segunda ronda de selección fue realizada utilizando el fago enriquecido recuperado de la primera ronda de selección. Esto fue realizado exactamente como se describe anteriormente y los títulos producidos estuvieron en el intervalo de 2.5×10^7 a 1.2×10^8 TU/ml.

Una tercera ronda de selección fue realizada utilizando el fago enriquecido recuperado de la segunda ronda de selección. Estas fueron realizadas como se describe anteriormente pero con una concentración de antígeno de 1
5 $\mu\text{g/ml}$. Los títulos producidos estuvieron en el intervalo de 5.1×10^7 a 7.5×10^8 TU/ml.

Para monitorizar el progreso de las selecciones, se llevaron a cabo ELISAs de fago monoclonal después de las rondas 2 y 3. Muestra de colonias individuales fueron
10 recogidas en 200 μL de 2xTY suplementado con 15 $\mu\text{g/ml}$ de tetraciclina e incubados toda la noche a 37°C con agitación a 250 rpm en placas de cultivo de células de 96 pozos Costar (Corning Incorporated, Estados Unidos). Los cultivos fueron centrifugados para concentrar las células, y los
15 sobrenadantes fueron evaluados mediante ELISA de enlace al antígeno para los dAbs de fago que se enlazan a CD40. Todos los lavados fueron realizados utilizando 3 lavados de 250 μl de PBST seguido por 3 lavados de 250 μl de PBS. Las inmunoplasacas MaxiSorp de 96 pozos (Nunc, Estados Unidos)
20 fueron recubiertas toda la noche a 4°C con 50 μl /pozo de CD40-Fc a 0.5 $\mu\text{g/ml}$ (BMS) en amortiguador de carbonato-bicarbonato 0.2 M, pH 9.4. Las placas fueron lavadas y luego bloqueadas con 250 μl de MPBS al 2% por 1 hora a temperatura ambiente. Las placas fueron lavadas y los sobrenadantes del
25 fago fueron agregados a un volumen igual de 2% de MPBS e

incubados por 1 hora a temperatura ambiente. Las placas fueron lavadas, y los fagos enlazados fueron detectados con un conjugado anti-M13-HRP (GE Healthcare, Reino Unido) diluido 1:5000 en 2% de MPBS e incubado por 1 hora a temperatura ambiente. Las placas fueron lavadas, y el ELISA fue desarrollado utilizando la solución de peroxidasa para micropozos SureBlue 1-Component TMB MicroWell (KPL Inc, Estados Unidos). Los dAbs de fago específicos fueron identificados mediante comparación a las placas recubiertas con Fc libre.

Los genes de dAb provenientes de cada una de las rondas anteriores dos y tres de los productos de selección, fueron subclonados, como un combinado, dentro del vector de expresión soluble pDOM5 en la cepa HB2151 de *E. coli*. Este vector permitió la expresión del dAb libre con una etiqueta c-myc (Roche Diagnostics GmbH) en *E. coli* y la secreción al sobrenadante.

Los dAbs que se enlazan a CD40 provenientes de selecciones pasivas fueron identificados como sigue. Noventa y seis colonias individuales (en pDOM5) fueron recogidas de cada producto en 200 μ L de caldo Terrific que contenía el medio de Autoinducción OnEx (Novagen, Reino Unido) toda la noche a 37°C con agitación a 250 rpm en placas de cultivo de células de 96 pozos Costar 96 (Corning Incorporated, Estados Unidos). Los cultivos fueron centrifugados fueron

centrifugados para concentrar las células, y los sobrenadantes fueron evaluados mediante ELISA de enlace al antígeno para los dAbs que se enlazan a CD40. Las inmunoplaacas de 96 pozos MaxiSorp (Nunc, Estados Unidos) fueron recubiertas toda la noche a 4°C con 50 µl/pozo de CD40-Fc a 0.5 µg/ml (BMS) en amortiguador de carbonato-bicarbonato 0.2 M, pH 9.4. Todos los lavados fueron como se describe para el ELISA de fago. Las placas fueron bloqueadas por 1 hora a temperatura ambiente con 250 µl de PBS que contenía 1% de Tween 20 (PBST). El sobrenadante de cultivo que contenía el dAb, clarificado, fue agregado a la placa de ELISA con un volumen igual de 0.1% de PBST. Las placas fueron incubadas por 1 hora a temperatura ambiente y luego lavadas. El dAb enlazado fue detectado utilizando un proceso de dos pasos: primeramente el 9E10 biotinilado (IgG anti-myc, Sigma-Aldrich, Reino Unido) diluido 1:2000 en 0.1% de PBST fue agregado por 1 hora a temperatura ambiente, luego lavado, seguido por estreptavidina-HRP (Bender MedSystems, Austria) diluido 1:5000 en 0.1% de PBST por 1 hora a temperatura ambiente. Las placas fueron lavadas y el ELISA desarrollado utilizando SureBlue 1-Component TMB. Los dAbs específicos fueron identificados mediante comparación a las placas recubiertas con Fc libre.

Los clones específicos para CD40 fueron probados ya sea en el ensayo de enlace al receptor basado en esferas o

basado en ELISA (RBA) para evaluar la inhibición del enlace al ligando de CD40. Las mediciones de la potencia obtenidas a partir de RBA se dan en la Tabla 5 (esfuerzo de Selección Primaria). Los anticuerpos de dominio que mostraron
 5 inhibición en el RBA fueron probados en el ensayo de proliferación de células B y luego en una variedad de otros ensayos celulares *in vitro*.

BMS3h-210 a -225

BMS3h-210 a -225 fueron aislados de las selecciones
 10 contra las células enteras. El fago proveniente de las bibliotecas de dAb 4G y 6G Domantis, intactas, fueron combinados como sigue antes de iniciar las selecciones:

- 1) 4G + 6G VH CDR3 longitudes entre 7 - 9 aminoácidos.
- 2) 4G + 6G VH CDR3 longitudes entre 10 - 12 aminoácidos.
- 15 3) 4G + 6G VH CDR3 longitudes entre 13 - 15 aminoácidos.
- 4) 4G y 6G VK

Para la ronda uno una línea celular DG44 CHO establemente transfectada con el CD40 humano expresado sobre la superficie celular (suministrado por BMS) fue utilizado
 20 como el antígeno. Antes de la selección contra estas células, los combinados de la biblioteca descritos anteriormente fueron incubados con las células CHO no transfectadas para agotarlas de los dAbs de visualización de fago específicos para los antígenos de la superficie celular
 25 diferentes de la CD40. Ambos tipos de células fueron

cosechados por incubación con Versene (Invitrogen) antes de la evaluación para la viabilidad. Seis millones de células CHO no transfectadas, viables, fueron resuspendidas en 4 ml de PBS con 2% (w/v) de BSA (PBS/BSA) y rotadas extremo sobre extremo a 4°C por 1 hora para el bloqueo. Todos los pasos subsiguientes fueron realizados a 4°C a no ser que se indicara de otro modo. Las células fueron centrifugadas a 185 g por 5 minutos y el sobrenadante, que contenía el fago de biblioteca agotado, fue transferido a un tubo fresco. A éste se agregaron 6×10^6 células CHO-CD40 viables en 1 ml PBS/BSA y la mezcla fue rotada por 1 hora. Las células fueron luego lavadas cinco veces por centrifugación a 185 g por 5 minutos y resuspendidas en 10 ml PBS/BSA. Después del lavado final, las células fueron concentradas como se describió previamente y fueron luego resuspendidas en 0.5 ml de 1 mg/ml de tripsina tipo XIII proveniente de páncreas bovino (Sigma Aldrich, Reino Unido) en PBS suplementado con Tris-HCl 5 mM pH 7.4, CaCl_2 0.1 mM y transferidas a un tubo para microcentrífuga. Las células fueron luego rotadas a temperatura ambiente por 10 minutos antes de centrifugar a 16000 g por 5 minutos. Los fagos eluidos en el sobrenadante fueron utilizados para infectar *E. coli* y se determinó que los títulos de fagos producidos estaban entre 5.1×10^5 y 2.7×10^6 TU/ml (unidades de transformación por ml).

Se realizó una segunda ronda de selección

utilizando el fago enriquecido recuperado de la primera ronda de selección. Estos fueron realizados como se describió anteriormente pero sin el paso de agotamiento inicial (des-selección) y utilizando las células B humanas RAMOS (ATCC) en vez de CHO-CD40. Los títulos producidos estuvieron en el intervalo de 2.3×10^5 a 7.5×10^5 TU/ml.

Se realizó una tercera ronda de selección como para la segunda ronda. Los títulos producidos estuvieron en el intervalo de 1.9×10^8 a 3.5×10^8 TU/ml.

Los genes de dAb provenientes de cada una de las rondas anteriores dos y tres de productos de selección, fueron subclonados, como un combinado, dentro del vector de expresión soluble pDOM5 en *E. coli* cepa HB2151. Este vector permitió la expresión del dAb libre con una etiqueta c-myc en *E. coli* y la secreción hacia el sobrenadante.

Los clones específicos para CD40 fueron probados ya sea en el ensayo de enlace al receptor de células CHO (RBA) para evaluar la inhibición del enlace al ligando CD40. Los anticuerpos de dominio que mostraron inhibición en RBA fueron probados en el ensayo de proliferación de células B y luego en una variedad de otros ensayos celulares *in vitro*.

Maduración por Afinidad por PCR propensa a error

Las bibliotecas de fagos propensas a error fueron construidas para 13 dAbs BMS3h que mostraron actividad de neutralización en el ensayo de proliferación de células B

descrito más adelante en el ejemplo 6 (ver TABLA 17). Esto fue realizado mediante el uso de la polimerasa Mutazyme II (parte del kit GeneMorph II de Agilent Technologies) para introducir aleatoriamente errores en el gen dAb durante la
5 amplificación mediante la reacción en cadena de polimerasa (PCR). Los genes de dAb mutados fueron clonados como una fusión genética con la proteína del gen III del fago fd bajo el control de la secuencia guía GAS1 en el vector pDOM4, que contenía todos los genes de fd necesarios para generar
10 partículas de fago infecciosas. Estas bibliotecas fueron aproximadamente de 1×10^8 UFC (unidades formadoras de colonias) en tamaño, con una proporción de errores de 2-5 aminoácidos por gen de dAb.

Los fagos generados a partir de estas bibliotecas
15 fueron sometidos a tres rondas de selección contra el CD40 humano biotinilado, soluble. La primera ronda de la selección del fago fue realizada mediante el premezclado de la biblioteca de fago con 2% de MPBS (solución salina amortiguada con fosfato suplementada con 2% (p/v) de leche en
20 polvo descremada deshidratada Marvel y agregando CD40 humano biotinilado (BMS) a una concentración final de 20 nM en un volumen final de 1 ml. La mezcla fue incubada por al menos una hora a temperatura ambiente con mezclado extremo sobre extremo. Los complejos antígeno-fago fueron luego capturados
25 utilizando 50 μ l de estreptavidina M-280 Dynabeads®

(Invitrogen) y lavados 7 veces con 1 ml de PBST seguido por un lavado simple en 1 ml de PBS. Los fagos lavados fueron eluidos del complejo antígeno/esfera por incubación con 0.5 ml de tripsina tipo XIII a una concentración de 1 mg/ml
5 proveniente de páncreas bovino (Sigma Aldrich, Reino Unido) en PBS suplementado con Tris-HCl 5 mM pH 7.4, cloruro de calcio 0.1 mM. Los fagos eluidos fueron utilizados para infectar *E. coli* y los títulos de fagos producidos fueron determinados como entre 2×10^5 y 9×10^7 TU/ml (unidades de
10 transformación por ml).

Se realizó una segunda ronda de selección utilizando el fago enriquecido recuperado de la primera ronda de selección, con una concentración final de CD40 biotinilado 2 nM seguido por la captura utilizando esferas de
15 estreptavidina como se describió anteriormente. Los títulos producidos estuvieron en el intervalo de 3×10^4 a 5×10^6 TU/ml.

Fue realizada una tercera ronda de selección utilizando el CD40 biotinilado 2 nM seguido por la captura utilizando esferas de estreptavidina. Los títulos de los
20 fagos eluidos estuvieron en el intervalo de 8×10^4 a 4×10^6 TU/ml.

Selección BIAcore^{MR}

Los genes de dAb provenientes de cada uno de las tres rondas de selección producidas, fueron subclonados, como
25 un combinado, dentro del vector de expresión soluble pDOM13

(Domantis) en *E. coli* HB2151. El vector pDOM13 es también conocido como pDOM33 y es descrito en WO/2008/149143. Este vector permitió la expresión del dAb libre en *E. coli* y la secreción hacia el sobrenadante. Cuarenta y siete colonias
5 individuales fueron recogidas de cada uno de los productos y expresados en 200 µl de caldo Terrific (TB) que contenía el medio de Autoinducción Novagen Overnight Express (Merck Chemicals, Reino Unido) toda la noche a 37°C con agitación a 250 rpm en placas de cultivo de células de 96 pozos Costar
10 (Corning Incorporated, Estados Unidos). En la misma placa, se inoculó un pozo simple con *E. coli* que expresa el dAb progenitor apropiado (de tipo silvestre). Los cultivos fueron centrifugados para concentrar las células y los sobrenadantes fueron seleccionados sobre un instrumento
15 BIAcore^{MR} 3000 (GE Healthcare) para mejoramientos en la "velocidad de apagado" (por ejemplo la constante de la velocidad de disociación, k_d) en comparación al dAb progenitor.

Aproximadamente 1600 unidades de respuesta (RU) del
20 CD40 humano biotinilado (BMS) fueron inmovilizadas sobre una celda de flujo de un chip de estreptavidina (SA) BIAcore^{MR}. Una segunda celda de flujo sin ningún ligando inmovilizado, sirvió como una celda de flujo de referencia para la referencia en línea. Cada sobrenadante de dAb que iba a ser
25 analizado fue diluido 1:3 en amortiguador de HBS-EP (HEPES

0.01 M pH 7.4 con cloruro de sodio 0.15 M, EDTA 3 mM y 0.005% v/v de Surfactante P20, GE Healthcare). Diez microlitros de cada sobrenadante de dAb fueron inyectados, utilizando la función KINJECT del instrumento, a través de las celdas de flujo de referencia e inmovilizadas con CD40, en serie, con la sustracción en línea de la señal proveniente de la celda de referencia. El experimento fue realizado a 25°C y con una velocidad de flujo de 10 μ l/min de HBS-EP. Después de que cada inyección había sido completada, el dAb se dejó dissociar del ligando en amortiguador por 120 segundos antes de la regeneración con una inyección de 5 μ l de glicina 10 mM pH 2.0. El software BIAevaluation 4.1 (GE Healthcare) fue utilizado para sustraer los trazos de la celda de flujo de referencia de cada trazo de analito. Se utilizó el mismo software para realizar un ajuste aproximado de un modelo cinético 1:1 (Langmuir) a la fase de disociación de los trazos de analitos. Este modelo produjo constantes de velocidad de disociación aproximadas ("velocidad de apagado" o k_d) para cada clon y permitió que se realizaran comparaciones relativas con el dAb de tipo silvestre.

Los clones con velocidades de apagado mejoradas fueron identificados para todas las líneas excepto BMS3h-129 y 197. Los clones con velocidades de apagado mejoradas fueron probados ya sea en el ensayo de enlace al receptor basado en esferas o basado en ELISA (RBA), para evaluar la

potencia mejorada como se describió anteriormente. Las mediciones de potencia obtenidas a partir del RBA se dan en las tablas etiquetadas "Clones Madurados Propensos a Error". Los clones que fueron más potentes en el RBA fueron subsecuentemente probados en un ensayo de proliferación de células B para evaluar la potencia biológica mejorada, y estas mediciones obtenidas se dan en la TABLA 17. Los anticuerpos de dominio que tuvieron potencia mejorada en el ensayo de proliferación de células B fueron también probados en una variedad de otros ensayos de células *in vitro*.

Maduración por afinidad mediante diversificación de exploración de triplete

Los cinco dAbs de potencia mejorada, aislados de la maduración propensa a errores, BMS3h-37-2, -38-2, -56-2, -193-25 y -217-23, fueron elegidos para ser posteriormente madurados por afinidad mediante diversificación de exploración de triplete. Las bibliotecas de fagos fueron construidas con base en estos progenitores como se describe anteriormente para las bibliotecas propensas a errores excepto que, en vez de utilizar la PCR propensa a errores, se utilizaron una serie de oligonucleótidos triplete degenerados, traslapados, para diversificar las regiones de determinación de la complementariedad (CDR) de cada dAb. Para cada dAb que iba a ser madurado por afinidad, se utilizaron los oligonucleótidos que contenían los triplete

del codón NNS ver Arkin et al. (1992) *Proc. Nat'l Acad. Sci. USA* 89:7811-7815) para elaborar un número de bibliotecas para cada CDR mediante el empalme por PCR de extensión de traslape (SOE). Los triplete diversificados por los oligonucleótidos para un CDR dado se traslaparon por dos codones, dando como resultado dos a cuatro bibliotecas por CDR. Los residuos de aminoácidos diversificados en las bibliotecas de BMS3h-37-2 estuvieron en las posiciones 30, 31, 32, 33, 35, 50, 52, 53, 55, 56, 95, 96, 97, y 98 (numeración de Kabat). Los residuos diversificados en las bibliotecas BMS3h-38-2 fueron como para 37-2, pero con la adición de la posición 100. Los residuos diversificados en las bibliotecas BMS3h-56-2 fueron como para 37-2, pero con la adición de las posiciones 100 y 101. Los residuos diversificados en la bibliotecas BMS3h-193-25 estuvieron en las posiciones 217-23 27, 28, 30, 31, 32, 34, 49, 50, 51, 53, 89, 91, 92, 93, 94, y 96.

Los fagos generados a partir de estas bibliotecas fueron combinados por CDR y las selecciones fueron realizadas como se describe anteriormente, excepto que, para BMS3h-37-2, -38-2, -56-2 y -193-25, la concentraciones del antígeno utilizado fueron de 10, 1 y 0.1 nM para las rondas uno dos y tres, respectivamente. Para BMS3h-217-23 las concentraciones del antígeno utilizado fueron de 20, 2 y 0.2 nM para las rondas, dos y tres, respectivamente. Para BMS3h-193-25, la cual es de reactividad cruzada para CD40 de cynomolgus, las

selecciones fueron también realizadas contra cyno CD40 en paralelo. Además, las rondas de selección dos y tres fueron realizadas en presencia o ausencia de un exceso de 100 veces y 1000 veces de CD40 no marcado, respectivamente. La adición
5 a este competidor fue realizada después de la incubación inicial de una hora del fago con el antígeno biotinilado y la mezcla fue luego incubada, como se describió anteriormente, por una hora adicional. Este paso de competencia fue incluido con el objetivo de mejorar la selección de los dAbs
10 con una velocidad de apagado más lenta. Los títulos de la ronda uno estuvieron en el intervalo de 1.4×10^6 a 1.4×10^9 . Los títulos en la ronda 2 fueron de 1.3×10^5 a 4.0×10^8 sin competencia y 8.6×10^4 a 1.3×10^8 con competencia. Los títulos en la ronda 3 fueron de 1.2×10^5 a 1.9×10^8 sin competencia y
15 6.0×10^5 a 1.2×10^8 con competencia.

Estos productos de selección fueron subclonados y seleccionados como se describe para la maduración de afinidad propensa a errores. Los clones con las velocidades de apagado mejoradas fueron identificados para todas las líneas
20 excepto BMS3h-193-25. Los clones con velocidades de apagado mejoradas fueron probados en el ensayo de enlace al receptor de ELISA (RBA) para evaluar la potencia mejorada. Las mediciones de potencia obtenidas a partir del RBA se dan en las Tablas etiquetadas "Clones Madurados Adicionales". Los
25 clones que fueron más potentes en el RBA fueron

subsecuentemente probados en un ensayo de proliferación de células B para evaluar la potencia biológica mejorada, y estas mediciones obtenidas se dan en la TABLA 17. Los anticuerpos de dominio que tuvieron potencia mejorada en el
 5 ensayo de proliferación de células B fueron también probados en una variedad de otros ensayos de células *in vitro*.

Ejemplo 2

Selección Utilizando Ensayos de Enlace al Receptor (RBA)

Se utilizaron varios enlace al receptor (RBA) *in vitro* para determinar la afinidad por CD40 de las secuencias de aminoácidos del dominio variable anti-CD40 humano, generadas en el ejemplo 1. Se utilizaron tres formatos de RBA: (1) un RBA de esferas, (2) un RBA de ELISA, y (3) un RBA de células CHO.

15 RBA de esferas:

Partículas de poliestireno con estreptavidina Sphero lavadas con solución salina amortiguada con fosfato (PBS) (Saxon Europe, Reino Unido) fueron recubiertas con 0.5 µg/ml de IZ-CD40L humano biotinilado (BMS). Después del
 20 recubrimiento, las partículas de CD40L biotiniladas fueron lavadas en PBS y diluidas 1:10 en albúmina sérica bovina al 0.1% (p/v) (BSA) (Sigma-Aldrich, Reino Unido) en el amortiguador de ensayo de PBS. En una placa de paredes negras, con fondo claro de 384 pozos (Applied Biosystems) un
 25 intervalo de dilución del dAb purificado, 0.25 µg/ml de CD40

humano (BMS, CY24FEB06-01), clon GG-7 del mAb de ratón anti-IgG (Fc) humano 1 en 5000 (Sigma-Aldrich, Reino Unido), 0.25 µg/ml de ALEXA Fluor 647 de cabra anti-ratón (Invitrogen, Molecular probes, Reino Unido) y las partículas de poliestireno con CD40L biotinilado, fueron combinados igualmente y se dejaron incubar a temperatura ambiente por 6 horas en ausencia de luz. Después de la incubación, fue evaluado el enlace competitivo del dAb vs. el CD40 humano a las partículas de CD40L biotiniladas, utilizando la fluorescencia relativa con el mecanismo de detección celular AB8200 (Applied Biosystems).

RBA de ELISA:

Placas de 384 pozos High Bind, de pared clara (Corning, Reino Unido) fueron recubiertas con 25 µl de Neutravidina a una concentración de 1 µg/ml en amortiguador de carbonato-bicarbonato 0.2 M, pH 9.4 toda la noche a 4°C. Al día siguiente, las placas de ensayo fueron lavadas con 0.1% (v/v) de amortiguador de Tween PBS, bloqueadas con 1% (p/v) de BSA en PBS por 1 hora a temperatura ambiente y lavadas nuevamente. Después de la eliminación del amortiguador de lavado en exceso, se incubaron 25 µl de IZ-CD40L humano biotinilado (BMS) a una concentración de 1 µg/ml con las placas de ensayo por 1 hora a temperatura ambiente. Simultáneamente, un intervalo de dilución del dAb purificado y 1 µg/ml de CD40 humano (BMS, CY24FEB06-01) fueron formados

en complejo en una proporción 1:1. Después del lavado de la placa de ensayo, el complejo dAb:CD40 humano fue incubado en la placa de ensayo a temperatura ambiente por 2 horas con agitación suave. El enlace competitivo del dAb vs. CD40 humano al CD40L biotinilado fue detectado con incubaciones 5 secuenciales del clon GG-7 del mAb anti-IgG (Fc) humano de ratón 1 en 5000 (Sigma-Aldrich, Reino Unido) seguido por el anticuerpo de detección secundario de cabra anti-IgG (Fc) de ratón, conjugado a peroxidasa de rábano (HRP) 1 en 10,000 10 (Sigma-Aldrich, Reino Unido). La señal de absorbancia fue medida utilizando un lector de placas SpectraMax M5^e (Molecular Devices) a 450 nm después de la neutralización con la solución de HCl 1M.

Ensayos celulares: RBA de células CD40 CHO:

15 Las células CHO-DG44 que expresan CD40, humanas, establemente transfectadas, o las células CHO-DG44 nativas (ambas BMS) fueron desprendidas de los matraces de cultivo de células utilizando Versene (Invitrogen). Cuarenta mil células por pozo fueron sembradas en placas de fondo claro, 20 de pared negra, de 96 pozos High Bind, (Corning, Reino Unido) en amortiguador de ensayo BSA PBS al 0.1% (p/v) con un intervalo de dilución del dAb, 0.25 µg/ml del IZ-CD40L humano biotinilado (BMS), y 0.25 µg/ml estreptavidina Alexa Fluor 647 (Invitrogen, Molecular Probes, Reino Unido). La mezcla 25 fue incubada en ausencia de luz por 6 horas. Después de la

incubación, el enlace competitivo del dAb vs. las células CD40 CHO humanas al IZ-CD40L biotinilado, soluble, fue evaluado utilizando la fluorescencia relativa con el mecanismo de detección celular AB8200 (Applied Biosystems).

5 Las TABLAS 5-7 respectivamente muestran los resultados de un esfuerzo de selección primaria ("clones intactos") y las rondas subsecuentes por maduración por afinidad ("clones madurados propensos a errores" y "clones madurados adicionales") para los dAbs anti-CD40 humano,
10 probados.

TABLA 5

Esfuerzo de Selección Primaria:

15	Clon intacto	EC₅₀ RBA de esferas (nM)	EC₅₀ RBA de ELISA (nM)	EC₅₀ RBA de células (CHO-CD40) (nM)
	BMS3h-37	100, 200		
	BMS3h-38	600, 650		>10000
	BMS3h-41	2000, 1600		>10000
20	BMS3h-43	100, 50, 50		5000
	BMS3h-56	1000, 500		
	BMS3h-106	300, 1000, 500, 400		>10000
	BMS3h-129	5000		
25	BMS3h-131	500, >1000		

	Clon intacto	EC₅₀ RBA de esferas (nM)	EC₅₀ RBA de ELISA (nM)	EC₅₀ RBA de células (CHO-CD40) (nM)
5	BMS3h-193	1000		
	BMS3h-197	30		
	BMS3h-198	80		600
	BMS3h-202	3000, 3700		>10000
	BMS3h-217	800		1400
10	BMS3h-231		670, 870	
	BMS3h-233		2770	
	BMS3h-257		3210, 1340	
	BMS3h-242		390, 210	
	BMS3h-262		1770, 1160	
15	BMS3h-263		3130	
	BMS3h-271		370, 210	
	BMS3h-285		168, 258	
	BMS3h-287		>10000, 6758	
20	BMS3h-289		2390, >10000	

TABLA 6

Clones Madurados Propensos a Errores:

	Clon	EC ₅₀ RBA de ELISA (nM)	EC ₅₀ RBA de células (CHO-CD40) (nM)
5	BMS3h-37-2		32
	BMS3h-37-4		45
	BMS3h-37-11		27
	BMS3h-38-5		1000
	BMS3h-38-8		2800
10	BMS3h-41-3		200
	BMS3h-41-10		4300
	BMS3h-43-3		320
	BMS3h-43-5		90
	BMS3h-56-1	7.1	
15	BMS3h-56-2	17.0	
	BMS3h-56-5	4.9, 7.5, 4.7	18, 28
	BMS3h-56-7	5.5	
	BMS3h-56-8	6.2	
	BMS3h-56-9	4.4, 5.5	
20	BMS3h-56-16	7.0	
	BMS3h-56-17	66	
	BMS3h-56-18	6.5	
	BMS3h-56-19	5.5, 5.1	

	Clon	EC₅₀ RBA de ELISA (nM)	EC₅₀ RBA de células (CHO-CD40) (nM)
	BMS3h-56-20	6.8	
	BMS3h-56-21	6.5, 6.2	
5	BMS3h-56-22	6.5	
	BMS3h-56-23	24.5	
	BMS3h-56-24	11.7	
	BMS3h-56-25	5.5	
	BMS3h-56-26	5.0	
10	BMS3h-56-27	16.3	
	BMS3h-56-28	8.9	
	BMS3h-56-29	9.7	
	BMS3h-56-30	24.2	
	BMS3h-56-31	61.0	
15	BMS3h-193-5	>300	
	BMS3h-193-7	300	
	BMS3h-193-10	200	
	BMS3h-193-11	300	
	BMS3h-193-12	200	
20	BMS3h-193-15		300
	BMS3h-193-18	100	
	BMS3h-193-19	100	
	BMS3h-193-25	140	
25	BMS3h-193-26	100	

	Clon	EC ₅₀ RBA de ELISA	EC ₅₀ RBA de células
		(nM)	(CHO-CD40) (nM)
5	BMS3h-193-27	100	
	BMS3h-193-29	360, 114	
	BMS3h-193-30	290, 116	
	BMS3h-198-1	12	70
	BMS3h-198-2		115
10	BMS3h-198-3		330
	BMS3h-198-9	20	
	BMS3h-198-10	35	
	BMS3h-198-11	20	
	BMS3h-198-14	9	
15	BMS3h-198-17	20	
	BMS3h-198-19	7.9	
	BMS3h-198-22	10	
	BMS3h-198-31	6.1	
	BMS3h-198-32	24.7	
20	BMS3h-198-33	8.7	
	BMS3h-198-34	32.6	
	BMS3h-198-37	15.1	
	BMS3h-198-38	7.2	
	BMS3h-202-10		7200
	BMS3h-202-11		8300

	Clon	EC₅₀ RBA de ELISA (nM)	EC₅₀ RBA de células (CHO-CD40) (nM)
	BMS3h-217-1	23	
	BMS3h-217-2	78	
5	BMS3h-217-3	32	
	BMS3h-217-4	parcial, 15	
	BMS3h-217-5	65	
	BMS3h-217-6	26	
	BMS3h-217-7	39	
10	BMS3h-217-8	6	
	BMS3h-217-9	53	
	BMS3h-217-14	8	
	BMS3h-217-15	21	
	BMS3h-217-16	9	
15	BMS3h-217-17	60	
	BMS3h-217-23	16	

TABLA 7

Clones Madurados Adicionales:

20	Clon	EC₅₀ RBA de ELISA (nM)	EC₅₀ Ensayo celular ICAM1 (nM)	EC₅₀ RBA de células (CHO-CD40) (nM)
25	BMS3h-37-202	4.1, 35		

	Clon	EC₅₀ RBA de ELISA (nM)	EC₅₀ Ensayo celular ICAM1 (nM)	EC₅₀ RBA de células (CHO-CD40) (nM)
5	BMS3h-37-205	3.1, 4.4		
	BMS3h-37-206	3.2, 8.9		
	BMS3h-37-207	2.5, 6.6		
	BMS3h-37-212	24		
	BMS3h-37-213	16		
10	BMS3h-38-201	3.4, inactivo		
	BMS3h-38-202	4.8		
	BMS3h-38-203	5.5		
	BMS3h-38-204	4.8		
	BMS3h-38-205	4.5, 11.1		
15	BMS3h-38-209	10.2		
	BMS3h-38-211	2.3, 13.8		
	BMS3h-38-215	2.3, 3.6		
	BMS3h-38-217	1.8, 2.2		
	BMS3h-38-218	3.0		
20	BMS3h-38-219	1.8, 7.1		
	BMS3h-38-223	5.7		
	BMS3h-38-224	6.3		
	BMS3h-38-225	8.8		
25	BMS3h-38-226	18.1		

	Clon	EC₅₀ RBA de ELISA (nM)	EC₅₀ Ensayo celular ICAM1 (nM)	EC₅₀ RBA de células (CHO-CD40) (nM)
5	BMS3h-38-228	4		
	BMS3h-38-231	4.4		
	BMS3h-38-235	1.5		
	BMS3h-38-237	2		
	BMS3h-38-238	5.1		
10	BMS3h-56-201	3.7, 2.3	10.0	
	BMS3h-56-202	3.4, 3.2	80.0	
	BMS3h-56-203	5.2, 4.3	70.0	
	BMS3h-56-204	4.5		
	BMS3h-56-205	9.0		
15	BMS3h-56-206	2.9, 2.3	5.0	
	BMS3h-56-207	7.3		
	BMS3h-56-215	3.2, 4.6	40.0	
	BMS3h-56-217	2.1, 12.6		
	BMS3h-56-220	4.2		
20	BMS3h-56-223	5.0		
	BMS3h-56-224	2.1, 4.2		
	BMS3h-56-225	2.9		
	BMS3h-56-229	4.1		
25	BMS3h-56-232	2.8, 3.7		

	Clon	EC₅₀ RBA de ELISA (nM)	EC₅₀ Ensayo celular ICAM1 (nM)	EC₅₀ RBA de células (CHO-CD40) (nM)
5	BMS3h-56-239	2.7		
	BMS3h-56-243	9.9		
	BMS3h-56-244	6.0		
	BMS3h-56-246	11.1		
	BMS3h-56-248	0.7		
10	BMS3h-56-253	1.3		
	BMS3h-56-258	5.2	23.0	15
	BMS3h-56-261	5.7	42.4	17
	BMS3h-56-262	4.0	135.0	42
	BMS3h-56-265	18.8	289.0	88
15	BMS3h-56-266	3.8	31.9	27
	BMS3h-56-269	3.3	34.2	24
	BMS3h-56-270	11.3	93.8	91
	BMS3h-193-2501	114		
	BMS3h-193-2502	170		
20	BMS3h-193-2503	3000		
	BMS3h-193-2504	140		
	BMS3h-193-2505	500		
	BMS3h-193-2506	180		
25	BMS3h-193-2507	160		

	Clon	EC ₅₀ RBA de	EC ₅₀ Ensayo	EC ₅₀ RBA de
		ELISA (nM)	celular ICAM1 (nM)	células (CHO-CD40) (nM)
5	BMS3h-193-2510	170		
	BMS3h-193-2511	270		
	BMS3h-193-2512	600		
	BMS3h-193-2513	130		
	BMS3h-193-2514	525		
10	BMS3h-193-2515	100		
	BMS3h-193-2516	100		

Ejemplo 3

Cinéticas de Enlace a CD40

Las cinéticas de enlace fueron determinadas para los dAbs anti-CD40 humanos, identificados en el esfuerzo de selección primaria ("clones intactos") y en rondas subsiguientes de maduración por afinidad ("clones madurados propensos a errores"). Los métodos utilizados miden directamente la afinidad de los dAbs para CD40.

Se utilizó un instrumento BIAcore^{MR} 3000 (GE Healthcare) para analizar las cinéticas de enlace de los dAbs específicos de CD40, para CD40. Aproximadamente 600 unidades de respuesta (RU) de CD40 humano biotinilado (BMS) fueron inmovilizadas sobre una celda de flujo de un chip BIAcore^{MR} de

estreptavidina (SA). Una segunda celda de flujo sin ningún ligando inmovilizado, sirvió como una celda de flujo de referencia para referencie en línea. Una serie de diluciones duplicadas apropiadas de cada dAb que iba a ser analizado, fue preparada en el amortiguador HBS-EP (HEPES 0.01 M pH 7.4 con NaCl 0.15 M, EDTA 3 mM y 0.005% v/v de surfactante P20, GE Healthcare). Ciento ochenta microlitros de cada dAb fueron inyectados por duplicado utilizando la función KINJECT del instrumento. Cada dAb fue inyectado a través de las celdas de flujo inmovilizadas con CD40 y de referencia, en serie con sustracción en línea de la señal a partir de la celda de referencia. El experimento fue realizado a 25°C y a una velocidad de flujo de 30 µl/min de HBS-EP. Después de que cada inyección había sido completada, el dAb se dejó disociar del ligando en amortiguador por 300 segundos antes de la regeneración con una inyección de 10 µl de glicina 10 mM de pH 2.0. Una inyección de referencia del testigo de amortiguador HBS-EP (que no contenía analito) fue también realizada bajo las mismas condiciones, para servir como una segunda referencia para la sustracción de cada trazo de analito. Se utilizó el software BIAevaluation 4.1 (GE Healthcare) para sustraer el trazo de la celda de flujo de referencia y el trazo del testigo de amortiguador de cada trazo de analito. Se utilizó el mismo software para realizar un ajuste global simultáneo de un modelo cinético 1:1

(Langmuir) para las fases de asociación y disociación de los trazos en serie de dilución del analito. Este modelo produjo constantes de la velocidad de asociación y disociación (k_a y k_d , respectivamente) y la constante de disociación en equilibrio (K_D) de la interacción; esto se detalla en las

5 TABLAS 8 y 9.

TABLA 8

Clones intactos:

Clon	$\text{BIAcore}^{\text{MR}} k_a$ ($\text{M}^{-1}\text{s}^{-1}$)	$\text{BIAcore}^{\text{MR}} k_d$ (s^{-1})	$\text{BIAcore}^{\text{MR}} K_D$ (M)
BMS3h-37	<u>1.9E+04</u>	<u>3.6E-03</u>	<u>1.9E-07</u>
BMS3h-38	<u>2.1E+04</u>	<u>6.2E-03</u>	<u>3.0E-07</u>
BMS3h-41	<u>9.9E+03</u>	<u>8.3E-03</u>	<u>8.4E-07</u>
BMS3h-43	<u>1.4E+03</u>	<u>3.1E-03</u>	<u>2.1E-06</u>
15 BMS3h-56	<u>2.3E+04</u>	<u>4.0E-03</u>	<u>1.8E-07</u>
BMS3h-106	<u>1.3E+05</u>	<u>4.6E-02</u>	<u>3.5E-07</u>
BMS3h-107	<u>2.0E+05</u>	<u>1.7E-01</u>	<u>8.5E-07</u>
BMS3h-129	<u>4.7E+05</u>	<u>5.1E-01</u>	<u>1.1E-06</u>
BMS3h-131	<u>2.4E+04</u>	<u>2.2E-02</u>	<u>9.3E-07</u>
20 BMS3h-197	<u>8.1E+04</u>	<u>1.4E-02</u>	<u>1.8E-07</u>
BMS3h-198	<u>1.6E+03</u>	<u>3.8E-04</u>	<u>2.4E-07</u>
BMS3h-202	<u>1.7E+03</u>	<u>3.5E-03</u>	<u>2.0E-06</u>

TABLA 9

Clones Madurados Propensos a Errores:

	Clon	BIACore ^{MR}	BIACore ^{MR}	BIACore ^{MR}
		k_a ($M^{-1}s^{-1}$)	k_d (s^{-1})	K_D (M)
5	BMS3h-37-2	<u>1.0E+05</u>	<u>4.1E-04</u>	<u>4.0E-09</u>
	BMS3h-37-5	<u>3.9E+04</u>	<u>2.2E-04</u>	<u>5.5E-09</u>
	BMS3h-37-9	<u>1.5E+04</u>	<u>1.8E-04</u>	<u>1.2E-08</u>
10	BMS3h-38-1	<u>3.2E+04</u>	<u>1.1E-03</u>	<u>3.3E-08</u>
	BMS3h-38-2	<u>6.1E+04</u>	<u>7.5E-04</u>	<u>1.2E-08</u>
	BMS3h-38-3	<u>7.5E+04</u>	<u>4.1E-04</u>	<u>5.5E-09</u>
	BMS3h-41-1	<u>5.1E+04</u>	<u>5.6E-04</u>	<u>1.1E-08</u>
	BMS3h-43-1	<u>4.4E+03</u>	<u>6.3E-04</u>	<u>1.4E-07</u>
15	BMS3h-43-3	<u>3.1E+04</u>	<u>5.9E-04</u>	<u>1.9E-08</u>
	BMS3h-56-1	<u>9.8E+04</u>	<u>5.4E-04</u>	<u>5.5E-09</u>
	BMS3h-56-2	<u>1.1E+05</u>	<u>6.0E-04</u>	<u>5.3E-09</u>
	BMS3h-56-5	<u>1.1E+05</u>	<u>6.3E-04</u>	<u>5.9E-09</u>
	BMS3h-56-7	<u>1.3E+05</u>	<u>4.7E-04</u>	<u>3.5E-09</u>
20	BMS3h-56-9	<u>1.5E+05</u>	<u>3.9E-04</u>	<u>2.6E-09</u>
	BMS3h-131-2	<u>7.9E+04</u>	<u>1.7E-03</u>	<u>2.1E-08</u>
	BMS3h-193-25	<u>4.6E+05</u>	<u>3.7E-02</u>	<u>8.1E-08</u>
	BMS3h-198-1	<u>1.5E+04</u>	<u>1.8E-04</u>	<u>1.3E-08</u>
	BMS3h-202-5	<u>4.4E+03</u>	<u>1.3E-03</u>	<u>3.0E-07</u>

Ejemplo 4**Caracterización Biofísica**

Los dAbs anti-CD40 humano, identificados en el esfuerzo de selección primaria ("clones intactos") y la
 5 rondas subsecuentes de maduración por afinidad ("clones madurados propensos a errores" y "clones madurados adicionales") fueron además caracterizados por análisis de parámetros biofísicos. Para medir la estabilidad relativa de los dAbs, su punto de fusión fue determinado mediante
 10 calorimetría de exploración diferencial (DSC). Los dAbs con una temperatura de fusión más alta son más estables. Para determinar si los dAbs formar agregados multiméricos en solución, los dAbs fueron analizados mediante cromatografía de exclusión de tamaño/dispersión del luz laser de ángulos
 15 múltiples (SEC-MALLS). Los resultados son mostrados en las TABLAS 10-12.

TABLA 10**Clones nativos:**

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Clon	DSC (T_m/°C)	Estado en solución de SEC-MALS
BMS3h-38	59	Monómero y dímero (<5%)
BMS3h-41	59	Monómero y equilibrio de monómero- dímero (<5%)
BMS3h-43		<u>Dímero y trímero</u>

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	Clon	DSC (T_m/°C)	Estado en solución de SEC-MALS
	BMS3h-56	57	Monómero y dímero (<10%)
	BMS3h-106		Monómero
5	BMS3h-107	63	Monómero
	BMS3h-129	59	Monómero
	BMS3h-193	56	Monómero
	BMS3h-197	62 & 53	Monómero y dímero (<5%)
	BMS3h-198	61	Monómero
10	BMS3h-202	60	Monómero y equilibrio de monómero-dímero (<2%)
	BMS3h-207		<u>Dímero y tetrámero</u>
	BMS3h-208		<u>Monómero y dímero</u>
	BMS3h-217	57	Dímero
15	BMS3h-233		Monómero
	BMS3h-242		Monómero y monómero-dímero
	BMS3h-262		Monómero
	BMS3h-265		Dímero
	BMS3h-271		Dímero
20	BMS3h-285		Monómero

TABLA 11

Clones Madurados Propensos a Errores:

	Clon	DSC Tm/°C	Estado en solución de SEC-MALS
5	BMS3h-37-1	57.2	
	BMS3h-37-2	56.2	
	BMS3h-37-9	59.7	
	BMS3h-37-11	60.0	
10	BMS3h-56-1	49.6	Monómero
	BMS3h-56-2	63.0	Monómero y dímero (<2%)
	BMS3h-56-3	64.0	Monómero (>98%)
	BMS3h-56-5	51.2	
15	BMS3h-41-1	56	Monómero (~99%)
	BMS3h-41-2	53.4	
	BMS3h-41-3	51.8	
	BMS3h-41-9	61	Monómero y equilibrio rápido de Monómero/Dímero (<2%)
20	BMS3h-41-12	49.8	Monómero/Dímero
	BMS3h-41-13		Monómero/Dímero
	BMS3h-43-1	53	Monómero (~99%)
	BMS3h-43-3	51.2	
25	BMS3h-43-5	48.2	Monómero/Dímero
	BMS3h-43-10	51.8	
	BMS3h-43-11	54.8	

	Clon	DSC T_m/°C	Estado en solución de SEC-MALS
	BMS3h-43-12		Dímero (60%) y Monómero (40%)
	BMS3h-56-1	59.2	Monómero/Dímero
	BMS3h-56-2	60.1	Monómero/Dímero
5	BMS3h-56-5	57	Monómero (>95%)
	BMS3h-56-6	57.5	Monómero/Dímero
	BMS3h-56-7	61	Monómero + equilibrio rápido de Monómero/Dímero (<5%)
	BMS3h-56-8	58	Monómero (>98%)
10	BMS3h-56-9	61	Monómero + dímero (<5%)
	BMS3h-56-14	60.1	Monómero
	BMS3h-193-8	60	
	BMS3h-193-12	52	
	BMS3h-193-16	54.5 y 65.7	Monómero
15	BMS3h-193-19	56.8	Monómero
	BMS3h-193-25	55.8	Monómero
	BMS3h-193-29	60	Monómero
	BMS3h-193-30	58	
	BMS3h-198-1	52.5	Monómero
20	BMS3h-198-2		Monómero
	BMS3h-198-3	59	
	BMS3h-198-5	55.6	
	BMS3h-198-19	60.7	

	Clon	DSC T _m /°C	Estado en solución de SEC-MALS
	BMS3h-198-24	59.9	Monómero
	BMS3h-198-28	60.3	Monómero
	BMS3h-202-1	56.8	Monómero
5	BMS3h-202-5	55.5	Trímero (60%) y Monómero/Dímero (40%)
	BMS3h-202-10	58.3	Trímero (60%) y Monómero/Dímero (40%)
	BMS3h-217-1		Monómero/Dímero
10	BMS3h-217-2		Dímero
	BMS3h-217-3		Dímero
	BMS3h-217-4		Monómero/Dímero
	BMS3h-217-5		Dímero
	BMS3h-217-6		Dímero
15	BMS3h-217-8		Dímero
	BMS3h-217-14		Monómero/Dímero
	BMS3h-217-15		Dímero
	BMS3h-217-16		Dímero
	BMS3h-217-17		Monómero/Dímero
20	BMS3h-217-23		Dímero

TABLA 12

Clones Madurados Adicionales:

	Clon	DSC Tm/°C	Estado en solución de SEC-MALS
5	BMS3h-37-206		<u>Monómero (73%) y dímero (20%) + HMW</u>
	BMS3h-37-212		<u>Dímero</u>
	BMS3h-38-201		<u>Monómero (75%) y Dímero (15%)</u>
	BMS3h-38-228		<u>Monómero (90%) y Trímero (10%)</u>
	BMS3h-38-231		<u>Monómero (90%) y Dímero (10%)</u>
10	BMS3h-38-235		<u>Monómero (90%) y Trímero-Dímero</u>
	BMS3h-38-237		<u>Monómero (90%) y Tetrámero (10%)</u>
	BMS3h-38-238		<u>Monómero (95%) y Dímero-Monómero</u>
	BMS3h-56-201	<u>57.4 + 61.8</u>	<u>Monómero y Dímero (15%)</u>
	BMS3h-56-202		<u>Monómero</u>
15	BMS3h-56-203		<u>Monómero y Trímero</u>
	BMS3h-56-206		<u>Monómero</u>
	BMS3h-56-215		<u>Monómero, Dímero (2%) y Trímero (9%)</u>
	BMS3h-56-217	<u>52.8 + 54.6</u>	
	BMS3h-56-232	<u>51.0 + 56.1</u>	<u>Monómero (95%) y Dímero (5%)</u>
20	BMS3h-56-239	<u>53.5</u>	<u>Monómero</u>
	BMS3h-56-243	<u>51.9</u>	<u>Monómero y Pentámero</u>
	BMS3h-56-244		<u>Monómero (90%) y Trímero (10%)</u>
	BMS3h-56-248		<u>Monómero (60%), Dímero y Tetrámero</u>
	BMS3h-56-253		<u>Monómero</u>
25	BMS3h-56-258	<u>62.5 + 57.5</u>	

Clon	DSC T _m /°C	Estado en solución de SEC-MALS
BMS3h-56-261	<u>58.6 + 61.5</u>	
BMS3h-56-266	<u>61.3 + 62.3</u>	
BMS3h-56-269	<u>64.5 + 67.2</u>	

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Ejemplo 5

Análisis de Competencia

Se utilizó un instrumento BIAcore^{MR} 3000 (GE Healthcare) para analizar si los dAbs específicos del CD40 se enlazaban o no al mismo epítipo de CD40. Fueron inmovilizadas aproximadamente 600 unidades de respuesta (RU) del CD40 humano biotinilado (BMS) sobre una celda de flujo de un chip BIAcore^{MR} de estreptavidina (SA). Una segunda celda de flujo sin ningún ligando inmovilizado sirvió como una celda de flujo de referencia para la referencia en línea. Una dilución apropiada de cada dAb o Fab que iba a ser analizado, fue preparada en el amortiguador HBS-EP (HEPES 0.01 M pH 7.4 con NaCl 0.15 M, EDTA 3 mM y 0.005% v/v de tensioactivo P20, GE Healthcare). La dilución elegida fue una la cual, cuando se inyectó como se describe más adelante, dio como resultado >80% de la RU enlazada posible, máxima, para el inhibidor particular, típicamente 1 - 10 µM. En seguida, se preparó una mezcla del mismo dAb o Fab que se describe anteriormente (a la misma concentración final) con

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un segundo dAb o Fab que iba a ser analizado para competencia. Se utilizó la función COINJECT del instrumento para inyectar 60 μ l de la dilución del inhibidor simple a través de las celdas de flujo inmovilizadas con CD40 y de referencia, en serie, seguido inmediatamente por una inyección de 60 μ l de la mezcla de dos inhibidores. La sustracción en línea de la señal proveniente de la celda de referencia fue realizada por el software de control del instrumento. El experimento fue realizado a 25°C y a una velocidad de flujo de 30 μ l/min de HBS-EP. Después de que cada co-inyección había sido terminada, los inhibidores se dejaron disociar del ligando en el amortiguador por 60 segundos antes de la regeneración con una inyección de 10 μ l de glicina 10 mM pH 2.0. La RU máxima obtenida para la segunda inyección (la mezcla de los dos inhibidores) se anotó y fue expresada como un porcentaje de la RU obtenida para el mismo inhibidor cuando se inyectó solo.

Si el segundo inhibidor conservada al menos 100% de la RU usualmente enlazada cuando se inyectó solo, entonces esto implicó que los dos inhibidores se enlazaran a epítomos discretos. Si menos del 100% de enlace del segundo inhibidor fue observado, entonces esto fue indicador de la competencia entre los dos inhibidores para el enlace a CD40. Existieron varias posibles razones para esta competencia: los dos inhibidores pueden reticularse al mismo o a epítomos

traslapados, puede existir inhibición estérica del enlace, o el enlace del primer inhibidor puede inducir un cambio conformacional en el antígeno, lo cual previene o reduce el enlace del segundo inhibidor.

5 Un clon ejemplar proveniente de cada línea (excepto BMS3h-217) fue probado para la competencia con otros dAbs en los grupos traslapados. Todos los dAbs probados parecen competir uno con el otro para el enlace a CD40, como se muestra en las TABLAS 13 y 14. Estos datos sugieren que
10 todos los polipéptidos anticuerpos seleccionados del grupo que consiste de las líneas BMS3h-37, BMS3h-38, BMS3h-41, BMS3h-43, BMS3h-56, BMS3h-131, BMS3h-198, y BMS3h-202 deben competir con el enlace de un dAb proveniente de cualquiera de estas líneas al CD40 humano.

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TABLA 13**BIAcore^{MR} de competencia:**

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Primera Inyección	RU primer dAb solo	Segunda Inyección (% RU de dAb simple)				
		<i>BMS3h-56-5</i>	<i>BMS3h-37-11</i>	<i>BMS3h-131-2</i>	<i>BMS3h-198-1</i>	<i>BMS3h-202-11</i>
<i>BMS3h-56-5</i>	245		-15	17	0.6	7.3
<i>BMS3h-37-11</i>	158	15		25	16	0.3
<i>BMS3h-131-2</i>	220	22	-3.7		23.2	10.3

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<i>BMS3h-198-1</i>	176	28	6.4	41		18
<i>BMS3h-202-11</i>	124	50	42	57	39	

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TABLA 14

Primera Inyección	RU primer dAb solo	Segunda Inyección (% RU de dAb simple)			
		<i>BMS3h-38-2</i>	<i>BMS3h-41-9</i>	<i>BMS3h-43-1</i>	<i>BMS3h-56-5</i>
<i>BMS3h-38-2</i>	170		11	29	29
<i>BMS3h-41-9</i>	150	27		44	47
<i>BMS3h-43-1</i>	210	20	19		39
<i>BMS3h-56-5</i>	190	4	0	22	

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Similarmente, fueron probados diversos dAbs para la competencia con Fab' de Chi220, como se muestra en las TABLAS 15 y 16. En este caso, todos los dAbs no compiten con el Fab' de Chi220, excepto BMS3h-217, el cual muestra competencia. Los dAbs BMS3h-56-5 y BMS3h-193-12 se enlazaron con al menos 100% de la RU de dAb simple en presencia de Fab' de Chi220 G28-5 enlazado, sugiriendo que los Fab's se enlazan a uno o varios epítomos diferentes de los dAbs. El Fab' de

Chi220 mostró una reducción de RU enlazada en presencia de G28-5. El mismo resultado fue observado en el orden opuesto de enlace. Esto sugiere que Fab' G28-5 se enlaza al mismo epítipo que Fab' de Chi220.

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TABLA 15

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Primera Inyección	RU primer dAb/Fab solo	Segunda Inyección (% de RU de dAb/Fab simple)			
		<i>BMS3h-56-5</i>	<i>Chi220 Fab</i>	<i>G28-5 Fab</i>	<i>BMS3h-193-12</i>
<i>BMS3h-56-5</i>	193		98	94	64
<i>Chi220 Fab</i>	1089	105		11	109
<i>G28-5 Fab</i>	730	125	39		116
<i>BMS3h-193-12</i>	282	44	98	93	

TABLA 16

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Nombre del Clon	μM de dAb o Fab probado	RU de dAb simple	% de RU de dAb simple (Chi220+dAb)
BMS3h-38-2	5	156	121
BMS3h-41-13	5	162	109
BMS3h-43-3	5	300	101
BMS3h-38-2	5	175	114

BMS3h-56-5	5	193	105
BMS3h-106	10	165	111
BMS3h-107	10	35	146
BMS3h-129	10	156	121
BMS3h-193-12	5	282	98
BMS3h-197	1	177	116
BMS3h-217	10	85	25
G28-5 Fab	1	730	11

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Ejemplo 6

Ensayos de Actividad de CD40

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Los dAbs anti-CD40 humanos fueron evaluados funcionalmente para su habilidad de antagonizar las actividades de CD40. Las actividades de CD40 probadas fueron la proliferación de células B y la producción de citocina por la activación promovida por hCD40L de las células dendríticas derivadas de monocitos humanos primarios (DCs). A no ser que se indique de otro modo, todos los ensayos fueron realizados en el medio RPMI suplementado con 10% de suero fetal de ternera (FCS). Los resultados utilizando los diversos ensayos se muestran en la TABLA 17.

Proliferación de células B humanas primarias, promovida por IZ-hCD40L soluble:

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1×10^5 células B humanas tonsilares fueron incubadas

con 0.6 µg/ml de IZ-hCD40L junto con titulaciones variantes del polipéptido anticuerpo en un volumen final de 200 µl/pozo en una placa de fondo redondo de 96 pozos. Las placas fueron incubadas a 37°C por 72 horas, luego se agregó timidina (³H; 5 0.5 µci/pozo) por 6 horas. La proliferación de células B fue cuantificada con base en la incorporación de la timidina.

Proliferación de células B humanas primarias, promovida por CHO-hCD40L:

Las células CHO fueron transfectadas con CD40L 10 humano para generar una línea celular estable que expresa altos niveles de CD40L sobre la superficie celular. Las células CHO-CD40L fueron irradiadas a 10,000 Rads antes de la incubación con las células B humanas. 1x10⁵ células B humanas tonsilares fueron incubadas con 1x10³ células CHO- 15 CD40L (proporción 1:100 de CHO-CD40L: células B humanas) junto con titulaciones variantes del polipéptido anticuerpo en un volumen final de 200 µl/pozo en una placa de fondo redondo de 96 pozos. Las placas fueron incubadas a 37°C por 72 horas después de lo cual se agregó ³H-timidina (0.5 20 µci/pozo) por 6 horas. La proliferación de células B fue cuantificada con base en la incorporación de timidina.

Proliferación de células B humanas esplénicas cyno, promovida por IZ-hCD40L soluble:

1x10⁵ células B esplénicas cyno fueron incubadas 25 con 0.5 µg/ml de IZ-hCD40L junto con titulaciones variantes

de polipéptido anticuerpo en un volumen final de 200 µl/pozo en una placa de fondo redondo de 96 pozos. Las placas fueron incubadas a 37°C por 72 horas después de lo cual se agregó ³H-timidina (0.5 µci/pozo) por 6 horas. La proliferación de
5 células B fue cuantificada con base en la incorporación de timidina.

Proliferación de células B humanas, promovida por células B primarias:

Las células T fueron aisladas de células
10 mononucleares de sangre periférica humana (PBMC) y enriquecidas utilizando rosetas de células sanguíneas rojas de oveja (SRBC). Las células B tonsilares humanas fueron aisladas mediante homogeneización del tejido tonsilar a una suspensión de células simples. Los leucocitos fueron
15 obtenidos mediante separación por Ficoll, luego las células B fueron negativamente seleccionadas utilizando formación de rosetas de SRBC y enriquecidas mediante descarte de las células en rosetas.

Las células T humanas enriquecidas fueron
20 cultivadas con PM-LCLs (un línea de células B transformadas por EBV; irradiada a 10,000 Rads) a una proporción 5:1 (T:LCL) por 6 días a 37°C para generar una población de células T alogénicas. En el día 6, las células T expandidas fueron aisladas e irradiadas a 3000 Rads, y luego cultivadas
25 (5×10^4 células T/pozo) con las células B tonsilares humanas

primarias (1×10^5 células B/pozo) a una proporción 1:2 en una placa de fondo plano de 96 pozos recubierta con el mAb anti-CD3 (OKT3). Titulaciones variantes de los polipéptidos anticuerpos fueron agregadas a cada pozo; el volumen final en
 5 cada pozo fue de 200 μ l. Las placas de prueba fueron incubadas a 37°C por 3 días. La proliferación de células B humanas fue determinada vía la adición de ^3H -timidina (0.5 μ ci/pozo) a los cultivos por al menos 18 horas.

Activación promovida por CHO-hCD40L de las células

10 ***dendríticas derivadas de monocitos humanos primarios (DCs):***

Las PBMCs humanas fueron enriquecidas para monocitos por agotamiento de las células T, vía la formación de rosetas de SRBC. Las PBMCs enriquecidas con monocitos fueron cultivadas con 10 ng/ml de GM-CSF y 5 ng/ml de IL-4 en
 15 placas de 6 pozos por 6 días a 37°C. Las placas cultivadas fueron reabastecidas con medio fresco (con GM-CSF e IL-4) en los días 2 y 5. Las células dendríticas inmaduras (DCs) fueron utilizadas en ensayos celulares en el día 6. 8×10^4 DCs inmaduras fueron cultivadas con 4×10^3 células CHO-hCD40L
 20 (irradiadas a 10,000 Rads) junto con titulaciones variantes de los polipéptidos anticuerpos en una placa de 96 pozos de fondo plano. Después de 24 horas, los sobrenadantes fueron cosechados y probados para la presencia de diversas citocinas (IL-12, TNF, IL-23). La activación de DC fue determinada por
 25 los niveles de producción de citocina.

TABLA 17

Clon	EC50 (nM) de la proliferación de células B humanas, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B Cyno, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B humanas, promovida por CHO- hCD40L-	EC50 (nM) de MLR de células T	EC50 (nM) de la IL-12 activación por DC promovida por CHO- hCD40L
3h-5	>7000		>7000		
3h-8	>7000		>7000		
3h-28	>7000		>7000		
3h-33	>7000		>7000		
3h-48	>7000		>7000		
3h-52	>7000		>7000		
3h-57	>7000		>7000		
3h-61	>7000		>7000		
3h-88	>7000				
3h-102	>7000				
3h-106	437.0 ± 214.0	>7000			
3h-107	>7000	>7000			

5	Clon	EC50 (nM) de la proliferación de células B humanas, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B Cyno, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B humanas, promovida por CHO- hCD40L-	EC50 (nM) de MLR de células T	EC50 (nM) de la IL-12 activación por DC promovida por CHO- hCD40L
10	3h-112	>7000				
	3h-129	2100.0 ± 1000.0				
	3h-197	360.0 ± 500.0	>7000			
15	3h-207	>7000				
	3h-208	>7000				
	3h-37	3400.0 ± 2900.0	>7000			
20	3h-37-1	250.0 ± 100.0				
	3h-37-2	5.0 ± 2.0	>7000		198 ± 35	13.0 ± 7.3
	3h-37- 202	0.6 ± 0.2			83 ± 18	10.0
25	3h-37-	2.0 ± 1.0				6.6

5	Clon	EC50 (nM) de la proliferación de células B humanas, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B Cyno, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B humanas, promovida por CHO- hCD40L-	EC50 (nM) de MLR de células T	EC50 (nM) de la IL-12 activación por DC promovida por CHO- hCD40L
10	205					
	3h-37- 206	5.0 ± 0.8				23.0
	3h-37- 207	4.0 ± 2.0				15.5 ± 8.0
15	3h-37- 212	1.0 ± 0.05				
	3h-37- 213	0.7 ± 0.2				
	3h-37-11	8.0 ± 7.0				
20	3h-38	2800.0 ± 400.0	>7000			
	3h-38-1	142.0 ± 86.0				
25	3h-38-2	10.0 ± 6.0	>7000	723.0 ± 185.0	986 ± 383	289.0 ± 315.0

5	Clon	EC50 (nM) de la proliferación de células B humanas, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B Cyno, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B humanas, promovida por CHO- hCD40L-	EC50 (nM) de MLR de células T	EC50 (nM) de la IL-12 activación por DC promovida por CHO- hCD40L
	3h-38- 201	>70.0		>7000		>800.0
10	3h-38- 205	4.0 ± 2.0		1100.0 ± 141.0		29.0
	3h-38- 211	2.0 ± 1.0		82.0 ± 4.0	200 ± 1	18.0 ± 19.0
15	3h-38- 215	1.0 ± 0.0		65.0 ± 1.0	163 ± 14	6.0 ± 4.0
	3h-38- 217	0.8 ± 0.2		34.0 ± 6.0	74 ± 22	1.7 ± 0.4
20	3h-38- 219	2.0 ± 0.5		93.0 ± 26.0	164 ± 3	9.0 ± 5.0
	3h-38- 228	0.7 ± 0.05				
25	3h-38-	0.66 ± 0.2				

5	Clon	EC50 (nM) de la proliferación de células B humanas, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B Cyno, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B humanas, promovida por CHO- hCD40L-	EC50 (nM) de MLR de células T	EC50 (nM) de la IL-12 activación por DC promovida por CHO- hCD40L
10	231					
	3h-38- 235	0.4 ± 0.2				
	3h-38- 237	0.4 ± 0.2				
15	3h-38- 238	0.7 ± 0.03				
	3h-38-3	10.0 ± 7.0				
	3h-41	>7000				
	3h-41-1	104.0 ± 56.0				
20	3h-41-2	47.0 ± 67.0				
	3h-41-3	12.0 ± 7.0	>7000			
	3h-41-9	148.0 ± 98.0				
	3h-41-12	104.0 ± 50.0				
25	3h-41-13	208.0 ± 90.0				

5	Clon	EC50 (nM) de la proliferación de células B humanas, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B Cyno, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B humanas, promovida por CHO- hCD40L-	EC50 (nM) de MLR de células T	EC50 (nM) de la IL-12 activación por DC promovida por CHO- hCD40L
10	3h-43	83.0 ± 40.0	>7000			
	3h-43-1	53.0 ± 20.0				
	3h-43-3	87.0 ± 19.0				
	3h-43-5	180.0 ± 130.0				
15	3h-43-10	143.0 ± 131.0				
	3h-43-11	30.0 ± 19.0				
	3h-43-12	12.0 ± 6.0				
20	3h-56	713.0 ± 133.0	>7000			
	3h-56-1	7.0 ± 5.0				
	3h-56-2	3.0 ± 1.0		326.0 ± 79.0	276 ± 29	444.0, >2000.0
25	3h-56-	0.12 ± 0.04		11.0 ± 6.0	7.25 ± 0.96	0.93 ± 0.7

5	Clon	EC50 (nM) de la proliferación de células B humanas, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B Cyno, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B humanas, promovida por CHO- hCD40L-	EC50 (nM) de MLR de células T	EC50 (nM) de la IL-12 activación por DC promovida por CHO- hCD40L
10	201					
	3h-56- 202	0.6 ± 0.2		39.0 ± 16.0	50 ± 9.8	2.9 ± 2.6
	3h-56- 203	0.45 ± 0.1		51.0 ± 29.0	52 ± 23	3.7 ± 4.0
15	3h-56- 206	0.1 ± 0.01		6.0 ± 2.0	5.25 ± 0.5	0.7± 0.4
	3h-56- 215	0.2 ± 0.03		41.0 ± 15.0	31 ± 7	11.0± 12.0
20	3h-56- 217	0.1 ± 0.04		13.0 ± 5.0	16 ± 6.7	9.4 ± 8.0
	3h-56- 224	0.5 ± 0.2		26.0 ± 5.0	47 ± 11	18.0 ± 22.0
	3h-56- 232	0.27 ± 0.1		37.0 ± 0.7	42 ± 10	7.3 ± 6.6

5	Clon	EC50 (nM) de la proliferación de células B humanas, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B Cyno, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B humanas, promovida por CHO- hCD40L-	EC50 (nM) de MLR de células T	EC50 (nM) de la IL-12 activación por DC promovida por CHO- hCD40L
10	3h-56- 239	0.11 ± 0.0		18.0 ± 4.0	13.5 ± 4.76	5.8 ± 6.5
	3h-56- 243	0.15 ± 0.007		13.5 ± 2.0	14.2 ± 4.6	8.8 ± 10.0
15	3h-56- 244	0.17 ± 0.02		26.0 ± 3.0	21 ± 4.1	12.6 ± 16.0
	3h-56- 246	0.24 ± 0.06		34.0 ± 14.0	23.8 ± 6.2	23.2 ± 22.0
	3h-56- 248	0.36 ± 0.1				
20	3h-56- 253	0.4 ± 0.2				
	3h-56- 258	0.079 ± 0.003		11.0 ± 3.0	8.7 ± 1.9	1.52 ± 1.6
25	3h-56-	0.17 ± 0.09		25.5 ± 6.0	17 ± 5.4	3.0 ± 1.8

5	Clon	EC50 (nM) de la proliferación de células B humanas, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B Cyno, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B humanas, promovida por CHO- hCD40L-	EC50 (nM) de MLR de células T	EC50 (nM) de la IL-12 activación por DC promovida por CHO- hCD40L
10	261					
	3h-56- 262	0.31 ± 0.007				
	3h-56- 265	0.36 ± 0.06				
15	3h-56- 266	0.19 ± 0.04		19.5 ± 6.0	13.8 ± 2.4	2.8 ± 2.3
	3h-56- 269	0.14 ± 0.02		15.0 ± 5.0	9.7 ± 1.9	1.8 ± 1.2
20	3h-56- 270	0.31 ± 0.1				
	3h-56-5	6.0 ± 4.0	>7000			
	3h-56-6	4.0 ± 3.0				
	3h-56-7	8.0 ± 6.0				
25	3h-56-8	5.0 ± 2.0				

5	Clon	EC50 (nM) de la proliferación de células B humanas, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B Cyno, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B humanas, promovida por CHO- hCD40L-	EC50 (nM) de MLR de células T	EC50 (nM) de la IL-12 activación por DC promovida por CHO- hCD40L
10	3h-56-9	3.0 ± 0.6				
	3h-56-15	2.0 ± 0.9				
	3h-56-19	3.0 ± 2.0				
	3h-56-21	2.0 ± 1.0				
15	3h-131	2700.0 ± 1000.0	>7000			
	3h-131-2	55.0 ± 53.0	>7000			
	3h-131-6	141.0 ± 37.0				
	3h-131- 14	24.0 ± 4.0				
20	3h-193	>7000				
	3h-193- 12	277.0 ± 167.0				
	3h-193- 16	387.0 ± 173.0				

5	Clon	EC50 (nM) de la proliferación de células B humanas, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B Cyno, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B humanas, promovida por CHO- hCD40L-	EC50 (nM) de MLR de células T	EC50 (nM) de la IL-12 activación por DC promovida por CHO- hCD40L
10	3h-193- 19	233.0 ± 110.0				
	3h-193- 25	303.0 ± 214.0	2200.0 ± 1200.0			
15	3h-193- 29	1380.0 ± 721.0				
	3h-198	554.0 ± 186.0	>7000			
	3h-198-1	64.0 ± 47.0				
20	3h-198-2	207.0 ± 158.0				
	3h-198-5	9.0 ± 6.0				
	3h-198- 19	19.0 ± 14.0				
25	3h-198-	34.0 ± 37.0				

5	Clon	EC50 (nM) de la proliferación de células B humanas, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B Cyno, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B humanas, promovida por CHO- hCD40L-	EC50 (nM) de MLR de células T	EC50 (nM) de la IL-12 activación por DC promovida por CHO- hCD40L
10	24					
	3h-198- 28	20.0 ± 9.0				
	3h-202	6400.0 ± 1300.0	>7000			
15	3h-202-1	192.0 ± 77.0	>7000			
	3h-202-5	6500.0 ± 1000.0				
	3h-202- 10	289.0 ± 158.0				
20	3h-202- 11	201.0 ± 103.0				
	3h-217	3200.0 ± 2030.0	>7000, 5300, 1690			
25	3h-217-1	45.0 ± 26.0	35.0 ± 8.0			

5	Clon	EC50 (nM) de la proliferación de células B humanas, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B Cyno, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B humanas, promovida por CHO- hCD40L-	EC50 (nM) de MLR de células T	EC50 (nM) de la IL-12 activación por DC promovida por CHO- hCD40L
10	3h-217-2	8.0 ± 4.0	7.0			335.0
	3h-217-4	61.0 ± 20.0	27.0			
	3h-217-5	13.0 ± 5.0	15.0			
	3h-217-6	11.0 ± 3.0	10.0			
	3h-217-7	220.0 ± 20.0				
15	3h-217-8	33.0 ± 10.0	14.0			
	3h-217-9	380.0 ± 170.0				
	3h-217-14	26.0 ± 10.0	8.0			
20	3h-217-15	47.0 ± 21.0	20.0			
	3h-217-16	5.0 ± 2.0	7.0			1125.0
25	3h-217-	1950.0 ±				

5	Clon	EC50 (nM) de la proliferación de células B humanas, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B Cyno, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B humanas, promovida por CHO- hCD40L-	EC50 (nM) de MLR de células T	EC50 (nM) de la IL-12 activación por DC promovida por CHO- hCD40L
10	17	110.0				
	3h-217- 23	16.0 ± 6.0	15.0			
	3h-217- 2305	11.0 ± 4.0				
15	3h-217- 30	80.0 ± 9.0				>7700
	3h-217- 31	>700.0				
20	3h-231	328.0 ± 144.0	>7000			
	3h-233	184.0 ± 75.0	>7000			1492.0, >2000
	3h-240	>7000	>7000			
25	3h-242	219.0 ± 53.0	435.0 ± 62.0			2050.0

5	Clon	EC50 (nM) de la proliferación de células B humanas, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B Cyno, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B humanas, promovida por CHO- hCD40L-	EC50 (nM) de MLR de células T	EC50 (nM) de la IL-12 activación por DC promovida por CHO- hCD40L
10	3h-257	135.0 ± 28.0	>7000			704.0 ± 445.0
	3h-262	548.0 ± 121.0	>700			998.0
	3h-263	>700.0	>700			
15	3h-264	1200.0 ± 400.0	>7000			>2000
	3h-265	2400.0 ± 1000.0	>7000			>2000
	3h-271	295.0 ± 92.0	446.0			>2000
20	3h-274	1200, >7000	>7000			
	3h-275	157.0 ± 11.0	>7000			
	3h-285	49.0 ± 0.7	155.0			
25	3h-287	287.0 ± 156.0	918.0			

Clon	EC50 (nM) de la proliferación de células B humanas, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B Cyno, promovida por hIZCD40L	EC50 (nM) de la proliferación de células B humanas, promovida por CHO- hCD40L-	EC50 (nM) de MLR de células T	EC50 (nM) de la IL-12 activación por DC promovida por CHO- hCD40L
3h-289	2300.0 ± 1200.0	4300.0			
3h-290	>7000	5650.0			
3h-294	>7000	>7000			
3h-295	>7000	>7000			
3h-296	306.0 ± 55.0	>7000			
3h-309	648.0 ± 268.0	838.0			
3h-312	1100.0 ± 346.0	>7000			

Ejemplo 7

dAbs específicos dobles que se enlazan a CD40 y a la Albúmina Sérica

Los dAbs específicos dobles que se enlazan
específicamente a CD40 y a la albúmina sérica humana (HSA) o

albúmina sérica de cynomolgus (CSA) fueron contruidos y probados para la actividad en ensayos basados en células. Los dAbs específicos de albúmina son llamados "AlbudAbs." En este ejemplo, las fusiones AlbudAb comprenden un dAb BMS3h
 5 que se enlaza a CD40 o a otro anticuerpo de dominio, DOM7h, que reconoce HSA. Los dos dAbs son fusionados intraestructuralmente a los extremos amino y carboxilo de un ligador de aminoácidos para formar un polipéptido de fusión en línea (ILF). El polipéptido de ILF es expresado
 10 recombinantemente como una proteína de fusión simple. Los RBAs que demuestran actividad de los ILFs AlbudAb son descritos más adelante, y los resultados se muestran en la TABLA 18. La TABLA 19 resumen las secuencias ligadoras utilizadas en los ILFs AlbudAb probados. Los datos de enlace
 15 cinético determinados por el ensayo BIAcore^{MR} se muestran en la TABLA 20.

ELISA de células CD40-CHO para la detección de los dAbs en un sobrenadante:

Las células CHO-DG44 que expresan CD40 humano,
 20 establemente transfectadas, o las células CHO-DG44 nativas (ambas BMS) fueron desprendidas de los matraces de cultivo celular utilizando EDTA tripsinizado a 0.25%, y 100,000 células por pozo fueron sembradas en el medio de crecimiento dentro de las placas tratadas de cultivo de tejido de 96
 25 pozos (NUNC). Las células se dejaron adherir toda la noche

en una atmósfera humidificada a 37°C, con 5% de CO₂. En el día del ensayo, la lámina celular fue lavada con PBS antes de ser fijada con 2% de paraformaldehído (Sigma-Aldrich) por 20 minutos. Después de la fijación, la lámina celular fue
5 nuevamente lavada en PBS antes de un paso de bloqueo de 1 hora con suero fetal bovino al 15% (FBS, PAA) en PBS. Las placas fueron lavadas una vez más antes de la adición de 100 µl/pozo del sobrenadante del dAb e incubadas por 2 horas a temperatura ambiente. Después de la incubación de los
10 sobrenadantes de dAb con células, las placas fueron lavadas y el enlace del dAb fue detectado con incubación de la anti-proteína A o L conjugada a peroxidasa de rábano (HRP), dependiendo de si los dAbs son dominios de V_H o V_L. La señal de absorbancia fue medida utilizando un lector de placas
15 SpectraMax M5^e (Molecular Devices) a 450 nm después de la neutralización con HCl 1 M.

Ensayo celular de suprarregulación de ICAM-1:

Las células COS que expresan CD40L humano, establemente transfectadas, fueron desprendidas de los
20 matraces de cultivo celular utilizando Versene (Invitrogen). 20,000 células por pozo fueron sembradas dentro de las placas de fondo claro, de pared negra Highbind de 96 pozos, (Corning, Reino Unido) en amortiguador de ensayo (RPMI 1640 sin rojo de fenol (Sigma-Aldrich, Reino Unido) + 1% de
25 penicilina/estreptomicina + 10% de FBS Gold (ambos de PAA

Laboratories, Reino Unido). Las células se dejaron adherir toda la noche en una atmósfera humidificada a 37°C con 5% de CO₂. Al siguiente día, el amortiguador de ensayo agotado que no contenía células adheridas fue reabastecido con 100 µl de amortiguador de ensayo fresco. A éste se agregaron 20,000 células RAMOS/pozo en amortiguador de ensayo en adición a un intervalo de dilución de dAb. La placa de ensayo fue regresada a la atmósfera humidificada a 37°C con 5% de CO₂ por 24 horas. Para los pozos control negativo, no fueron agregadas células RAMOS. La habilidad del dAb para inhibir la suprarregulación de ICAM-1 sobre la superficie celular de células RAMOS, en respuesta a la exposición a CD40L sobre la superficie celular de las células COS, fue evaluada por la adición de 0.5 µg/ml del anticuerpo de ratón anti-ICAM-1 humano (R&D Systems) y 0.2 µg/ml de anticuerpo de cabra anti-ratón ALEXA flour 647 (Invitrogen, Molecular probes, Reino Unido). Después de un periodo de incubación de 3 horas en ausencia de luz, se detectó la fluorescencia relativa, medida por la plataforma de detección celular AB8200 (Applied Biosystems).

Análisis de la cinética de fusión en línea (ILF) del enlace a la albúmina sérica:

Se utilizó un instrumento BIAcore^{MR} 3000 (GE Healthcare) para analizar la cinética de enlace de los ILFs anti-CD40-AlbudAb a la albúmina sérica humana y de

cynomolgus. Aproximadamente 400 unidades de respuesta (RU) de la albúmina sérica humana (HSA) o de la albúmina sérica del cynomolgus (CSA) fueron inmovilizadas sobre una celda de flujo de un chip BIAcore^{MR} CM5 utilizando un kit de
5 acoplamiento de amina (Amine Coupling Kit) (GE Healthcare). Una segunda celda de flujo sin ningún ligando inmovilizado sirvió como una celda de flujo de referencia para la referencia en línea. Una serie apropiada de diluciones duplicadas de cada dAb que iba a ser analizado se preparó en
10 amortiguador HBS-EP (HEPES 0.01 M pH 7.4 con NaCl 0.15 M, EDTA 3 mM y 0.005% v/v de tensioactivo P20, GE Healthcare). Doscientos microlitros de cada ILF fueron inyectados por duplicado utilizando la función KINJECT del instrumento. Las inyecciones fueron realizadas a través de las celdas de
15 flujo inmovilizadas con albúmina sérica y de referencia, en serie, con sustracción en línea de la señal proveniente de la celda de referencia. El experimento fue realizado a 25°C y a una velocidad de flujo de 40 µl/min de HBS-EP. Después de que cada inyección había sido terminada, el dAb se dejó
20 disociar del ligando en amortiguador por 120 segundos antes de la regeneración con una inyección de 10 µl de glicina 10 mM de pH 2.0. Una inyección de referencia del testigo amortiguador HBS-EP (que no contenía analito) fue también inyectada bajo las mismas condiciones para servir como una
25 segunda referencia para la sustracción de cada trazo de

analito. Se utilizó el software BIAevaluation 4.1 (GE Healthcare) para sustraer el trazo de la celda de flujo de referencia y el trazo del testigo amortiguador de cada trazo de analito. Se utilizó el mismo software para realizar un
 5 ajuste global simultáneo de un modelo cinético 1:1 (Langmuir) a las fases de asociación y disociación de los trazos en serie de diluciones de analito. Este modelo produjo las constantes de velocidad de asociación y disociación (k_a y k_d , respectivamente) y la constante de disociación en equilibrio
 10 (K_D) de la interacción. Los valores paramétricos se muestran en la TABLA 20.

TABLA 18

DMS No.	dAb de extremo N	Ligador	dAb de extremo C	EC ₅₀ (nM) de RBA de células CHO-CD40		EC ₅₀ (nM) del ensayo de células ICAM-1	
				0.1% BSA	50 μ M HSA	10% de suero bovino	10% de suero humano
DMS0654	BMS3h-56-201	AST	DOM7h-11-3	15	8.6		
DMS0655	BMS3h-56-201	AST	DOM7h-11-87	6.3	2.7		
DMS0656	BMS3h-56-258	AST	DOM7h-11-3	11.8	26.8		
DMS0657	BMS3h-56-258	AST	DOM7h-11-87	6.8	16.6		
DMS0658	DOM7h-11-3	TVAAPS	BMS3h-56-201	12.2	9.1		
DMS0659	DOM7h-11-87	TVAAPS	BMS3h-56-201	7.2	3.3		
DMS0660	DOM7h-11-3	TVAAPS	BMS3h-56-258	21.8	13.1		
DMS0661	DOM7h-11-87	TVAAPS	BMS3h-56-258	4.1	5.7		
DMS0662	DOM7h-11-90	TVAAPS	BMS3h-56-201			33.5	>1000

DMS No.	dAb de extremo N	Ligador	dAb de extremo C	EC ₅₀ (nM) de RBA de células CHO-CD40		EC ₅₀ (nM) del ensayo de células ICAM-1	
				0.1% BSA	50 µM HSA	10% de suero bovino	10% de suero humano
DMS0663	DOM7h-11-86	TVAAPS	BMS3h-56-201			21.4	>1000
DMS0664	DOM7h-11-69	TVAAPS	BMS3h-56-201			16.5	>1000
DMS0677	DOM7h-11-90	TVA	BMS3h-56-258			21.7	20.35
DMS0679	DOM7h-11-90	G ₄ S	BMS3h-56-258			21.7	39.2
DMS0680	DOM7h-11-90	(G ₄ S) ₃	BMS3h-56-258			39.3	74.2
DMS0681	DOM7h-11-90	(G ₄ S) ₅	BMS3h-56-258			43.6	53.3
DMS0682	BMS3h-56-258	TVA	DOM7h-11-90			10.2	94.8
DMS0683	BMS3h-56-258	ASTSGPS	DOM7h-11-90			32.4	50.9
DMS0684	BMS3h-56-258	G ₄ S	DOM7h-11-90			37.9	74.3
DMS0685	BMS3h-56-258	(G ₄ S) ₃	DOM7h-11-90			31.9	62.4
DMS0686	BMS3h-56-258	(G ₄ S) ₅	DOM7h-11-90			48.3	66.6

TABLA 19

Secuencias Ligadoras Representativas

AST	SEQ ID NO: 5
TVAAPS	SEQ ID NO: 6
TVA	SEQ ID NO: 7
GGGGS	SEQ ID NO: 1207
(GGGGS) ₃	SEQ ID NO: 1208
(GGGGS) ₅	SEQ ID NO: 1209
ASTSGPS	SEQ ID NO: 8

TABLA 20
Análisis BIAcore^{MR}

DMS No.	dAb de extremo N	Ligador ("TVAAPS" descrito como SEQ ID NO: 6)	dAb de extremo C	Albúmina Sérica Humana			Albúmina Sérica de Cyno		
				k_a (1/Ms) $\times 10^{-6}$	k_d (1/s) $\times 10^3$	K_D (nM)	k_a (1/Ms) $\times 10^{-6}$	k_d (1/s) $\times 10^3$	K_D (nM)
DMS 0659	DOM7h-11- 87	TVAAPS	BMS3h-56- 201	0.85, 2.85, 2.6	1.17, 1.69, 1.2	1.37, 0.60, 0.45	0.85, 2.79, 2.9	2.37, 3.37, 2.4	2.79, 1.21, 0.83
DMS 0662	DOM7h-11- 90	TVAAPS	BMS3h-56- 201	1.1, 1.19	1.33, 1.47	1.21, 1.23	1.01, 1.10	2.52, 2.66	2.5, 2.42
DMS 0663	DOM7h-11- 86	TVAAPS	BMS3h-56- 201	1.25, 1.32	1.40, 1.60	1.12, 1.21	1.18, 1.18	2.81, 2.96	2.38, 2.52
DMS 0664	DOM7h-11- 69	TVAAPS	BMS3h-56- 201	2.5, 0.93	1.42, 1.49	0.57, 1.59	2.51, 0.92	2.73, 2.72	1.09, 2.97

La TABLA 21 lista secuencias de aminoácidos de los ILFs de AlbuAb representativos que pueden reticularse específicamente a CD40 y a HSA o CSA. La designación de cada ILF identifica la secuencia ligadora particular: "GxS" significa que el ligador tiene "x" residuos de glicina seguidos por serina, y "(GxS)y" significa que el ligador tiene y unidades repetidas de GxS. La TABLA 22 describe los ácidos nucleicos representativos que codifican para las secuencias de ILF listadas en la TABLA 21. Como es conocido en la técnica, múltiples codones pueden codificar para el mismo aminoácido. Los ácidos nucleicos que codifican para una secuencia de proteína incluyen de este modo ácidos

nucleicos que tiene degeneración de codón.

TABLA 21

Secuencias de Aminoácidos de dAb de Especificidad Doble

(La Tabla 21 describe "AST," "TVAAPS," "TVA,"

5 "G4S," "(G4S)3," "(G4S)5," y "ASTSGPS" descritas como SEQ ID Nos.: 5-7, 1207-1209 y 8, respectivamente)

DMS0654 BMS3h-56-201-AST-DOM7h-11-3

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSV

KGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFQEWGQGTLVTVSSASTDIQMTQSPS

10 SLSASVGDRVTITCRASRPIGTTL SWYQQKPGKAPKLLILWNSRLQSGVPSRFSGSGSGTDFTL
TISSLQPEDFATYYCAQAGTHPTTFGQGTKVEIKR (SEQ ID NO: 1210)

DMS0655 BMS3h-56-201-AST-DOM7h-11-87

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYA

DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFQEWGQGTLVTVSSASTDIQ

15 MTQSPSSLSASVGDRVTITCRASRPIGTML SWYQQKPGKAPKLLILAFSRLQSGVPSRFSG
SGSGTDFTLTISLQPEDFATYYCAQAGTHHTTFGQGTKVEIKR (SEQ ID NO:
1211)

DMS0656 BMS3h-56-258-AST-DOM7h-11-3

EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYA

20 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGTLVTVSSASTDIQ
MTQSPSSLSASVGDRVTITCRASRPIGTTL SWYQQKPGKAPKLLILWNSRLQSGVPSRFSG
SGSGTDFTLTISLQPEDFATYYCAQAGTHPTTFGQGTKVEIKR (SEQ ID NO:
1212)

DMS0657 BMS3h-56-258-AST-DOM7h-11-87

25 EVQLLESGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYA

DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGT LVT VSSASTDIQ
 MTQSPSSLSASVGDRVTITCRASRP IGTMLS WYQQKPGKAPKLLILAFSRLQSGVPSRFSG
 SGSGSGTDFTLTISS LQPEDFATYYCAQAGTHHTTFGQGTKVEIKR (SEQ ID NO:
 1213)

5 DMS0658 DOM7h-11-3-TVAAPS-BMS3h-56-201

DIQMTQSPSSLSASVGDRVTITCRASRP IGTMLS WYQQKPGKAPKLLILWNSRLQSGVPSR
 FSGSGSGTDFTLTISS LQPEDFATYYCAQAGTHPTTFGQGTKVEIKRTVAAPSEVQLLESG
 GGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFT
 ISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFQEWGQGT LVT VSS (SEQ ID NO:

10 1214)

DMS0659 DOM7h-11-87-TVAAPS-BMS3h-56-201

DIQMTQSPSSLSASVGDRVTITCRASRP IGTMLS WYQQKPGKAPKLLILAFSRLQSGVPSR
 FSGSGSGTDFTLTISS LQPEDFATYYCAQAGTHHTTFGQGTKVEIKRTVAAPSEVQLLESG
 GGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFT

15 ISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFQEWGQGT LVT VSS (SEQ ID NO:
 1215)

DMS0660 DOM7h-11-3-TVAAPS-BMS3h-56-258

DIQMTQSPSSLSASVGDRVTITCRASRP IGTMLS WYQQKPGKAPKLLILWNSRLQSGVPSR
 FSGSGSGTDFTLTISS LQPEDFATYYCAQAGTHPTTFGQGTKVEIKRTVAAPSEVQLLESG

20 GGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYADSVKGRFT
 ISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGT LVT VSS (SEQ ID NO:
 1216)

DMS0661 DOM7h-11-87-TVAAPS-BMS3h-56-258

DIQMTQSPSSLSASVGDRVTITCRASRP IGTMLS WYQQKPGKAPKLLILAFSRLQSGVPSR

25 FSGSGSGTDFTLTISS LQPEDFATYYCAQAGTHHTTFGQGTKVEIKRTVAAPSEVQLLESG

GGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPQGTRTTYADSVKGRFT
 ISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGTLLTVSS (SEQ ID NO:
 1217)

DMS0662 DOM7h-11-90-TVAAPS-BMS3h-56-201

5 DIQMTQSPSSLSASVGDRVTITCRASRPITMLSWYQQKPGKAPKLLILAFSRLQSGVPSR
 FSGSGSGTDFTLTISNLPEDFATYYCAQAGTHPTTFGQGTKVEIKRTVAAPSEVQLLESG
 GGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPQGTRTTYADSVKGRFT
 ISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFYFQEWGQGTLLTVSS (SEQ ID NO:
 1218)

10 DMS0663 DOM7h-11-86-TVAAPS-BMS3h-56-201

DIQMTQSPSSLSASVGDRVTITCRASRPITMLSWYQQKPGKAPKLLILAFSRLQSGVPSR
 FSGSGSGTDFTLTISNLPEDVATYYCAQAGTHPTTFGQGTKVEIKRTVAAPSEVQLLESG
 GGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPQGTRTTYADSVKGRFT
 ISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFYFQEWGQGTLLTVSS (SEQ ID NO:

15 1219)

DMS0664 DOM7h-11-69-TVAAPS-BMS3h-56-201

DIQMTQSPSSLSASVGDRVTITCRASRPITMLSWYQQKPGKAPKLLILAFSRLQSGVPSR
 FSGSGSGTDFTLTISNLPEDFATYYCAQAGVHPTTFGQGTKVEIKRTVAAPSEVQLLESG
 GGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERSAINPQGTRTTYADSVKGRFT

20 ISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFYFQEWGQGTLLTVSS (SEQ ID NO:
 1220)

DMS0667 DOM7h-11-3-TVAAPS-BMS3h-38-240

DIQMTQSPSSLSASVGDRVTITCRASRPITMLSWYQQKPGKAPKLLILWNSRLQSGVPSR
 FSGSGSGTDFTLTISNLPEDFATYYCAQAGTHPTTFGQGTKVEIKRTVAAPSEVQLLESG

25 GGLVQPGGSLRLSCAASGFTFEEEMIWVRQAPGKGLEWVSAISRNGYSTYYADSVKGRFT

ISRDNSKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ ID NO:
1221)

DMS0668 BMS3h-38-240-AST-DOM7h-11-3

EVQLLES GGGGLVQPGGSLRLSCAASGFTFE EEEEMIWVRQAPGKGLEWVSAISRNGYSTYYA

5 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSSASTDIQ
MTQSPSSLSASVGDRVTITCRASRP IGTTL SWYQQKPGKAPKLLILWNSRLQSGVPSRFSG
SGSGTDFTLTISSLQPEDFATYYCAQAGTHPTTFGQGTKVEIKR (SEQ ID NO:
1222)

DMS0669 DOM7h-14-10-TVAAPS-BMS3h-38-240

10 DIQMTQSPSSLSASVGDRVTITCRASQWIGS QLSWYQQKPGKAPKLLIMWRSSLQSGVPSR
FSGSGSGTDFTLTISSLQPEDFATYYCAQGLRHPKTFGQGTKVEIKRTVAAPSEVQLLES G
GGGLVQPGGSLRLSCAASGFTFE EEEEMIWVRQAPGKGLEWVSAISRNGYSTYYADSVKGRFT
ISRDNSKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSS (SEQ ID NO:
1223)

15 DMS0670 BMS3h-38-240-AST-DOM7h-14-10

EVQLLES GGGGLVQPGGSLRLSCAASGFTFE EEEEMIWVRQAPGKGLEWVSAISRNGYSTYYA

DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSSASTDIQ
MTQSPSSLSASVGDRVTITCRASQWIGS QLSWYQQKPGKAPKLLIMWRSSLQSGVPSRFSG
SGSGTDFTLTISSLQPEDFATYYCAQGLRHPKTFGQGTKVEIKR (SEQ ID NO:
20 1224)

DMS0671 BMS3h-38-235-AST-DOM7h-11-3

EVQLLAS GGGGLVQPGGSLRLSCAASGFTFE EEEEMIWVRQAPGKGLEWVSAISRNGYSTYYA

DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGTLVTVSSASTDIQ
MTQSPSSLSASVGDRVTITCRASRP IGTTL SWYQQKPGKAPKLLILWNSRLQSGVPSRFSG
25 SGSGTDFTLTISSLQPEDFATYYCAQAGTHPTTFGQGTKVEIKR (SEQ ID NO:

1225)

DMS0672 BMS3h-38-235-AST-DOM7h-11-90

EVQLLASGGGLVQPGGSLRLSCAASGFTFEEMIWVRQAPGKGLEWVSAISRNGYSTYYA

DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGT LVT VSSASTDIQ

5 MTQSPSSLSASVGDRV TITCRASRP IGTMLSWYQQKPGKAPKLLILAFSRLQSGVPSRFSG

SGSGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKR (SEQ ID NO:

1226)

DMS0674 DOM7h-11-3-TVAAPS-BMS3h-38-235

DIQMTQSPSSLSASVGDRV TITCRASRP IGTMLSWYQQKPGKAPKLLILWNSRLQSGVPSR

10 FSGSGSGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKRTVAAPSEVQLLASG

GGLVQPGGSLRLSCAASGFTFEEMIWVRQAPGKGLEWVSAISRNGYSTYYADSVKGRFT

ISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGT LVT VSS (SEQ ID NO:

1227)

DMS0675 DOM7h-11-90-TVAAPS-BMS3h-38-235

15 DIQMTQSPSSLSASVGDRV TITCRASRP IGTMLSWYQQKPGKAPKLLILAFSRLQSGVPSR

FSGSGSGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKRTVAAPSEVQLLASG

GGLVQPGGSLRLSCAASGFTFEEMIWVRQAPGKGLEWVSAISRNGYSTYYADSVKGRFT

ISRDN SKNTLYLQMNSLRAEDTAVYYCGKEPFRYDYWGQGT LVT VSS (SEQ ID NO:

1228)

20 DMS0677 DOM7h-11-90-TVA-BMS3h-56-258

DIQMTQSPSSLSASVGDRV TITCRASRP IGTMLSWYQQKPGKAPKLLILAFSRLQSGVPSR

FSGSGSGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKRTVAEVQLLESGGGL

VQPGGSLRLSCAASGFTFRDYEMWWVRQAPGGLERVSAINPQGTRTYADSVKGRFTISR

DN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGT LVT VSS (SEQ ID NO:

25 1229)

DMS0678 DOM7h-11-90-ASTSGPS-BMS3h-56-258

DIQMTQSPSSLSASVGDRVITITCRASRPIGTMLSWYQQKPGKAPKLLILAFSRLQSGVPSR
FSGSGSGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKRASTSGPSEVQLLES
GGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVKGRF

5 TISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGT LVTVSS (SEQ ID NO:
1230)

DMS0679 DOM7h-11-90-G4S-BMS3h-56-258

DIQMTQSPSSLSASVGDRVITITCRASRPIGTMLSWYQQKPGKAPKLLILAFSRLQSGVPSRFSG
SGSGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKRGGGGSEVQLLES GGGLVQPG

10 GSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYADSVKGRFTISRDN SKNT
LYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGT LVTVSS (SEQ ID NO: 1231)

DMS0680 DOM7h-11-90-(G4S)3-BMS3h-56-258

DIQMTQSPSSLSASVGDRVITITCRASRPIGTMLSWYQQKPGKAPKLLILAFSRLQSGVPSR
FSGSGSGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKRGGGGSGGGGSGGGG

15 SEVQLLES GGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTY
ADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGT LVTVSS (SEQ
ID NO: 1232)

DMS0681 DOM7h-11-90-(G4S)5-BMS3h-56-258

DIQMTQSPSSLSASVGDRVITITCRASRPIGTMLSWYQQKPGKAPKLLILAFSRLQSGVPSR
20 FSGSGSGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKRGGGGSGGGGSGGGG

SGGGGSGGGGSEVQLLES GGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSA
INPQGTRTTYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGT L
VTVSS (SEQ ID NO: 1233)

DMS0682 BMS3h-56-258-TVA-DOM7h-11-90

25 EVQLLES GGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTTYA

DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGT LVTVSSTVADIQ
 MTQSPSSLSASVGDRVTITCRASRP IGTMLSWYQQKPGKAPKLLILAFSRLQSGVPSRFSG
 SGSGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKR (SEQ ID NO:
 1234)

5 DMS0683 BMS3h-56-258-ASTSGPS-DOM7h-11-90

EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGT LVTVSSASTSGP
 SDIQMTQSPSSLSASVGDRVTITCRASRP IGTMLSWYQQKPGKAPKLLILAFSRLQSGVPS
 RFSGSGSGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKR (SEQ ID NO:
 10 1235)

DMS0684 BMS3h-56-258-G4S-DOM7h-11-90

EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGT LVTVSSGGGGSD
 IQMTQSPSSLSASVGDRVTITCRASRP IGTMLSWYQQKPGKAPKLLILAFSRLQSGVPSRF
 15 SGSGSGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKR (SEQ ID NO:
 1236)

DMS0685 BMS3h-56-258- (G4S) 3-DOM7h-11-90

EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGT LVTVSSGGGGSG
 20 GGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASRP IGTMLSWYQQKPGKAPKLLILAFS
 RLQSGVPSRFSGSGSGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKR (SEQ
 ID NO: 1237)

DMS0686 BMS3h-56-258- (G4S) 5-DOM7h-11-90

EVQLLES GGGGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYYA
 25 DSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGT LVTVSSGGGGSG

GGGSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASRPIGTMLSWYQQKPGK
 APKLLILAFSRLQSGVPSRFSGSGSGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTK
 VEIKR (SEQ ID NO: 1238)

DMS0688 DOM7h-11-90-TVAAPS-BMS3h-56-258

5 DIQMTQSPSSLSASVGDRVTITCRASRPIGTMLSWYQQKPGKAPKLLILAFSRLQSGVPSR
 FSGSGSGTDFTLTISNLQPEDFATYYCAQAGTHPTTFGQGTKVEIKRTVAAPSEVQLLESG
 GGLVQPGGSLRLSCAASGFTFRDYEMWWVRQAPGKGLERVSAINPQGTRTYADSVKGRFT
 ISRDNSKNTLYLQMNSLRAEDTAVYYCAKLPFYFHEWGQGLTVTVSS (SEQ ID NO:
 1239)

10

TABLA 22

Polinucleótidos que Codifican para dAbs de Especificidad

Doble

(La Tabla 22 describe "AST," "TVAAPS," "TVA,"
 "G4S," "(G4S)3," "(G4S)5," y "ASTSGPS" descritas como SEQ ID

15 Nos.: 5-7, 1207-1209 y 8, respectivamente)

DMS0654 BMS3h-56-201-AST-DOM7h-11-3

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 20 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAACTTCCG
 TTTTACTTTTCAGGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCGAC
 ATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACATC
 ACTTGCCGGGCAAGTCGTCCGATTGGGACGACGTTAAGTTGGTACCAGCAGAAACCAGGG
 AAAGCCCCTAAGCTCCTGATCCTTTGGAATTCCCGTTTGCAAAGTGGGGTCCCATCACGT
 25 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAA

GATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCCTACGACGTTTCGGCCAAGGG
ACCAAGGTGGAAATCAAACGG (SEQ ID NO: 1240)

DMS0655 BMS3h-56-201-AST-DOM7h-11-87

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GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCG
TTTTACTTTTCAGGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCGAC
ATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACATC
ACTTGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCAGGG
AAAGCCCCTAAGCTCCTGATCCTTGCTTTTTTCCCGTTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAA
GATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCATAACGACGTTTCGGCCAAGGG
ACCAAGGTGGAAATCAAACGG (SEQ ID NO: 1241)

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DMS0656 BMS3h-56-258-AST-DOM7h-11-3

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GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCG
TTTTACTTTTCAGGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCGAC
ATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACATC
ACTTGCCGGGCAAGTCGTCCGATTGGGACGACGTTAAGTTGGTACCAGCAGAAACCAGGG
AAAGCCCCTAAGCTCCTGATCCTTTGGAATTCCCGTTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAA

25

GATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCCTACGACGTTTCGGCCAAGGG
ACCAAGGTGGAAATCAAACGG (SEQ ID NO: 1242)

DMS0657 BMS3h-56-258-AST-DOM7h-11-87

5 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGTGCAGCCTCCGGATTACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCG
TTTTACTTTTACGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCGAC
10 ATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACATC
ACTTGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCAGGG
AAAGCCCCTAAGCTCCTGATCCTTGCTTTTTTCCCGTTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAA
GATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCATAACGACGTTTCGGCCAAGGG
ACCAAGGTGGAAATCAAACGG (SEQ ID NO: 1243)

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DMS0658 DOM7h-11-3-TVAAPS-BMS3h-56-201

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCGTCCGATTGGGACGACGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCCTTTGGAATTCCCGTTTGCAAAGTGGGGTCCCATCA
20 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCCTACGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCACCATCTGAGGTGCAGCTGTTGGAG
TCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGA
TTCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAG
CGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGC
25 CGGTTCAACATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTG

CGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTACTTTTCAGGAGTGG
GGTCAGGGAACCCCTGGTCACCGTCTCCAGC (SEQ ID NO: 1244)

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GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCCTAAGCTCCTGATCCTTGCTTTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCATAACGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCACCATCTGAGGTGCAGCTGTTGGAG
TCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGA
TTCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAG
CGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGC
CGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTG
CGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTACTTTTCAGGAGTGG
GGTCAGGGAACCCCTGGTCACCGTCTCCAGC (SEQ ID NO: 1245)

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DMS0660 DOM7h-11-3-TVAAPS-BMS3h-56-258

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GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCGTCCGATTGGGACGACGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCCTAAGCTCCTGATCCTTTGGAATTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCCTACGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCACCATCTGAGGTGCAGCTGTTGGAG
TCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGA
TTCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAG
CGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGC
CGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTG

25

CGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTACTTTACGAGTGG
GGTCAGGGAACCCTGGTCACCGTCTCCAGC (SEQ ID NO: 1246)

DMS0661 DOM7h-11-87-TVAAPS-BMS3h-56-258

5 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCCTAAGCTCCTGATCCTTGCTTTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCATAACGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCACCATCTGAGGTGCAGCTGTTGGAG
10 TCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGA
TTCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAG
CGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGC
CGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTG
CGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTACTTTACGAGTGG
GGTCAGGGAACCCTGGTCACCGTCTCCAGC (SEQ ID NO: 1247)

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DMS0662 DOM7h-11-90-TVAAPS-BMS3h-56-201

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCCTAAGCTCCTGATCCTTGCTTTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
20 GAAGATTTTGCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCACCATCTGAGGTGCAGCTGTTGGAG
TCCGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGA
TTCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAG
CGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGC
CGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTG
25

CGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTACTTTTCAGGAGTGG
GGTCAGGGAACCCTGGTCACCGTCTCCAGC (SEQ ID NO: 1248)

DMS0663 DOM7h-11-86-TVAAPS-BMS3h-56-201

5 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCCTAAGCTCCTGATCCTTGCTTTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATGTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCCTACGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCACCATCTGAGGTGCAGCTGTTGGAG
10 TCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGA
TTCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAG
CGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGC
CGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTG
CGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTACTTTTCAGGAGTGG
GGTCAGGGAACCCTGGTCACCGTCTCCAGC (SEQ ID NO: 1249)

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DMS0664 DOM7h-11-69-TVAAPS-BMS3h-56-201

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCCTAAGCTCCTGATCCTTGCTTTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
20 GAAGATTTTGCTACGTACTACTGTGCGCAGGCTGGGGTGCATCCTACGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCACCATCTGAGGTGCAGCTGTTGGAG
TCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGA
TTCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAG
CGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGC
CGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTG
25

CGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTACTTTTCAGGAGTGG
GGTCAGGGAACCCTGGTCACCGTCTCCAGC (SEQ ID NO: 1250)

DMS0667 DOM7h-11-3-TVAAPS-BMS3h-38-240

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GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACC
ATCACTTGCCGGGCAAGTCGTCCGATTGGGACGACGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCTAAGCTCCTGATCCTTTGGAATTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCCTACGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCACCATCTGAGGTGCAGCTGTTGGAG
TCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGA
TTCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAG
TGGGTCTCAGCTATTAGTAGGAACGGTTACAGCACATACTACGCAGACTCCGTGAAGGGC
CGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTG
CGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACTGG
GGTCAGGGAACCCTGGTCACCGTCTCCAGC (SEQ ID NO: 1251)

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DMS0668 BMS3h-38-240-AST-DOM7h-11-3

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GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTC
TCCTGCGCAGCCTCCGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAGGAACGGTTACAGCACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCG
TTTCGTTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCGAC
ATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATC
ACTTGCCGGGCAAGTCGTCCGATTGGGACGACGTTAAGTTGGTACCAGCAGAAACCAGGG
AAAGCCCCTAAGCTCCTGATCCTTTGGAATTCCCGTTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAA

25

GATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCCTACGACGTTTCGGCCAAGGG
ACCAAGGTGGAAATCAAACGG (SEQ ID NO: 1252)

DMS0669 DOM7h-14-10-TVAAPS-BMS3h-38-240

5 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACC
ATCACTTGCCGGGCAAGTCAGTGGATTGGGTCTCAGTTATCTTGGTACCAGCAGAAACCA
GGGAAAGCCCCCTAAGCTCCTGATCATGTGGCGTTCCCTCGTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCTCAGGGTTTGAGGCATCCTAAGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCACCATCTGAGGTGCAGCTGTTGGAG
10 TCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGA
TTCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAG
TGGGTCTCAGCTATTAGTAGGAACGGTTACAGCACATACTACGCAGACTCCGTGAAGGGC
CGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTG
CGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACTGG
GGTCAGGGAACCCTGGTCACCGTCTCCAGC (SEQ ID NO: 1253)

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DMS0670 BMS3h-38-240-AST-DOM7h-14-10

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGCGCAGCCTCCGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAGGAACGGTTACAGCACATACTAC
GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
20 CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCG
TTTCGTTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCGAC
ATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACCATC
ACTTGCCGGGCAAGTCAGTGGATTGGGTCTCAGTTATCTTGGTACCAGCAGAAACCAGGG
AAAGCCCCCTAAGCTCCTGATCATGTGGCGTTCCCTCGTTGCAAAGTGGGGTCCCATCACGT
25 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAA

GATTTTGCTACGTACTACTGTGCTCAGGGTTTGAGGCATCCTAAGACGTTTCGGCCAAGGG
ACCAAGGTGGAAATCAAACGG (SEQ ID NO: 1254)

DMS0671 BMS3h-38-235-AST-DOM7h-11-3

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GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCT
CCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAGGAACGGTTACAGCACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCG
TTTCGTTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGCGCTTCAACCGAC
ATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACCATC
ACTTGCCGGGCAAGTCGTCCGATTGGGACGACGTTAAGTTGGTACCAGCAGAAACCAGGG
AAAGCCCCTAAGCTCCTGATCCTTTGGAATTCCCGTTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAA
GATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCCTACGACGTTTCGGCCAAGGG
ACCAAGGTGGAAATCAAACGG (SEQ ID NO: 1255)

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DMS0672 BMS3h-38-235-AST-DOM7h-11-90

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GAGGTGCAGCTGTTGGCGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
TCCTGCGCAGCCTCCGGATTACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCC
CCAGGGAAGGGTCTAGAGTGGGTCTCAGCTATTAGTAGGAACGGTTACAGCACATACTAC
GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
CTGCAAATGAACAGCCTGCGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCG
TTTCGTTATGACTACTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGCGCTTCAACCGAC
ATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAACCATC
ACTTGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCAGGG
AAAGCCCCTAAGCTCCTGATCCTTGCTTTTTCCCGTTTGCAAAGTGGGGTCCCATCACGT
TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCTGAA

25

GATTTTGCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTTCGGCCAAGGG
ACCAAGGTGGAAATCAAACGG (SEQ ID NO: 1256)

DMS0674 DOM7h-11-3-TVAAPS-BMS3h-38-235

5 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCGTCCGATTGGGACGACGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCCTAAGCTCCTGATCCTTTGGAATTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
GAAGATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCCTACGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGGACCGTGGCGGCGCCGAGTGAGGTGCAGCTGTTGGCG
10 TCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGA
TTCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAG
TGGGTCTCAGCTATTAGTAGGAACGGTTACAGCACATACTACGCAGACTCCGTGAAGGGC
CGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTG
CGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACTGG
GGTCAGGGAACCCCTGGTCACCGTCTCCAGC (SEQ ID NO: 1257)

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DMS0675 DOM7h-11-90-TVAAPS-BMS3h-38-235

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCCTAAGCTCCTGATCCTTGCTTTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
20 GAAGATTTTGCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGGACCGTGGCGGCGCCGAGTGAGGTGCAACTGTTGGCG
TCTGGGGGAGGCTTGGTACAGCCTGGGGGTCCCTGCGTCTCTCCTGCGCAGCCTCCGGA
TTCACCTTTGAGGAGGAGGAGATGATTTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAG
TGGGTCTCAGCTATTAGTAGGAACGGTTACAGCACATACTACGCAGACTCCGTGAAGGGC
CGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTG
25

CGTGCCGAGGATACCGCGGTATATTACTGTGGGAAAGAGCCGTTTCGTTATGACTACTGG
GGTCAGGGAACCCTGGTCACCGTCTCCAGC (SEQ ID NO: 1258)

DMS0677 DOM7h-11-90-TVA-BMS3h-56-258

5 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCCTAAGCTCCTGATCCTTGCTTTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
GAAGATTTTGCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGTACGGTGGCGGAGGTGCAGCTGTTGGAGTCTGGGGGA
10 GGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGATTACCTTT
CGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCA
GCTATTAATCCGCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGGTTCACC
ATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAG
GACACCGCGGTATATTACTGTGCGAACTTCCGTTTTACTTTCACGAGTGGGGTCAGGGA
ACCCTGGTCACCGTCTCCAGC (SEQ ID NO: 1259)

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DMS0678 DOM7h-11-90-ASTSGPS-BMS3h-56-258

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCCTAAGCTCCTGATCCTTGCTTTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
20 GAAGATTTTGCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGGGCTAGCACCTCAGGTCCATCGGAGGTGCAGCTGTTG
GAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCC
GGATTACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTA
GAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCAGACTCCGTGAAG
GGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGC
25

CTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTACTTTTCACGAG
TGGGGTCAGGGAACCCTGGTCACCGTCTCCAGC (SEQ ID NO: 1260)

DMS0679 DOM7h-11-90-G4S-BMS3h-56-258

5 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCCTAAGCTCCTGATCCTTGCTTTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
GAAGATTTTGCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGGGGTGGAGGTGGCTCTGAGGTGCAGCTGTTGGAGTCT
10 GGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGATT
ACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGG
GTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGG
TTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGCGT
GCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTACTTTTCACGAGTGGGGT
CAGGGAACCCTGGTCACCGTCTCCAGC (SEQ ID NO: 1261)

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DMS0680 DOM7h-11-90- (G4S) 3-BMS3h-56-258

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCAAC
ATCACTTGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
GGGAAAGCCCCCTAAGCTCCTGATCCTTGCTTTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
20 GAAGATTTTGCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTTCGGCCAA
GGGACCAAGGTGGAAATCAAACGGGGTGGAGGTGGCTCTGGAGGTGGCGGTAGCGGCGGA
GGCGGTTTCAGAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCC
CTGCGTCTCTCCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGT
CGCCAGGCTCCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGT
ACATACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAAC
25

ACGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCG
 AAACCTCCGTTTTACTTTTACGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCCAGC (SEQ ID NO:
 1262)

DMS0681 DOM7h-11-90- (G4S) 5-BMS3h-56-258

5 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACC
 ATCACTTGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
 GGGAAAGCCCCCTAAGCTCCTGATCCTTGCTTTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
 GAAGATTTTGCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTCCGGCCAA
 10 GGGACCAAGGTGGAAATCAAACGGGGTGGAGGTGGCTCTGGAGGTGGCGGTAGCGGCGGT
 GGCGGTTTCAGGTGGCGGAGGTTCTGGAGGCGGTGGATCTGAGGTGCAGCTGTTGGAGTCT
 GGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGATTCT
 ACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAGCGG
 GTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGCCGG
 TTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGCGT
 15 GCCGAGGACACCGCGGTATATTACTGTGCGAACTTCCGTTTTACTTTTACGAGTGGGGT
 CAGGGAACCCTGGTCACCGTCTCCAGC (SEQ ID NO: 1263)

DMS0682 BMS3h-56-258-TVA-DOM7h-11-90

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 20 TCCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAACTTCCG
 TTTTACTTTTACGAGTGGGGTCAGGGAACCCTGGTCACCGTTTCGAGCACGGTGGCGGAC
 ATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTACCATC
 25 ACTTGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCAGGG

AAAGCCCCTAAGCTCCTGATCCTTGCTTTTTTCCCGTTTGCAAAGTGGGGTCCCATCACGT
 TTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCTGAA
 GATTTTGCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTTCGGCCAAGGG
 ACCAAGGTGGAAATCAAACGG (SEQ ID NO: 1264)

5

DMS0683 BMS3h-56-258-ASTSGPS-DOM7h-11-90

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
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 CCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCG
 TTTTACTTTTACGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGCGCTAGCACCTCA
 GGTCCATCGGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGAC
 CGTGTCAACATCACTTGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAG
 CAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCCTTGCTTTTTTCCCGTTTGCAAAGTGGG
 GTCCCATCACGTTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAAT

10

CTGCAACCTGAAGATTTTGCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACG
 TTCGGCCAAGGGACCAAGGTGGAAATCAAACGG (SEQ ID NO: 1265)

15

DMS0684 BMS3h-56-258-G4S-DOM7h-11-90

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATTCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCG
 TTTTACTTTTACGAGTGGGGTCAGGGAACCCTGGTCACCGTCTCGAGCGGTGGAGGCGGC
 TCTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTC
 ACCATCACTTGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAA

20

25

CCAGGGAAAGCCCCTAAGCTCCTGATCCTTGCTTTTTCCCGTTTGCAAAGTGGGGTCCCA
 TCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAA
 CCTGAAGATTTTGCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTTCGGC
 CAAGGGACCAAGGTGGAAATCAAACGG (SEQ ID NO: 1266)

5

DMS0685 BMS3h-56-258- (G4S) 3-DOM7h-11-90

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCG
 TTTTACTTTTACGAGTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGCGGTGGAGGTGGC
 TCTGGAGGTGGCGGTAGCGGCGGTGGCGGTTTCAGACATCCAGATGACCCAGTCTCCATCC
 TCCCTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTCGTCCGATT
 GGGACGATGTTAAGTTGGTACCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCCTT
 GCTTTTTTCCCGTTTGCAAAGTGGGGTCCCATCACGTTTTCAGTGGCAGTGGATCTGGGACA

10

GATTTCACTCTCACCATCAGCAATCTGCAACCTGAAGATTTTGCTACGTACTACTGCGCG
 CAGGCTGGGACGCATCCTACGACGTTTCGGCCAAGGGACCAAGGTGGAAATCAAACGG (SEQ ID NO:
 1267)

15

DMS0686 BMS3h-56-258- (G4S) 5-DOM7h-11-90

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTC
 TCCTGTGCAGCCTCCGGATTCACCTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCT
 CCAGGGAAGGGTCTAGAGCGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTAC
 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACACGCTGTAT
 CTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCG
 TTTTACTTTTACGAGTGGGGTCAGGGAACCTTGGTCACCGTCTCGAGCGGTGGAGGTGGC
 TCTGGAGGTGGCGGTAGCGGCGGTGGCGGTTTCAGGTGGCGGAGGTTCTGGAGGCGGTGGA

20

25

TCTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTC
 ACCATCACTTGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAA
 CCAGGGAAAGCCCCCTAAGCTCCTGATCCTTGCTTTTTTCCCGTTTGCAAAGTGGGGTCCCA
 TCACGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAA
 CCTGAAGATTTTGCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTTCGGC
 5 CAAGGGACCAAGGTGGAAATCAAACGG (SEQ ID NO: 1268)

DMS0688 DOM7h-11-90-TVAAPS-BMS3h-56-258
 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACCGTGTCACC
 ATCACTTGCCGGGCAAGTCGTCCGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCA
 10 GGGAAAGCCCCCTAAGCTCCTGATCCTTGCTTTTTTCCCGTTTGCAAAGTGGGGTCCCATCA
 CGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAATCTGCAACCT
 GAAGATTTTGCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTTCGGCCAA
 GGGACCAAGGTGGAAATCAAACGGACCGTAGCGGCGCCGAGTGAGGTGCAGCTGTTGGAG
 TCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTCTCTCCTGTGCAGCCTCCGGA
 TTCACCTTTTCGGGATTATGAGATGTGGTGGGTCCGCCAGGCTCCAGGGAAGGGTCTAGAG
 15 CGGGTCTCAGCTATTAATCCGCAGGGTACGCGTACATACTACGCAGACTCCGTGAAGGGC
 CGGTTACCATCTCCCGCGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTG
 CGTGCCGAGGACACCGCGGTATATTACTGTGCGAAACTTCCGTTTTACTTTACGAGTGG
 GGTCAGGGAACCCTGGTCACCGTCTCCAGC (SEQ ID NO: 1269)

Ejemplo 8

20

dAbs Anti-CD40 de Cynomolgus

25

Los métodos descritos en la presente para generar polipéptidos anticuerpos que se enlazan específicamente a CD40 humano pueden ser utilizados para generar polipéptidos anticuerpos que se enlazan específicamente a CD40 de otras

especies. Por ejemplo, los polipéptidos anticuerpos anti-CD40 de cynomolgus (anti-cyno) pueden ser producidos utilizando los métodos actualmente descritos. Los polipéptidos anticuerpos anti-cyno CD40 pueden ser generados
5 utilizando el mismo esquema de selección inicial/primaria y maduración por afinidad como los dAbs anti-CD40 humano, por ejemplo. Los métodos para obtener los dAbs anti-cynoCD40 son descritos, y los ejemplos representativos de los dAbs anti-cynoCD40 son proporcionados en la TABLA 23 siguiente.

10

RBA de ELISA:

Placas de 384 pozos Highbind de pared clara (Corning, Reino Unido) fueron recubiertas con 25 µl de neutravidina con concentración de 1 µg/ml en amortiguador de carbonato toda la noche a 4°C. Al siguiente día, las placas
15 de ensayo fueron lavadas con 0.1% de amortiguador Tween PBS, bloqueadas con 1% de BSA en PBS por 1 hora a temperatura ambiente, y lavadas nuevamente. Después de la eliminación del amortiguador de lavado en exceso, se incubaron 25 µl de 1 µg/ml de IZ-CD40L humano biotinilado (BMS, concentración
20 patrón de 1.2 mg/ml) con las placas de ensayo por 1 hora a temperatura ambiente. Simultáneamente, un intervalo de diluciones del dAb purificado y 1 µg/ml de cynoCD40 (BMS) fueron formados en complejo en una proporción 1:1. Después del lavado de la placa de ensayo, el complejo de dAb:cyno
25 CD40 fue incubado en la placa de ensayo a temperatura

ambiente por 2 horas con agitación suave. El enlace competitivo del dAb versus cynoCD40 al CD40L biotinilado fue detectado con el anticuerpo secundario anti-humano (Fc) conjugado a peroxidasa de rábano (HRP) (Sigma-Aldrich, Reino Unido). La señal de absorbancia fue medida utilizando un lector de placas Spectromax M5e (Molecular Devices) a 450 nm después de la neutralización con HCl 1M.

RBA de células CHO cynoCD40 utilizando AB8200 FMAT:

Las células CHO-DG44 que expresan cynoCD40, establemente transfectadas o las células CHO-DG44 nativas (BMS) fueron desprendidas de los matraces de cultivo celular utilizando Versene (Invitrogen). 40,000 células por pozo fueron sembradas en las placas de fondo claro de pared negra de 96 pozos Highbind (Corning, Reino Unido) en amortiguador de ensayo BSA PBS al 0.1% con un intervalo de dilución del dAb, 0.25 µg/ml de IZ-CD40L humano biotinilado (BMS, 1.2 mg/ml de concentración patrón), y 0.25 µg/ml de estreptavidina Alexa Fluor 647 (Invitrogen, Molecular probes, Reino Unido). La mezcla fue incubada en ausencia de luz por 6 horas. Después de la incubación, fue evaluado el enlace competitivo del dAb versus las células cynoCD40 CHO a IZ-CD40L biotinilado, soluble, utilizando la fluorescencia relativa medida mediante la plataforma protección celular AB8200 (Applied Biosystems).

Proliferación de células B humanas primarias promovida por CHO-hCD40L:

Las células CHO (ATCC) fueron transfectadas con CD40 humano para generar una línea celular estable que
5 expresa altos niveles de CD40L sobre la superficie celular. Las células CHO-CD40L fueron irradiadas a 10,000 Rads antes de la incubación con células B humanas. 1×10^5 células B humanas tonsilares fueron incubadas con 1×10^3 células CHO-CD40L (proporción 1:100 de células CHO-CD40L: células B
10 humanas) junto con la titulación variante del dAb o el anticuerpo monoclonal en un volumen final de 200 μ l/pozo en una placa de fondo redondo de 96 pozos. Las placas fueron incubadas a 37°C por 72 horas, después de lo cual se agregó timidina (3H; 0.5 μ ci/pozo) por 6 horas. La proliferación de
15 células B fue cuantificada con base en la incorporación de timidina. Todos los ensayos, a no ser que se indique de otro modo, fueron realizados en el medio RPMI suplementado con 10% de suero fetal de ternera (FCS).

Proliferación de células B esplénicas de cynomolgus,
20 **promovida por IZ-hCD40L soluble:**

1×10^5 células B aisladas de bazos de monos cynomolgus fueron incubadas con 0.5 μ g/ml de IZ-hCD40L junto con una titulación variante del dAb o el mAb en un volumen final de 200 μ l/pozo en una placa de fondo redondo de 96
25 pozos. Las placas fueron incubadas a 37°C por 72 horas,

después de lo cual fue agregada 3H-timidina (μ ci/pozo) por 6 horas. La proliferación de células B fue cuantificada con base en la incorporación de timidina. Todos los ensayos, a no ser que se indique de otro modo, fueron realizados en el medio RPMI suplementados con 10% de suero fetal de ternera (FCS).

TABLA 23

	Clon	RBA de ELISA (nM)	RBA celular (nM)	Ensayo de proliferación de células B (EC50 nM)	
				Humano	Cyno
10	BMS5c8				8,10,12,8,8
	BMS3c-85	370		>7000, >7000	747, 2700, 7000, 7000
	BMS3c-85-1	52, 8	12	2600, 1100	18, 39, 47
15	BMS3c-85-2	12, 4	4, 17	1800, 800	2, 5, 6, 1
	BMS3c-85-3	7	23	>7000, >7000	33, 31, 21, 31
	BMS3c-85-8	22	17.2	>7000, >7000	33, 33, 25
	BMS3c-85-9	10		>7000, >7000	>70, >70, 104
20	BMS3c-85-21	11	18		24
	BMS3c-85-24	8	13, 14		
	BMS3c-85-	62			

	Clon	RBA de ELISA (nM)	RBA celular (nM)	Ensayo de proliferación de células B (EC50 nM)	
				Humano	Cyno
5	25				
	BMS3c-85- 26	3		3300, 3900	>70, >70, 385
	BMS3c-85- 27	13	23		39
10	BMS3c-85- 31	13	11, 9		
	BMS3c-85- 32	21	56		111
	BMS3c-85- 33	15	10, 21.3		17
15	BMS3c-85- 34	48			
	BMS3c-85- 35	-	19, 1.5	>700	2
	BMS3c-85- 36	-	28		
20	BMS3c-85- 37	-	71		
	BMS3c-85-	-	17		

	Clon	RBA de ELISA (nM)	RBA celular (nM)	Ensayo de proliferación de células B (EC50 nM)	
				Humano	Cyno
5	38				
	BMS3c-85- 47	-	2.9	>700	<2, 0.5
	BMS3c-85- 49	-	10	>700	3, 3
10	BMS3c-85- 51	-	2.5	>700	3
	BMS3c-85- 52	-	8.5		
	BMS3c-85- 55	-	13.3, 6.7	>700	3, 3
15	BMS3c-85- 56	-	sin convergencia		
	BMS3c-85- 57	-	13.8, 5.3	>700	2, 4
	BMS3c-85- 62	-	9.9, 2.7, 2.0	>700	<2, 0.63
20	BMS3c-85- 63	-	80.9		
	BMS3c-85-	-	16.1		

	Clon	RBA de ELISA (nM)	RBA celular (nM)	Ensayo de proliferación de células B (EC50 nM)	
				Humano	Cyno
5	64				
	BMS3c-85- 65	-	13.9, 7.4	>700	3, 2
	BMS3c-85- 67	-	1.5		0.17
10	BMS3c-85- 69	-	1.8		0.33
	BMS3c-85- 72	-	2		0.16
	BMS3c-85- 73	-	2.3		
15	BMS3c-85- 77	-	2.3		0.2
	BMS3c-85- 84	-	1.3		0.21
	BMS3c-85- 88	-	3		0.25
20	BMS3c-85- 91	-	1.3		0.26

Ejemplo 9**dAbs Anti-CD40 Humano No Se Enlazan a CynoCD40**

CynoCD40 tiene un residuo Leu109 en vez de un residuo Trp109, como en CD40 humano. Las secuencias de aminoácidos de CD40 de *Macaca fascicularis* se reproducen en
 5 seguida:

```

1  MVRLPLQCVL WGCLLTAVYP EPPTACREKQ YLINSQCCSL CQPGQKLVSD
51 CTEFTETECL PCGESEFLDT WNRETRCHQH KYCDPNLGLR VQQKGTSETD
101 TICTCEEGLH CTSESCESCV PHRSCLPGFG VKQIATGVSD TICEPCPVGF
10 151 FSNVSSAFEK CRPWTSCETK DLVVQQAGTN KTDVVCGPQD RQRALVVIPI
201 CLGILFVILL LVLVFIKKVA KKPNDKVPHP KQEPQEINFP DDLPGSNPAA
251 PVQETLHGCQ PVTQEDGKES RISVQERQ (SEQ ID No.: 2)
  
```

Los dAbs deCD40 anti-humano fueron probados para la reactividad cruzada a las células B en sangre de mono cynomolgus, macaco rhesus y chimpancé, y linfocitos
 15 provenientes de sangre de mono tití utilizando métodos citométricos de flujo. Los procedimientos detallados más adelante resumen los métodos utilizados para la detección del dAb de CD40 en múltiples experimentos. Los resultados,
 20 mostrados en la TABLA 24, sugieren que los dAbs anti-CD40 humano no se enlazan a cynoCD40. Esto es consistente con la evidencia descrita anteriormente (ver Figuras 1 y 2) de que Trp109 en CD40 humano (que está ausente en cynoCD40) es importante para la formación de complejos entre los dAbs y el
 25 CD40 humano.

Métodos:

Los dAbs anti-CD40 humano, PEGilados (BMS3h-56-5C-40L y BMS3h38-2C-P40Br) o un dAb conjugado a la biotina (BMS3h38-2-biotina) fueron incubados con muestras de sangre de humano y de primate sobre un rotor por 1 hora a 37°C. 100 µl de cada muestra de sangre fueron repartidos en alícuotas hacia tubos de 12 x 75 mm y lavados 3 veces con amortiguador FACS (0.5% de FBS/PBS/0.1% de azida de sodio). Los tubos fueron centrifugados por 5 minutos a 1500 rpm, y los sobrenadantes fueron decantados entre los lavados. Después de los lavados, los tubos fueron colocados sobre hielo e incubados con IgG humano por 5 minutos para bloquear el enlace no específico vía los receptores de Fc.

Para la detección del dAb PEGilado, los anticuerpos anti-PEG (clon CH-2074, Silver Lake Research o clon 2-2, Open Biosystems) fueron agregados a los tubos e incubados por 30 minutos. Las muestras fueron lavadas una vez en amortiguador FACS, luego incubadas con un anticuerpo CD20 marcado con APC (clon 2H7, BD Biosciences) y la IgG anti-ratón marcada con PE (específico de Fcγ1 Calbiochem) por 30 minutos adicionales sobre hielo.

Para la detección del dAb conjugado a la biotina, fueron agregados estreptavidina marcada con PE (Invitrogen) y el anticuerpo CD20 marcado con APC (clon 2H7, BD Biosciences) a los tubos, e incubados por 30 minutos a temperatura

ambiente.

Además, para medir los niveles de CD40 sobre la sangre humano y de primate, una alícuota de cada muestra de sangre fue incubada con un anticuerpo CD20 marcado con APC
5 (clon 2H7, BD Biosciences) y un anticuerpo anti-CD40 humano marcado con PE, que reacciona cruzadamente con especies de primates (clon 5C3, BD Biosciences) por 30 minutos a temperatura ambiente.

Para lisar las células sanguíneas rojas y fijar las
10 células sanguíneas blancas después de la incubación del anticuerpo de detección, fue agregada Solución de Lisis de FACS (BD Biosciences) a todos los tubos, y las muestras fueron incubadas por 15 minutos a temperatura ambiente. Las muestras fueron centrifugadas y resuspendidas en Solución de
15 Lisis de FACS, y analizadas mediante citometría de flujo sobre un BD FACSCanto^{MR}, con entradas de células B CD20+ para el análisis. Para las muestras de mono tití, el anticuerpo CD20 no fue de reactividad cruzada, por lo tanto, el análisis fue realizado sobre todos los linfocitos como fueron
20 identificados por las propiedades de dispersión delantera y lateral (tamaño).

Resultados:

El enlace de los dAbs anti-CD40 humano, PEGilados y biotinilados, fue probado en muestras de sangre de humano y
25 de primate de acuerdo al método anterior. El enlace del dAb

anti-CD40 humano a las células B CD20+ en muestras de sangre humana, fue también detectado. En contraste, el enlace de los dAbs anti-CD40 PEGilados y biotinilados no fue detectado en células B CD20+ en muestras de sangre de cynomolgus, rhesus, o chimpancé o en linfocitos de muestras de sangre de mono tití. Los resultados para el dAb BMS3h-38-2C-P40Br se muestran en la Figura 3, Paneles A y B. Fueron obtenidos resultados similares para los otros dAbs. Niveles comparables de CD40 sobre las células B de especies humana y de primate fueron confirmados utilizando el anticuerpo anti-CD40 humano que reacciona cruzadamente con el CD40 de primate. Estos datos indican que los dAbs anti-CD40 humano provenientes de las líneas BMS3h-56 y BMS3h-38 son incapaces de reticularse a CD40 en especies de primate. Los datos son consistentes con la importancia del residuo Trp109 en la formación de un complejo entre CD40 y los dAbs anti-CD40, como se muestran en las Figuras 1 y 2.

Ejemplo 10

Cristalografía de Rayos X de un Complejo Entre CD40 y el dAb

BMS3h-56-5

Recolección y procesamiento de datos:

Se analizaron dos diferentes formas de cristales durante la determinación de la estructura del complejo CD40 humano (SEQ ID No.: 1)/BMS3h-56-5 (SEQ ID No.: 321). Los datos fueron recolectados de un cristal del complejo

CD40/BMS3h56-5, enfriado instantáneamente y mantenido a 100°K, y montado sobre un goniómetro Rigaku AFC-9. La fuente de rayos X fue un FR-E Rigaku utilizando un objetivo de cobre con ópticos confocales MicroMax^{MR} y un detector Saturn 92.

5 Los datos fueron recolectados a redundancia extremadamente alta para mejorar la señal de difracción anómala del azufre con la esperanza de utilizar esa señal para ejecutar por fases los datos. Los datos fueron procesados con HKL2000 (HKL Research; Otwinowski et al., En *Methods Enzymol.*
10 *Macromolecular Crystallography* part A, Carter et al., eds., vol. 276, p. 307-326, Academic Press, Inc., New York, NY (1997)). Las estadísticas de recolección de datos para este cristal se resumen en seguida en la Tabla 24:

Grupo Espacial: I222;

15 Celda Unitaria: a = 156.6 Å; b = 158.3 Å; c = 200.7 Å;

Mosaicidad 0.59-0.84; Observaciones Rechazadas: 1028; 0.06%.

TABLA 24

s09-167	Resolución, Å	Medido	Único	Redun.	% Completo	Valor R	I/ σ
Total	50.00-3.30	1603547	37772	42.5	99.8	0.137	33.7
Primera Capa	50.00-8.94	≥38193	1971	40.1	97.1	0.049	58.7
Última Capa	3.36-3.30	≥37054	1861	43.6	99.8	0.439	12.5

Una segunda forma cristalina fue recolectada de un cristal enfriado instantáneamente a 100°K y montado sobre un detector Rayonix MX-225 en la línea de haz de Fuente de Luz Canadiense CMCF1 (08-ID-1) y la longitud de onda fue de 0.9793 Å. Estos datos fueron recolectados por Shamrock Structures (R. Walter y G. Ranieri) y fueron procesados con HKL2000. Las estadísticas de recolección de datos para este cristal se resumen en seguida y en la Tabla 25:

Grupo Espacial: C2;

Celda Unitaria: a = 199.3 Å; b = 48.7 Å; c = 138.8 Å; β = 118.2°;

Mosaicidad 0.62-0.71; Observaciones rechazadas: 70; 0.08%.

TABLA 25

x09-275	Resolución, Å	Medido	Único	Redun.	% Completo	Valor R	I/ σ_1
Total	50.00-2.80	92545	29303	3.2	98.6	0.091	14.6
Primera Capa	50.00-6.03	9265	3060	3.0	98.5	0.052	18.0
Ultima Capa	2.90-2.80	8857	2882	3.1	98.0	0.421	3.4

Modelos de Reemplazo Molecular:

El modelo del dAb, BMS3h-56-5, fue derivado de los residuos 1-124 de la cadena E de PDB ID 2VYR con residuos secuenciales que responden a las CDRs 31-35, 50-57, y 99-111 eliminadas por SPLIT_PDB (que corresponde a la numeración de

Kabat 31-35, 50-56, y 95-100G) y luego corrido a través de MUTATE y finalmente reenumerado por RENUMBER. MUTATE cambia los residuos no idénticos al mínimo idéntico, por ejemplo, normalmente Ala o Gly, pero, por ejemplo Tyr→Phe y Phe→Tyr podrían dar como
 5 resultado Phe. Esto no construye átomos, aunque para Thr→Val, Val→Thr, Cys→Ser, y Ser→Cys, éste sustituirá el nombre del átomo apropiado pero no cambiará la posición. RENUMBER cambió la numeración a la numeración de Kabat (Kabat et al., *Sequences of Immunological Interest*, 5th ed., U.S. Dept. Health & Human
 10 Services, Washington, D.C. (1991)), que es un sistema de numeración estándar para anticuerpos que realiza la descripción de las CDRs y los residuos estructurales de manera directa.

Un modelo de CD40 fue construido a partir de PDB IDs 1JMA (cadena B), 1NCF (cadena A), 1TNR (cadena R), 2HEV (cadena
 15 R), 2HEY (cadenas R, T), y 2UWI (cadenas A, B) utilizando phenix.ensemble (Universidad de Cambridge, Reino Unido) para crear un conjunto de estructuras. Los extremos N (residuos 24-78) más un segmento de seis residuos (residuos 95-100) de estas moléculas fueron superponibles con una distancia de raíz cuadrada
 20 media aceptable para los átomos Ca, y que se utilizó como un modelo para la región N terminal de CD40.

Métodos de Reemplazo Molecular:

El programa PHASER (McCoy et al., *J. Appl. Crystallogr.* 40: 658-674 (2007)) fue utilizado para el reemplazo molecular.
 25 La función de traducción Z-score (TFZ) y el incremento en la

ganancia de probabilidad logarítmica fueron monitorizados para decidir si habían sido encontradas o no soluciones reales. Las calificaciones de TFZ de 8 y superiores en general representan una solución. Calificaciones de TFZ más bajas acompañadas por
 5 incrementos sustanciales (> 50) en la ganancia de probabilidad logarítmica son también indicadores aceptables.

Construcción de Modelos, Modificación de Densidad, y Métodos de Refinación Cristalográfica:

Las herramientas de construcción de modelos para los
 10 gráficos moleculares incluyeron el programa COOT (Emsley et al., *Acta Crystallogr Sect. D* 60: 2126-2132 (2004); Emsley et al., "Features y Development of Coot," *Acta Crystallogr Sect. D* 66: 486-501 (2010)). La modificación de la densidad utilizando el promedio de mapa de simetría no cristalográfico, se realizó
 15 utilizando los programas conocidos de modificación de densidad y otros programas para calcular los ángulos Eulerianos y las traslaciones entre moléculas. La refinación fue corrida utilizando autoBUSTER (GlobalPhasing,Ltd.: Bricogne et al., *Acta Crystallogr. Sect. D* 60: 2210-2221 (2004); Tronrud et al., *Acta*
 20 *Crystallogr. Sect. A* 43: 489-501 (1987)).

Sistema de numeración de Anticuerpo de Dominio:

El sistema de numeración de residuo para el anticuerpo de dominio sigue aquel de Kabat. La numeración de Kabat es comparada a la numeración secuencial directa siguiente para
 25 BMS3h-56-5:

15

25

En la numeración de Kabat BMS3h-56-5 tiene los residuos de inserción 52A, 82A, 82B, 82C y está faltando el residuo 100. En ambos sistemas de numeración, la Ser y la Thr en el extremo N que son parte de la construcción de expresión se dan con números negativos.

Determinación de la estructura del complejo CD40/BMS3h-56-5:

PHASER fue capaz de localizar cuatro moléculas de dAb de BMS3h-56-5 en la forma cristalina I222 y tres moléculas de dAb de BMS3h-56-5 en la forma cristalina C2. En la forma cristalina I222 las calificaciones de TFZ estuvieron en el intervalo de 7.6 a 41.0, y el incremento en la ganancia de probabilidad logarítmica estuvo en el intervalo de 77 a 446. Estas soluciones para las moléculas de dAb de BMS3h-56-5 formaron columnas helicoidales de moléculas de dAb a través del cristal de I222 que estuvieron separadas de otras columnas por canales grandes. En el cristal C2, las calificaciones de TFZ estuvieron en el intervalo de 7.7 a 16.5, y el incremento en la ganancia de probabilidad logarítmica estuvo en el intervalo de 110 a 150. El empaquetamiento de los dAbs en esta forma cristalina no fue repetitivo o simétrico.

Utilizando el modelo de conjuntos para el dominio N-terminal de CD40, cuatro moléculas del dominio N-terminal de CD40 pudieron ser colocadas en la forma cristalina I222 con las calificaciones de TFZ en el intervalo de 5.7 a 8.5, y el incremento en la ganancia de probabilidad logarítmica estuvo en el intervalo de 83 a 389. Los cuatro dominios N-terminales de CD40 en la forma cristalina I222 formaron un cúmulo igualmente centrado entre cuatro columnas de las moléculas de dAb. Sin embargo, éstas no tocaron las

moléculas de dAb BMS3h-56-5. En la forma cristalina C2 tres moléculas del dominio N-terminal de CD40 pudieron ser colocadas con las calificaciones de TFZ en el intervalo de 5.8 a 12.1, y el incremento en la ganancia de probabilidad
5 logarítmica estuvo en el intervalo de 100 a 198. En esta forma cristalina, los dominios N-terminales tampoco hicieron contacto con las moléculas de dAb BMS3h-56-5.

En la forma cristalina I222, el dominio N-terminal del CD40 proveniente del complejo CD40/Chi220 Fab y el
10 dominio N-terminal de 2UWI fueron superpuestos sobre el dominio N-terminal de CD40. La habilidad para asociar el extremo N con un dAb de BMS3h-56-5 particular permitió el uso de promedio de marca de simetría no cristalográfica (NCS). Los coeficientes de correlación iniciales para el promedio de
15 NCS dieron valores fuera de la diagonal de 0.71-0.81. Los valores fuera de diagonal finales fueron de 0.88-0.92. La densidad electrónica cercana a la región N-terminal fue clara, y pudo ser rastreada una trayectoria para CDR3 del dAb BMS3h-56-5. Los residuos 82-94 y 101-121 del complejo
20 CD40/Chi220 Fab' fueron superpuestos sobre los residuos correspondientes sobre 2UWI y luego se utilizó COOT para mejorar el ajuste manualmente. Esta posición para el segundo dominio (residuos 82-94 y 101-121) de CD40 fue luego transformada sobre los otros tres dominios N-terminales.

25 Un ciclo de refinación fue corrido con la

disminución libre de R desde 0.437 hasta 0.380 y el trabajo de R de 0.447 hasta 0.381 con mejoramiento en la unión de raíz cuadrada media y en las desviaciones angulares de lo ideal. El mapa de densidad electrónica resultante mostró que el residuo 109 tuvo una cadena lateral que fue consistente con Trp y esa densidad existió para al menos algunos residuos en los 70 residuos C-terminales de CD40.

Ya que CD40 tiene poca estructura secundaria, el ajuste de los ~ 70 residuos C-terminales al electrón, probaron ser difíciles, de modo que fue indagada la base de Datos de Proteínas Research Collaboratory for Structural Bioinformatics para un modelo adecuado para ayudar al rastreo de la cadena. Los dos aciertos superiores con 16 de las 44 identidades y 24 de las 44 concordancias fueron 2AW2 y 1JMA, que tienen la misma secuencia:

	125	130	140	150	160
CD40	̄CSPGFGVKQĪATGVSDTIC̄EP̄CPVGGFFSNV̄SSAFEK̄CHPW̄TSC̄E				
2AW2	CSPGYRVKEACGELTGTVC̄EPC̄PPGTYIAHLNGLSK̄C̄LQ̄C̄QM̄CD				
Consenso	CSPG* VK*	** T	CEGCP	G *	* KC C*
	.	.	.	.	.
	23	30	40	50	60 66
20	.	.	.	.	.
1JMA	19	30	40	50	62
(SEQ ID NOS 1270-1271)					

Residuos idénticos son anotados con el código apropiado de una sola letra sobre la línea de consenso, y residuos similares son anotados sobre la línea de consenso

como asteriscos. Éste fue el tramo de residuos para los residuos 41-84 del dominio N-terminal de CD40:

```

          41          50          60          70          80
          |          |          |          |          |
CD40      CQPGQ̄KLVSDCTEFTETEC̄LPC̄GESEFLDTWNRETHCHQH̄KYCD
CD40      CSPGFGVKQ̄IATGVSDTIC̄EPC̄PVGFFSNVSSAFEKCHPWTSC̄E
5 Consenso C PG * T **T C PC F * * *CH C*
          |          |          |          |          |
          125 130 - 140 - 150 - 160 -
(SEQ ID NOS 1272 y 1270)

```

Residuos idénticos son anotados con el código apropiado de una sola letra sobre la línea de consenso, y los
 10 residuos similares son anotados sobre la línea de consenso como asteriscos.

Enlaces disulfuro concordantes:

Comparación de Enlaces Disulfuro en los residuos 41-84 y 125-168 de CD40

```

15 Residuos      Residuos
    41-84        125-168
    C41-C59      C125-C143
    [C38]-C51
    C62-C77      C146-C161
20 C83[-C103]    C167[-C186]

```

Los residuos en corchetes caen fuera de los intervalos de residuos en la repetición secuencial.

Con el modelo 1JMA/2AW2 como una guía, se utilizó

el programa COOT para ajustar una de las cadenas de CD40. Este modelo ajustado fue luego superpuesto sobre una de las otras tres cadenas de CD40. Sin embargo, pareció que la posición de este nuevo tramo de residuos estuvo orientada de manera diferente en las otras dos cadenas de CD40, y éstas no fueron ajustadas esta vez. Fue corrido un ciclo de refinamiento libre de R que disminuye desde 0.393 hasta 0.366 y el trabajo R de 0.400 a 0.349 con mejoramiento considerable en el enlace de raíz cuadrada media y las desviaciones angulares de lo ideal.

El dAb BMS3h-56-5 proveniente de una de las moléculas en la forma cristalina I222 fue superpuesto sobre cada uno de los tres dAbs en la forma cristalina C2. Esa matriz de transformación fue utilizada para orientar el segundo dominio y el dominio C-terminal de la forma cristalina I222. El modelo fue reconstruido formado el programa COOT. Un ciclo de refinamiento fue corrido con libre de R que disminuye desde 0.361 hasta 0.334 y el trabajo R de 0.375 hasta 0.306 con unión mejorada de raíz cuadrada media y desviaciones angulares de lo ideal. El mapa resultante de la densidad de electrones proporcionó una guía para colocar muchos más residuos de CD40. Otro ciclo de refinamiento fue corrido con libre de R que disminuye desde 0.302 hasta 0.287 y el trabajo R de 0.299 a 0.270 con enlace mejorado de raíz cuadrada media y desviaciones angulares de

lo ideal.

La construcción del modelo convencional y el refinamiento fueron luego utilizados para completar la determinación de la estructura. Varias rondas más de optimización condujeron a un refinamiento final con las siguientes características: libre de R 0.260, trabajo R 0.228, enlaces de raíz cuadrada media 0.010 Å, ángulos de raíz cuadrada media 1.4°. Los coeficientes de correlación espacial real son de 0.92 para los átomos de cadena principal y 0.80 para los átomos de cadena lateral. El modelo final tuvo 13 moléculas de agua.

Utilizando el modelo del dominio C-terminal proveniente de la forma cristalina C2 como una guía, los modelos de CD40 en la forma cristalina I222 fueron adicionalmente refinados. Varios ciclos más de construcción de modelos utilizando el programa COOT y refinamiento con el programa autoBUSTER condujeron a las siguientes estadísticas: libre de R 0.323, trabajo R 0.292, enlaces de raíz cuadrada media 0.011 Å, ángulos de raíz cuadrada media 1.5°. Los coeficientes de correlación espacial real son de 0.91 para los átomos de cadena principal y de 0.80 para los átomos de cadena lateral. El modelo no contenía moléculas de agua.

Estructura General del complejo CD40/BMS3h-56-5:

Un BMS3h-56-5 dAb se enlaza a una molécula de CD40. Como se muestra en la Figura 1, BMS3h-56-5 se enlaza a un

epítopo que es distinto de aquel del anticuerpo Chi220, el cual se enlaza en la región N-terminal. Los residuos de CD40 (SEQ ID No.: 1) son mostrados en verde, excepto por los residuos de epítopos. Los residuos de CD40 para Chi220 son mostrados en azul; los residuos de epítopos del dAb BMS3h-56-5 son mostrados en ciano. El Fab Chi220 y las β -hebras de BMS3h-56-5 son mostrados en rojo, los residuos de CDR son mostrados en magenta, y otros bucles son mostrados en anaranjado. Los enlaces disulfuro son mostrados en las moléculas de CD40, Chi220, y BMS3h-56-5 con los átomos de azufre en amarillo.

La forma cristalina I222 contiene cuatro complejos CD40/BMS3h-56-5 cristalográficamente independientes, y el cristal C2 contiene tres complejos CD40/BMS3h-56-5 cristalográficamente independientes. La molécula de CD40 tiene una cierta cantidad de flexibilidad, y los dominios están acomodados de manera diferente en las siete versiones únicas del complejo, pero la naturaleza general de la interacción es conservada en todos los casos.

20 ***Residuos del epítopo de dAb BMS3h-56-5:***

El epítopo de CD40 mínimo para BMS3h-56-5 es definido como residuos de CD40 que contienen al menos un átomo en contacto por van der Waals o por puentes de hidrógeno con un átomo de BMS3h-56-5. El epítopo mínimo en todos los complejos contiene los siguientes residuos de CD40

con referencia a la SEQ ID No.: 1: Trp109, Leu121, His122, Ser124, Ser156, Ala157, Phe158, Glu159, y His162. Los siguientes residuos adicionales están en contacto de van der Waals o de puentes de hidrógeno en algunos complejos: Pro85, Asn86, Leu87, Gly88, Glu106, Glu107, Gly108, His110, Thr112, Cys119, Val120, Gln133, Ile134, Ala135, Thr136, Ser155, Lys160.

Un epítipo de CD40 máximo es definido como los residuos que contienen átomos que están enterrados por una esfera de sonda de 1.7 Å. Estos residuos incluyen todos los residuos anteriores, más Val154 en todos los complejos. En algunos complejos, los residuos enterrados adicionales son: Ser118, Arg123, Thr141, Phe151, Asp153, Cys161, y Pro163.

Una descripción de la superficie de BMS3h-56-5 con los residuos de contacto se muestra en la Figura 2. Se muestran los residuos BMS3h-56-5 de contacto. Los residuos enterrados son también mostrados. CD40 es representado como una caricatura con el anaranjado que representa la estructura secundaria no repetitiva y el magenta que representa los residuos de epítipo. También se muestran como barras (átomos de carbono en color ciano) los residuos de CD40 Trp109, Ala115, Leu121, Ser126, y His162, los cuales son cinco de los siete residuos que difieren entre el humano y el mono cynomolgus (*Macaca fascicularis*). Ala115 y Ser126 están sobre el lado opuesto de CD40 a partir del sitio de enlace

BMS3h-56-5. Trp109 y Leu121 se enlazan en una hendidura de BMS-h-56-5 que yace entre CDR-3 y FR-2 (residuos Leu45 y Arg47 de BMS-3h-56-5). His162 de CD40 interactúa con Arg56 de CDR-2 del dAb BMS3h-56-5. La mutación de Trp109 reduce o
 5 elimina considerablemente la actividad de BMS3h-56-5.

Dependiendo del complejo cristalográficamente independiente, 660-740 Å² del área superficial de CD40 están enterrados entre los residuos de contacto 16-21 representados a un nivel más fino con los átomos 46-67 de contacto. Para
 10 BMS3h-56-5, 660-780 Å² de área superficial están enterrados con los residuos 14-17 de contacto representados a un nivel más fino con los átomos 48-62 de contacto. Estos contactos producen 3-7 enlaces de hidrógeno y 111-142 interacciones de van der Waals, dependiendo del complejo cristalográficamente
 15 independiente.

Ejemplo 11

Identificación de los Epítopos de Enlace de dAb sobre CD40

Para identificar los epítopos de enlace de dAb sobre CD40, el enlace del dAb fue probado contra siete
 20 proteínas de fusión CD40-Fc que contenían sustituciones específicas de residuos de aminoácidos en los residuos 76, 109, ó 121. Estas proteínas de fusión CD40-Fc incluyen CD40 humano de tipo silvestre (wt-hCD40), CD40 de mono cynomolgus tipo silvestre (wt-cCD40), y cinco
 25 proteínas CD40 humanas mutantes (M1-M5) con residuos de

aminoácido específicos mutados al residuo correspondiente a partir de la secuencia CD40 de monomolgus (M1, M2, M4, M5) o de CD40 de chimpancé (M3). Las sustituciones de aminoácidos son listadas en la Tabla 26.

La secuencia del dominio extracelular de CD40 humano de tipo silvestre (1-193) es proveniente de REFSEQ: acceso NM_001250.3. Fueron generadas construcciones de Cynomolgus y mutantes utilizando la mutagénesis dirigida al sitio de la secuencia de tipo silvestre en las posiciones mostradas en la Tabla 26. Los dominios extracelulares fueron fusionados con un ligando escindible por trombina DPGGGGGRLVPRGFGTGDP (SEQ ID No.: 1273), que fue fusionado con el Fc de la IgG1 humana. Las proteínas fueron expresadas en células HEK-293-6E transfectadas con los vectores de expresión TIG-pYD7-GATE Durocher. Los sobrenadantes fueron cosechados después de cinco días. Cada proteína CD40 fue purificada a partir del medio condicionado utilizando la cromatografía de flujo rápido de proteína A. La columna fue lavada con PBS (fosfato de sodio 20 mM, NaCl 0.15 M, pH 7.2) y luego eluida utilizando acetato de sodio 80 mM, pH 3, en 1/5 del volumen de Tris-HCl 1 M, pH 8. El eluido fue corrido sobre una columna Superdex-200 en PBS.

TABLA 26

	Nombre	Nombre corto	Residuo 76	Residuo 109	Residuo 121
5	Fusión de Fc de CD40 humano de tipo silvestre	wt-hCD40	H	W	L
	Fusión de Fc de CD40 humano (H76R)	hCD40-M1	R	W	L
	Fusión de Fc de CD40 humano (W109L)	hCD40-M2	H	L	L
10	Fusión de Fc de CD40 humano (W109R) (<i>CD40 de Chimpancé</i>)	hCD40-M3	H	R	L
	Fusión de Fc de CD40 humano (W109L, L121P)	hCD40-M4	H	L	P
15	Fusión de Fc de CD40 humano (H76R, W109L, L121P)	hCD40-M5	R	L	P
20	Fusión de Fc de CD40 de mono cynomolgus, de tipo silvestre	wt-cyno-CD40	R	L	P

Los dAb's representativos provenientes de las líneas 3h217, 3h37, 3h38, y 3h56 fueron evaluados para su enlace a las proteínas de fusión CD40-Fc listadas en la Tabla

26. Los ensayos fueron realizados sobre instrumentos BioRad ProteOn XPR36 SPR. Las superficies de SPR fueron preparadas mediante la inmovilización de 8 µg/ml del anticuerpo anti-IgG (Fc) humano (Biacore/GE Healthcare) en acetato de sodio 10 mM de pH 4.5 sobre un chip sensor BioRad GLC utilizando la química estándar de etil(dimetilaminopropil)carbodiimida (EDC)/N-hidroxisuccinimida (NHS), con bloqueo con etanolamina. El amortiguador de corrida para la inmovilización y el análisis del enlace cinético fue fosfato de sodio 10 mM, cloruro de sodio 130 mM, 0.05% de tween 20, pH 7.1. Las proteínas de fusión CD40-Fc a concentraciones de 20 µg/ml fueron capturadas en la orientación vertical sobre estas superficies vía la cola Fc, y las superficies de referencia que carecen de las proteínas CD40-Fc fueron utilizadas para sustracción de referencia. Fueron realizados experimentos cinéticos mediante el flujo de los analitos de dAb de 405, 135, 45, 15, y 5 nM en la orientación horizontal sobre las superficies de CD40-Fc capturado a 25°C, utilizando un tiempo de asociación de 240 segundos y un tiempo de disociación de 420 segundos, a una velocidad de flujo de 30 µl/minuto. Las superficies fueron regeneradas en las orientaciones horizontal y vertical con pulsos de 30 segundos de cloruro de magnesio 3 M seguido por el amortiguador de corrida a 60 µl/minuto. Los datos del sensograma fueron con referencia doble y fueron luego ajustados a un modelo de

Langmuir 1:1 utilizando el software BioRad ProteOn Manager V.2.1.0.38, para determinar la constante de la velocidad de asociación (k_a), la constante de la velocidad de disociación (k_d), y la constante de la disociación en equilibrio (K_D).

5 Se encontró que todos los dAbs de las líneas 3h-37, 3h-38, y 3h-56 se enlazan con alta afinidad ($K_D < 10^{-8}$ M) a las proteínas de fusión CD40-Fc que contenían los residuos de CD40 humano, W109 y L121, pero el enlace fue significativamente reducido o no detectable a las proteínas

10 de fusión CD40-Fc con los residuos correspondientes provenientes de CD40 de mono cynomolgus (L109, P121) o CD49 de chimpancé (R109). Esto indica que los dAbs provenientes de cada de las líneas 3h37, 3h38--, y 3h56- se enlazan específicamente a un epítipo que incluye los residuos 109 y

15 121 del CD40 humano. En contraste, todos los miembros probados de la línea 3h-217 se enlazaron con afinidad similar a todo las proteínas de fusión CD40-Fc probadas, indicando que los miembros de la línea 3h-217 se enlazan a un sitio sobre CD40 que no incluye los residuos 76, 109, o 121. Por

20 lo tanto, la línea 3h-217 se enlaza a un epítipo diferente que las líneas 3h-37, 3h-38, y 3h-56. La Tabla 27 resume los valores de K_D determinados para el enlace de dAb a las proteínas de fusión CD40-Fc utilizando SPR sobre un instrumento ProteOn XPR36. Una "X" en la Tabla 27 significa

25 que no se encontró evidencia para el enlace bajo estas

condiciones.

TABLA 27

5		wt-hCD40	hCD40-M1 (H76R)	hCD40-M2 (W109L)	hCD40-M3 (W109R)	hCD40-M4 (W109L, L121P)	hCD40-M5 (H76R, W109L, L121P)	cyno CD40
10	3h-217-5	0.47, 0.48	0.94	0.99	0.72	0.93	1.0	0.9
	3h-217-16	0.22, 0.26	0.35	0.41	0.27	0.35	0.5	0.4
	3h-217-23	0.78, 1.5	1.6	2.0	1.2	1.6	2.2	1.9
	3h-37-2	2.0, 2.0	2.6	>1000	X	X	X	X
	3h-37-11	1.9, 2.3	2.4	>1000	X	X	X	X
	3h-38-2	5.1, 8.0	7.2	X	X	X	X	X
	3h-38-211	3.3, 6.1	4.0	>1000	X	X	X	X
15	3h-38-215	2.1, 6.0	3.0	>1000	X	X	X	X
	3h-38-217	2.3, 2.4	3.4	>1000	X	X	X	X
	3h-56-1	3.0, 5.4	4.2	29	>1000	X	X	X
	3h-56-2	3.8, 3.2	6.1	44	>1000	X	X	X
	3h-56-5	5.3, 4.7	7.2	65	>1000	X	X	X
	3h-56-202	2.3, 1.3	3.3	160	X	X	X	X
	3h-56-206	0.60, 1.4	1.0	55	X	X	X	X
20	3h-56-217	1.0, 1.9	1.4	2.5	23	X	X	X

La Tabla 28 muestra la constante de la velocidad de asociación (k_a), la constante de la velocidad de asociación (k_d), y la constante de disociación en equilibrio (K_D) determinada para dAb que se enlaza a las proteínas de fusión

de CD40-Fc utilizando SPR sobre un instrumento ProteOn XPR36. Una "X" en la Tabla 28 significa que no se encontró evidencia bajo el enlace para estas condiciones.

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TABLA 28

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Ligando	dAb	ka (1/Ms)	kd (1/s)	Kd (nM)
wt-hCD40	3h-217-5	2.71x10 ⁶	1.27x10 ⁻³	0.47
wt-hCD40 (repetición)	3h-217-5	2.03x10 ⁶	9.81x10 ⁻⁴	0.48
hCD40 M1 (H76R)	3h-217-5	3.17x10 ⁶	2.99x10 ⁻³	0.94
hCD40 M2 (W109L)	3h-217-5	2.55x10 ⁶	2.51x10 ⁻³	0.99
hCD40 M3 (W109R)	3h-217-5	2.73x10 ⁶	1.96x10 ⁻³	0.72
hCD40 M4 (W109L, L121P)	3h-217-5	2.78x10 ⁶	2.59x10 ⁻³	0.93
hCD40-M5 (H76R, W109L, L121P)	3h-217-5	2.44x10 ⁶	2.42x10 ⁻³	0.99
wt-cCD40	3h-217-5	2.46x10 ⁶	2.12x10 ⁻³	0.86
wt-hCD40	3h-217-16	4.47x10 ⁶	9.91x10 ⁻⁴	0.22
wt-hCD40 (repetición)	3h-217-16	3.30x10 ⁶	8.47x10 ⁻⁴	0.26
hCD40 M1 (H76R)	3h-217-16	4.83x10 ⁶	1.68x10 ⁻³	0.35
hCD40 M2 (W109L)	3h-217-16	4.06x10 ⁶	1.67x10 ⁻³	0.41
hCD40 M3 (W109R)	3h-217-16	3.78x10 ⁶	1.04x10 ⁻³	0.27
hCD40 M4 (W109L, L121P)	3h-217-16	4.39x10 ⁶	1.52x10 ⁻³	0.35
hCD40-M5 (H76R, W109L, L121P)	3h-217-16	3.65x10 ⁶	1.70x10 ⁻³	0.47

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	L121P)				
	wt-cCD40	3h-217-16	3.44×10^6	1.47×10^{-3}	0.43
	wt-hCD40	3h-217-23	1.64×10^6	1.27×10^{-3}	0.78
	wt-hCD40 (repetición)	3h-217-23	1.07×10^6	1.63×10^{-3}	1.52
5	hCD40 M1 (H76R)	3h-217-23	1.64×10^6	2.62×10^{-3}	1.59
	hCD40 M2 (W109L)	3h-217-23	1.49×10^6	2.91×10^{-3}	1.95
	hCD40 M3 (W109R)	3h-217-23	1.53×10^6	1.86×10^{-3}	1.22
	hCD40 M4 (W109L, L121P)	3h-217-23	1.67×10^6	2.68×10^{-3}	1.61
10	hCD40-M5 (H76R, W109L, L121P)	3h-217-23	1.30×10^6	2.87×10^{-3}	2.21
	wt-cCD40	3h-217-23	1.24×10^6	2.35×10^{-3}	1.90
	wt-hCD40	3h-37-2	2.12×10^5	4.17×10^{-4}	1.96
	wt-hCD40 (repetición)	3h-37-2	2.13×10^5	4.26×10^{-4}	2.00
15	hCD40 M1 (H76R)	3h-37-2	2.17×10^5	5.62×10^{-4}	2.58
	hCD40 M2 (W109L)	3h-37-2			>1000
	hCD40 M3 (W109R)	3h-37-2			X
	hCD40 M4 (W109L, L121P)	3h-37-2			X
	hCD40-M5 (H76R, W109L, L121P)	3h-37-2			X
20	wt-cCD40	3h-37-2			X
	wt-hCD40	3h-37-11	2.91×10^5	5.60×10^{-4}	1.92
	wt-hCD40 (repetición)	3h-37-11	2.81×10^5	6.40×10^{-4}	2.28
	hCD40 M1 (H76R)	3h-37-11	3.00×10^5	7.17×10^{-4}	2.39

5	hCD40 M2 (W109L)	3h-37-11			>1000
	hCD40 M3 (W109R)	3h-37-11			X
	hCD40 M4 (W109L, L121P)	3h-37-11			X
	hCD40-M5 (H76R, W109L, L121P)	3h-37-11			X
	wt-cCD40	3h-37-11			X
10	wt-hCD40	3h-38-2	1.20×10^5	6.08×10^{-4}	5.07
	wt-hCD40 (repetición)	3h-38-2	1.42×10^5	1.14×10^{-3}	8.04
	hCD40 M1 (H76R)	3h-38-2	1.40×10^5	1.00×10^{-3}	7.15
	hCD40 M2 (W109L)	3h-38-2			X
	hCD40 M3 (W109R)	3h-38-2			X
15	hCD40 M4 (W109L, L121P)	3h-38-2			X
	hCD40-M5 (H76R, W109L, L121P)	3h-38-2			X
	wt-cCD40	3h-38-2			X
	wt-hCD40	3h-38-211	1.11×10^5	3.62×10^{-4}	3.26
	wt-hCD40 (repetición)	3h-38-211	1.20×10^5	7.28×10^{-4}	6.08
20	hCD40 M1 (H76R)	3h-38-211	1.28×10^5	5.10×10^{-4}	3.98
	hCD40 M2 (W109L)	3h-38-211			>1000
	hCD40 M3 (W109R)	3h-38-211			X
	hCD40 M4 (W109L, L121P)	3h-38-211			X
	hCD40-M5 (H76R, W109L, L121P)	3h-38-211			X

5	wt-cCD40	3h-38-211			X
	wt-hCD40	3h-38-215	1.37×10^5	2.88×10^{-4}	2.10
	wt-hCD40 (repetición)	3h-38-215	1.36×10^5	8.20×10^{-4}	6.02
	hCD40 M1 (H76R)	3h-38-215	1.75×10^5	5.30×10^{-4}	3.03
	hCD40 M2 (W109L)	3h-38-215			>1000
10	hCD40 M3 (W109R)	3h-38-215			X
	hCD40 M4 (W109L, L121P)	3h-38-215			X
	hCD40-M5 (H76R, W109L, L121P)	3h-38-215			X
	wt-cCD40	3h-38-215			X
	wt-hCD40	3h-38-217	1.27×10^5	2.96×10^{-4}	2.34
15	wt-hCD40 (repetición)	3h-38-217	1.44×10^5	3.40×10^{-4}	2.37
	hCD40 M1 (H76R)	3h-38-217	1.41×10^5	4.81×10^{-4}	3.41
	hCD40 M2 (W109L)	3h-38-217			>1000
	hCD40 M3 (W109R)	3h-38-217			X
	hCD40 M4 (W109L, L121P)	3h-38-217			X
20	hCD40-M5 (H76R, W109L, L121P)	3h-38-217			X
	wt-cCD40	3h-38-217			X
	wt-hCD40	3h-56-1	2.52×10^5	7.50×10^{-4}	2.97
	wt-hCD40 (repetición)	3h-56-1	1.93×10^5	1.03×10^{-3}	5.35
	hCD40 M1 (H76R)	3h-56-1	2.31×10^5	9.67×10^{-4}	4.18
25	hCD40 M2 (W109L)	3h-56-1	1.92×10^5	5.57×10^{-3}	29.10

5	hCD40 M3 (W109R)	3h-56-1			>1000
	hCD40 M4 (W109L, L121P)	3h-56-1			X
	hCD40-M5 (H76R, W109L, L121P)	3h-56-1			X
	wt-cCD40	3h-56-1			X
	wt-hCD40	3h-56-2	2.46×10^5	9.27×10^{-4}	3.77
10	wt-hCD40 (repetición)	3h-56-2	1.97×10^5	6.24×10^{-4}	3.17
	hCD40 M1 (H76R)	3h-56-2	2.20×10^5	1.33×10^{-3}	6.05
	hCD40 M2 (W109L)	3h-56-2	1.89×10^5	8.30×10^{-3}	43.90
	hCD40 M3 (W109R)	3h-56-2			>1000
	hCD40 M4 (W109L, L121P)	3h-56-2			X
15	hCD40-M5 (H76R, W109L, L121P)	3h-56-2			X
	wt-cCD40	3h-56-2			X
	wt-hCD40	3h-56-5	1.78×10^5	9.38×10^{-4}	5.26
	wt-hCD40 (repetición)	3h-56-5	1.53×10^5	7.19×10^{-4}	4.69
	hCD40 M1 (H76R)	3h-56-5	1.69×10^5	1.21×10^{-3}	7.18
20	hCD40 M2 (W109L)	3h-56-5	1.38×10^5	8.89×10^{-3}	64.60
	hCD40 M3 (W109R)	3h-56-5			>1000
	hCD40 M4 (W109L, L121P)	3h-56-5			X
	hCD40-M5 (H76R, W109L, L121P)	3h-56-5			X
	wt-cCD40	3h-56-5			X

5	wt-hCD40	3h-56-202	1.82E+05	4.15×10^{-4}	2.27
	wt-hCD40 (repetición)	3h-56-202	1.77E+05	2.21×10^{-4}	1.25
	hCD40 M1 (H76R)	3h-56-202	1.76E+05	5.79×10^{-4}	3.29
	hCD40 M2 (W109L)	3h-56-202	1.35E+05	2.00×10^{-2}	155.00
	hCD40 M3 (W109R)	3h-56-202			X
10	hCD40 M4 (W109L, L121P)	3h-56-202			X
	hCD40-M5 (H76R, W109L, L121P)	3h-56-202			X
	wt-cCD40	3h-56-202			X
	wt-hCD40	3h-56-206	6.48E+05	3.89×10^{-4}	0.60
	wt-hCD40 (repetición)	3h-56-206	3.27E+05	4.72×10^{-4}	1.44
15	hCD40 M1 (H76R)	3h-56-206	5.65E+05	5.45×10^{-4}	0.96
	hCD40 M2 (W109L)	3h-56-206	3.38E+05	2.00×10^{-2}	54.70
	hCD40 M3 (W109R)	3h-56-206			X
	hCD40 M4 (W109L, L121P)	3h-56-206			X
	hCD40-M5 (H76R, W109L, L121P)	3h-56-206			X
20	wt-cCD40	3h-56-206			X
	wt-hCD40	3h-56-217	4.71E+05	4.70×10^{-4}	1.00
	wt-hCD40 (repetición)	3h-56-217	2.91E+05	5.46×10^{-4}	1.87
	hCD40 M1 (H76R)	3h-56-217	4.45E+05	6.35×10^{-4}	1.43
	hCD40 M2 (W109L)	3h-56-217	4.25E+05	1.05×10^{-3}	2.48
25	hCD40 M3 (W109R)	3h-56-217	2.91E+05	6.70×10^{-3}	23.00

hCD40 M4 (W109L, L121P)	3h-56-217			X
hCD40-M5 (H76R, W109L, L121P)	3h-56-217			X
wt-cCD40	3h-56-217			X

5

Ejemplo 12

Construcción de Polipéptidos de Fusión de Fc

Los polipéptidos anticuerpos que comprenden los dAbs pueden ser contruidos en diversas configuraciones, como se describe en la presente. En este ejemplo, diversos dAbs fueron fusionados con un dominio de Fc para generar los polipéptidos de fusión de Fc de las construcciones del dominio variable anti-CD40 humano tales como 3h37-202, 3h37-235, 3h37-258, y 3h37-202.

En un ejemplo representativo, el dAb BMS3h-56-269 (SEQ ID No.: 417) fue fusionado con un dominio Fc de IgG1 modificada (IgG1*) (SEQ ID No.: 1284). En el polipéptido de fusión del dominio Fc dAb-IgG1*, el extremo C del dAb BMS3h-56-269 fue fusionado a un tripéptido ligador que tiene la secuencia Ala-Ser-Thr, que a su vez fue fusionado con el dominio Fc de IgG1* (SEQ ID No.: 1284). El dominio Fc de IgG1* contenía la modificación C5S, con referencia a la numeración de las posiciones de la SEQ ID No.: 1284. C5 del dominio Fc de IgG1 normalmente forma un enlace disulfuro con

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un residuo Cys en la cadena ligera de una molécula de IgG. El dominio Fc de IgG1* también contenía las mutaciones C11S y C14S para eliminar los enlaces disulfuro intercatenarios en la región de bisagra de IgG1. Finalmente, el dominio Fc de
 5 IgG1* contenía una mutación P23S para disminuir la función efectora del dominio Fc. El polipéptido de fusión dAb-IgG1* Fc tiene la siguiente secuencia, donde el ligador Ala-Ser-Thr está en letras negritas y las modificaciones al dominio de Fc están en letras cursivas:

```

10 1   EVQLLESGGG LVQPGGSLRL SCAASGFTFR DYEMWWVRQA PGKGLERVSA
    51  INPQGTRTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLP
    101 FRFSDRGQGT LVTVSSASTE PKSSDKTHTS PPSPAPPELLG GSSVFLFPPK
    151 PKDTLMISRT PEVTCVVVDV SHEDPEVKFN WYVDGVEVHN AKTKPREEQY
    201 NSTYRVVSVL TVLHQDWLNG KEYKCKVSNK ALPAPIEKTI SKAKGQPREP
15 251 QVYTLPPSRD ELTKNQVSLT CLVKGFYPSD IAVEWESNGQ PENNYKTPP
    301 VLDSDGSFFL YSKLTVDKSR WQQGNVFSCS VMHEALHNHY TQKSLSLSPG
    351 K   (SEQ ID No.: 1286)
  
```

El polipéptido de fusión dAb-IgG1* Fc descrito en la SEQ ID No.: 1286 es un monómero que tiene un peso
 20 molecular calculado de 39,127 Da. Éste puede formar un dímero que tiene un peso molecular calculado de 78,254 Da.

El dAb BMS3h-56-269 (SEQ ID No.: 417) alternativamente fue fusionado con un dominio Fc de la IgG₄ humana (SEQ ID No.: 1285). El extremo C del dAb BMS3h-56-269
 25 fue nuevamente fusionado al ligador Ala-Ser-Thr, el cual fue

fusionado con el dominio Fc de la IgG₄ (SEQ ID No.: 1285). El dominio Fc de IgG₄ contenía la modificación S10P, con referencia a la numeración de las posiciones en la SEQ ID No.: 1285. El polipéptido de fusión BMS3h-56-269-IgG₄ Fc
 5 tiene la siguiente secuencia donde el ligador Ala-Ser-Thr está en letras negritas y la modificación S10P está en letras cursivas:

```

1   EVQLLESGGG LVQPGGSLRL SCAASGFTFR DYEMWWVRQA PGKGLERVSA
51  INPQGTRTYY ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCAKLP
10 101 FRFSDRGQGT LVTVSSASTE SKYGPPCPPC PAPEFLGGPS VFLFPPKPKD
151 TLMISRTPEV TCVVVDVSQE DPEVQFNWYV DGVEVHNAKT KPREEQFNST
201 YRVVSVLTVL HQDWLNGKEY KCKVSNKGLP SSIEKTISKA KGQPREPQVY
251 TLPPSQEEMT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTTPVLD
301 SDGSFFLYSR LTVDKSRWQE GNVFSCSVMH EALHNHYTQK SLSLSLGK
15 SEQ ID No.: 1287)

```

El polipéptido de fusión BMS3h-56-269-IgG₄ Fc descrito en la SEQ ID No.: 1287 es un monómero que tiene un peso molecular calculado de 38,867 Da. Éste puede formar un dímero que tiene un peso molecular calculado de
 20 77,734 Da.

Las secuencias de BMS3h-56-269 (SEQ ID No.: 417), el polipéptido de fusión BMS3h-56-269-IgG1* Fc (SEQ ID No.: 1286), y el polipéptido de fusión BMS3h-56-269-IgG₄ Fc (SEQ ID No.: 1287) están alineados en seguida, donde el inicio del
 25 dominio Fc está marcado por una flecha:

BMS3h56-269 (SEQ ID NO:417) (1)
 EVQLLES GGG L V Q P G G S L R L S C A A S G F T F R D Y E M W W V R Q A P G K G L E R V S A
 BMS3h56-269-CTL2 (SEQ ID NO:1286) (1)
 EVQLLES GGG L V Q P G G S L R L S C A A S G F T F R D Y E M W W V R Q A P G K G L E R V S A
 BMS3h56-269-Ig4 (SEQ ID NO:1287) (1)
 EVQLLES GGG L V Q P G G S L R L S C A A S G F T F R D Y E M W W V R Q A P G K G L E R V S A

5 BMS3h56-269 (SEQ ID NO:417) (34)
 INPQ G T R T Y Y A D S V K G R F T I S R D N S K N T L Y L Q M N S L R A E D T A V Y Y C A K L P
 BMS3h56-269-CTL2 (SEQ ID NO:1286) (51)
 INPQ G T R T Y Y A D S V K G R F T I S R D N S K N T L Y L Q M N S L R A E D T A V Y Y C A K L P
 BMS3h56-269-Ig4 (SEQ ID NO:1287) (51)
 INPQ G T R T Y Y A D S V K G R F T I S R D N S K N T L Y L Q M N S L R A E D T A V Y Y C A K L P

10 BMS3h56-269 (SEQ ID NO:417) (84)
 F R F S D R G Q G T L V T V S S -----
 BMS3h56-269-CTL2 (SEQ ID NO:1286) (101)
 F R F S D R G Q G T L V T V S S **A S T E** P K S S D K T H T S P P S P A P E L L G G S S V F L F P P K
 BMS3h56-269-Ig4 (SEQ ID NO:1287) (101)
 F R F S D R G Q G T L V T V S S **A S T E** S K Y G --- P P C P P C P A P E F L G G P S V F L F P P K

↑
 Inicio de Fc

15 BMS3h56-269 (SEQ ID NO:417) (117)

 BMS3h56-269-CTL2 (SEQ ID NO:1286) (151)
 P K D T L M I S R T P E V T C V V V D V S H E D P E V K F N W Y V D G V E V H N A K T K P R E E Q Y
 BMS3h56-269-Ig4 (SEQ ID NO:1287) (148)
 P K D T L M I S R T P E V T C V V V D V S Q E D P E V Q F N W Y V D G V E V H N A K T K P R E E Q F

20 BMS3h56-269 (SEQ ID NO:417) (117)

 BMS3h56-269-CTL2 (SEQ ID NO:1286) (201)
 N S T Y R V V S V L T V L H Q D W L N G K E Y K C K V S N K A L P A P I E K T I S K A K G Q P R E P
 BMS3h56-269-Ig4 (SEQ ID NO:1287) (198)
 N S T Y R V V S V L T V L H Q D W L N G K E Y K C K V S N K G L P S S I E K T I S K A K G Q P R E P

BMS3h56-269 (SEQ ID NO:417) (117) -----

 BMS3h56-269-CTL2 (SEQ ID NO:1286) (251)
 Q V Y T L P P S R D E L T K N Q V S L T C L V K G F Y P S D I A V E W E S N G Q P E N N Y K T T P P
 BMS3h56-269-Ig4 (SEQ ID NO:1287) (248)
 Q V Y T L P P S Q E E M T K N Q V S L T C L V K G F Y P S D I A V E W E S N G Q P E N N Y K T T P P

BMS3h56-269 (SEQ ID NO:417) (117)

 BMS3h56-269-CTL2 (SEQ ID NO:1286) (301)
 VLDS DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
 BMS3h56-269-Ig4 (SEQ ID NO:1287) (298)
 VLDS DGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLG

5 BMS3h56-269 (SEQ ID NO:417) (117) -
 BMS3h56-269-CTL2 (SEQ ID NO:1286) (351) K
 BMS3h56-269-Ig4 (SEQ ID NO:1287) (348) K

Los polipéptidos de fusión Fc fueron expresados utilizando los métodos de cultivo de células descritos en el Ejemplo 11. La columna fue
 10 lavada con PBS (fosfato de sodio 20 mM, NaCl 0.15 M, pH 7.2) y luego eluida utilizando acetato de sodio 80 mM, pH 3, en un 1/5 del volumen de Tris-HCl 1 M, pH 8. El eluido fue corrido sobre una columna Superdex-200 en PBS.

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Ejemplo 13

Ensayos de Actividad del Polipéptido de Fusión Fc de CD40

Los polipéptidos de fusión de Fc anti-CD40 humano fueron evaluados funcionalmente para su
 20 habilidad de antagonizar las actividades de CD40. Las actividades de CD40 probadas fueron la proliferación de células B y la producción de citocina por activación promovida por hCD40L de las células dendríticas derivadas de monocitos humanos

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primarios (DCs). La proliferación de células B y la producción de citocina fueron medidas utilizando los ensayos descritos en el Ejemplo 6. A no ser que se indique de otro modo, todos los ensayos fueron
5 realizados en el medio RPMI suplementado con 10% de suero fetal de ternera (FCS). Los polipéptidos de fusión del dominio de dAb-Fc mostraron inhibición potente (por ejemplo, antagonismo) de la activación dependiente de CD40. No existieron propiedades
10 agonistas percibidas entre ninguno de los polipéptidos de fusión del dominio de dAb-Fc específico de CD40 humano. Los resultados utilizando los diversos ensayos se muestran en la TABLA 29. 3h56-269-IgG4 fue evaluado para su enlace a CD40
15 humano inmovilizado, utilizando los ensayos descritos en el Ejemplo 11. Para 3h56-269-IgG4, el valor de Kd influenciado por la avidéz aparente, para el enlace a CD40 humano inmovilizado, es medido a 30 pM a 25°C y 40 pM a 37°C.

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TABLA 29

5	dAb-Fc	EC50 (nM) de la Proliferación de Células B Humanas, Promovida por hZCD40L	EC50 (nM) de la Proliferación de Células B Humanas, Promovida por la CHO-hCD40L	EC50 (nM) de Células T-B	EC50 (nM) de TNF de la Activación de DC Promovida por CHO-hCD40L	EC50 (nM) de IL-6 de la Activación de DC Promovida por CHO-hCD40L	EC50 (nM) de IL-12 de la Activación de DC Promovida por CHO-hCD40L
10	3h37-202-IgG4	0.16 ± 0.08	5.0, 3.0	5.0, 6.0			0.53 ± 0.1
	3h37-202-IgG1*	0.27, 0.22	3.0, 7.0				0.74 ± 0.2
15							
	3h38-235-IgG4	0.20, 0.15	6.0, 10.0	16.7 ± 5.7			0.67 ± 0.3
20	3h38-235-IgG1*	0.25 ± 0.1	4.0 ± 1.0				0.88 ± 0.3
25	3h56-258-IgG4	0.16 ± 0.05	1.0 ± 0.8	2.4 ± 0.99	0.22 ± 0.08	0.11 ± 0.05	0.3 ± 0.2

5	3h56- 258- IgG1*	0.063 ± 0.03	0.6 ± 0.4	2.0 ± 0.63			0.31 ± 0.1
	3h56- 269- IgG4	0.028 ± 0.01	0.27 ± 0.08	0.52 ± 0.07	0.16 ± 0.03	0.09 ± 0.02	0.092 ± 0.03
10	3h56- 269- IgG1*	0.025 ± 0.01	0.25 ± 0.04	0.53 ± 0.1	0.27 ± 0.06	0.15 ± 0.05	0.14 ± 0.06

Aunque las modalidades actuales han sido descritas con detalle con referencia a los ejemplos anteriores, se debe entender que pueden ser realizadas diversas modificaciones sin apartarse del espíritu de estas modalidades, y podría ser fácilmente conocido para la persona experta en la técnica.

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REIVINDICACIONES

1. Un polipéptido anticuerpo, caracterizado porque comprende un primer dominio variable, en donde el polipéptido anticuerpo se enlaza específicamente a un epítopo de CD40 humano, en donde el polipéptido anticuerpo compite con el enlace del anticuerpo de dominio (dAb) BMS3h-56-269 (SEQ ID NO: 417) a CD40, en donde CD40 comprende la secuencia de aminoácidos de la SEQ ID NO: 1, y en donde el epítopo comprende al menos un residuo de aminoácido de CD40 seleccionado del grupo que consiste de Trp109, Leu121, His122, Ser124, Ser156, Ala157, Phe158, Glu159, y His162.

2. El polipéptido anticuerpo de conformidad con la reivindicación 1, caracterizado porque el primer dominio variable comprende la secuencia de aminoácidos de uno de los polipéptidos anticuerpos seleccionados del grupo de líneas que consiste de BMS3h-37, BMS3h-38, BMS3h-56, and BMS3h-198, y en donde el primer dominio variable tiene una constante de enlace aparente de 1 pM a 100 nM.

3. El polipéptido anticuerpo de conformidad con cualquiera de las reivindicaciones 1-2, caracterizado porque el primer dominio variable comprende el aminoácido de uno de los polipéptidos anticuerpos seleccionados del grupo de líneas que consiste de BMS3h-37, BMS3h-38, y BMS3h-56, y en donde el primer dominio variable tiene una EC50 de proliferación de células B humanas, promovida por hIZCD40L,

de 0.01nM a 100.0 nM.

4. El polipéptido anticuerpo de conformidad con la reivindicación 1, caracterizado porque la secuencia de aminoácidos del primer dominio variable comprende:

- 5 (a) una región CDR1 que difiere de la región CDR1 de BMS3h-56-269 (SEQ ID NO: 417) por hasta dos aminoácidos,
- (b) una región CDR2 que difiere de la región CDR2 de BMS3h-56-269 (SEQ ID NO: 417) por hasta dos aminoácidos,
- (c) una región CDR3 que difiere de la región CDR3
10 de BMS3h-56-269 (SEQ ID NO: 417) por hasta dos aminoácidos,
- (d) una región FR1 que difiere de la región FR1 de BMS3h-56-269 (SEQ ID NO: 417) por hasta dos aminoácidos,
- (e) una región FR2 que difiere de la región FR2 de BMS3h-56-269 (SEQ ID NO: 417) por hasta dos aminoácidos,
- 15 (f) Una región FR3 que difiere de la región FR3 de BMS3h-56-269 (SEQ ID NO: 417) por hasta dos aminoácidos, y
- (g) una región FR4 que difiere de la región FR4 de BMS3h-56-269 (SEQ ID NO: 417) por hasta dos aminoácidos.

5. El polipéptido anticuerpo de conformidad con
20 la reivindicación 1, caracterizado porque los aminoácidos del primer dominio variable comprenden:

- (a) una región CDR1 que difiere de la región CDR1 de BMS3h-56-269 (SEQ ID NO: 417) por hasta dos aminoácidos,
- (b) una región CDR2 que difiere de la región CDR2
25 de BMS3h-56-269 (SEQ ID NO: 417) por hasta dos aminoácidos,

(c) una región CDR3 que difiere de la región CDR3 de BMS3h-56-269 (SEQ ID NO: 417) por hasta dos aminoácidos.

6. El polipéptido anticuerpo de conformidad con la reivindicación 1, caracterizado porque la secuencia de aminoácidos del primer dominio variable difiere de la secuencia de aminoácidos de BMS3h-56-258 (SEQ ID NO: 10) o BMS3h-56-269 (SEQ ID NO: 417) por hasta 10 aminoácidos.

7. El polipéptido anticuerpo de conformidad con la reivindicación 6, caracterizado porque la secuencia de aminoácidos del primer dominio variable difiere de la secuencia de aminoácidos de BMS3h-56-258 (SEQ ID NO: 10) o BMS3h-56-269 (SEQ ID NO: 417) por hasta 5 aminoácidos.

8. El polipéptido anticuerpo de conformidad con la reivindicación 7, caracterizado porque la secuencia de aminoácidos del primer dominio variable difiere de la secuencia de aminoácidos de BMS3h-56-258 (SEQ ID NO: 10) o BMS3h-56-269 (SEQ ID NO: 417) por hasta dos aminoácidos.

9. El polipéptido anticuerpo de conformidad con la reivindicación 8, caracterizado porque la secuencia de aminoácidos del primer dominio variable difiere de la secuencia de aminoácidos de BMS3h-56-258 (SEQ ID NO: 10) o BMS3h-56-269 (SEQ ID NO: 417) por un aminoácido.

10. El polipéptido anticuerpo de conformidad con cualquiera de las reivindicaciones 2-3, caracterizado porque el polipéptido anticuerpo se selecciona del grupo de líneas

de BMS3h-56, y en donde la secuencia de aminoácidos del primer dominio variable comprende:

(a) una región CDR1 que tiene una secuencia X_1 -Tyr-Glu- Y_1 -Trp (SEQ ID NO: 1274), en donde X_1 es Asp o Gly, e Y_1 es Met o Leu;

(b) una región CDR2 que tiene una secuencia Ala-Ile-Asn-Pro- X_2 -Gly- Y_2 - Z_2 -Thr-Tyr-Tyr-Ala-Asp-Ser-Val- A_2 -Gly (SEQ ID NO: 1275), en donde X_2 es Gln, Tyr, Pro, Trp, o Ala, Y_2 es Thr, Ser, Asn, Gly, Met, o Gln, Z_2 es Arg, Leu, Tyr, His, o Phe, y A_2 es Lys o Met; y

(c) una región CDR3 que tiene una secuencia X_3 -Pro- Y_3 - Z_3 -Phe- A_3 - B_3 (SEQ ID NO: 1276), en donde X_3 es Leu o Pro, Y_3 es Phe, Gln, Thr, o Met, Z_3 es Tyr, Pro, Leu, Thr, Ile, Phe, o Met, A_3 es Gln, His, Asp, Ser, Lys, Glu, o Gly, y B_3 es Glu, Asp, o Tyr.

11. El polipéptido anticuerpo de conformidad con la reivindicación 10, caracterizado porque la secuencia de aminoácidos del primer dominio variable comprende:

(a) una región FR1 que tiene una secuencia Glu-Val-Gln-Leu-Leu-Glu-Ser-Gly-Gly-Gly--Leu-Val-Gln-Pro-Gly-Gly-Ser- X_1 -Arg-Leu-Ser-Cys-Ala-Ala-Ser-Gly-Phe-Thr-Phe- Y_1 (SEQ ID NO: 1277), en donde X_1 es Leu o Arg, e Y_1 es Arg o Ala;

(b) una región FR2 que tiene una secuencia Trp-Val-Arg- X_2 -Ala-Pro-Gly- Y_2 - Z_2 -Leu-Glu-Arg-Val-Ser (SEQ ID NO: 1278), en donde X_2 es Gln o Arg, Y_2 es Lys o Arg, y Z_2 es Gly

o Val;

(c) una región FR3 que tiene una secuencia Arg-Phe-Thr-Ile-Ser-Arg-Asp-Asn-Ser-Lys-Asn-X₃-Lys-Tyr-Leu-Gln-Met-Asn-Ser-Leu-Arg-Ala-Y₃-Asp-Thr-Z₃-Val-Tyr-A₃-Cys-B₃-Lys (SEQ ID NO: 1279), en donde X₃ es Thr o Met, Y₃ es Glu o Asp, Z₃ es Ala o Ser, A₃ es Tyr o His, y B₃ es Ala o Thr; y

(d) una región FR4 que tiene una secuencia X₄-Gly-Y₄-Gly-Thr-Leu-Val-Thr-Val-Ser-Z₄ (SEQ ID NO: 1280), en donde X₄ es Trp o Arg, Y₄ es Gln o Pro, y Z₄ es Ser o Asn.

10 12. El polipéptido anticuerpo de conformidad con cualquiera de las reivindicaciones 2-3, caracterizado porque el primer dominio variable comprende la secuencia de aminoácidos de BMS3h-56-258 (SEQ ID NO: 10) o BMS3h-56-269 (SEQ ID NO:417).

15 13. El polipéptido anticuerpo de conformidad con cualquiera de las reivindicaciones 2-3, caracterizado porque el polipéptido anticuerpo se selecciona del grupo de líneas de BMS3h-37, en donde el primer dominio variable comprende la secuencia Glu-Val-Gln-Leu-Leu-Glu-Ser-Gly-Gly-Gly-Leu-Val-X₁-
20 Pro-Gly-Gly-Ser-Leu-Arg-Leu-Ser-Cys-Ala-Ala-Ser-Gly-Phe-Thr-Phe-Glu-Trp-Tyr-Glu-Met-Gln-Trp-Val-Arg-Arg-Ala-Pro-Gly-Lys-Gly-Leu-Glu-Trp-Val-Ser-Ala-Ile-Ser-Gly-Asp-Gly-Tyr-Arg-Thr-Tyr-Tyr-Ala-Asp-Ser-Val-Lys-Gly-Arg-Phe-Thr-Ile-Ser-Arg-Asp-Asn-Ser-Lys-Asn-Thr-Leu-Tyr-Leu-Gln-Met-Asn-Ser-Leu-Arg-Ala-
25 Glu-Asp-Thr-Ala-Val-Tyr-Tyr-Cys-Ala-Lys-Y₁-Leu-Z₁-A₁-Phe-Asp-

Tyr-B₁-Gly-Arg-Gly-Thr-Leu-Val-Thr-Val-Ser-Ser (SEQ ID NO: 1281); y

en donde X₁ es Gln o Arg; Y₁ es Glu o Gly; Z₁ es Ala, Leu, o Glu; A₁ es Phe o Tyr; y B₁ es Trp o Arg.

5 14. El polipéptido anticuerpo de conformidad con cualquiera de las reivindicaciones 2-3, caracterizado porque el polipéptido anticuerpo se selecciona del grupo de líneas de BMS3h-38, en donde el primer dominio variable comprende la secuencia Glu-Val-Gln-Leu-Leu-Ala-Ser-Gly-Gly-Gly-Leu-Val-Gln-
10 Pro-Gly-Gly-Ser-Leu-Arg-Leu-Ser-Cys-Ala-Ala-Ser-Gly-Phe-X₁-Phe-Glu-Glu-Glu-Glu-Met-Ile-Trp-Val-Arg-Gln-Ala-Pro-Gly-Lys-Gly-Leu-Glu-Trp-Val-Ser-Y₁-Ile-Ser-Z₁-A₁-Gly-B₁-C₁-Thr-Tyr-Tyr-Ala-Asp-Ser-Val-Lys-Gly-Arg-Phe-Thr-Ile-Ser-Arg-Asp-Asn-Ser-Lys-Asn-Thr-Leu-Tyr-Leu-Gln-Met-Asn-Ser-Leu-Arg-Ala-Glu-Asp-Thr-
15 Ala-Val-Tyr-Tyr-Cys-Gly-Lys-Glu-Pro-Phe-D₁-Tyr-Asp-Tyr-Trp-Gly-Gln-Gly-Thr-Leu-Val-Thr-Val-Ser-Ser (SEQ ID NO: 1282); y

en donde X₁ es Thr o Pro; Y₁ es Ala o Ser; Z₁ es Arg o Gly; A₁ es Arg, Ser, Asn, Gln, Gly, His, o Leu; B₁ es Tyr, Phe, Trp, o Gly; C₁ es Ser o Gly; y D₁ es Arg, Met, o Pro.

20 15. El polipéptido anticuerpo de conformidad con cualquiera de las reivindicaciones 2-3, caracterizado porque el polipéptido anticuerpo se selecciona del grupo de líneas de BMS3h-198, en donde el primer dominio variable comprende la secuencia Glu-Val-Gln-Leu-Leu-Glu-Ser-Gly-Gly-Gly-Leu-Val-
25 Gln-Pro-Gly-Gly-Ser-Leu-Arg-Leu-Ser-Cys-Ala-Ala-Ser-Gly-Phe-

Thr-Phe-Ala-Gly-Trp-Glu-X₁-Trp-Trp-Y₁-Arg-Gln-Ala-Pro-Gly-Lys-
 Gly-Leu-Glu-Arg-Val-Ser-Ala-Ile-Ser-Gly-Ser-Gly-Gly-Ser-Thr-
 Tyr-Tyr-Ala-Asp-Ser-Val-Lys-Gly-Arg-Phe-Thr-Ile-Ser-Arg-Asp-
 Z₁-A₁-Lys-Asn-Thr-Leu-Tyr-Leu-Gln-Met-Asn-Ser-Leu-Arg-Ala-Glu-
 5 Asp-Thr-Ala-Val-Tyr-B₁-Cys-Ala-C₁-D₁-Pro-Tyr-Ser-E₁-Asp-Tyr-F₁-
 G₁-H₁-Gly-Thr-Leu-Val-Thr-Val-Ser-Ser (SEQ ID NO: 1283); y

en donde X₁ es Met o Leu; Y₁ es Val o Phe; Z₁ es Asp
 o Asn; A₁ es Ser o Thr; B₁ es Tyr o His; C₁ es Lys o Arg; D₁
 es Asp o Glu; E₁ es Tyr o Phe; F₁ es Trp o Arg; G₁ es Gly o
 10 Arg; y H₁ es Gln o His.

16. El polipéptido de conformidad con cualquiera
 de las reivindicaciones 1-15, caracterizado porque el
 polipéptido anticuerpo es un anticuerpo de dominio (dAb).

17. El polipéptido de conformidad con cualquiera
 15 de las reivindicaciones 1-16, caracterizado porque el
 polipéptido anticuerpo es un polipéptido de fusión que
 comprende el primer dominio variable y un dominio de Fc.

18. El polipéptido de fusión de conformidad de
 reivindicación 17, caracterizado porque el polipéptido de
 20 fusión comprende un dominio Fc de IgG4.

19. El polipéptido de fusión de conformidad de
 reivindicación 18, caracterizado porque el polipéptido de
 fusión comprende un dominio Fc de IgG1.

20. El polipéptido de fusión de conformidad con
 25 cualquiera de las reivindicaciones 17-19, caracterizado

porque el polipéptido de fusión comprende la secuencia de aminoácidos de uno de los polipéptidos anticuerpos seleccionados del grupo de líneas que consisten de BMS3h-37, BMS3h-38, y BMS3h-56, y en donde el polipéptido de fusión
5 tiene una EC50 de proliferación de células B humanas promovida por hIZCD40L, de 0.001nM a 100.0 nM.

21. El polipéptido de fusión de conformidad con cualquiera de las reivindicación 1-20, caracterizado porque el polipéptido anticuerpo comprende además un segundo dominio
10 variable que se enlaza específicamente a un segundo antígeno, en donde el segundo antígeno es un antígeno diferente del CD40 humano.

22. El polipéptido anticuerpo de conformidad con la reivindicación 21, caracterizado porque el segundo
15 antígeno es un grupo de moléculas de diferenciación (CD) o una molécula de la clase II del complejo mayor de histocompatibilidad (MHC).

23. El polipéptido anticuerpo de conformidad con la reivindicación 21, caracterizado porque el segundo
20 antígeno es albúmina sérica (SA).

24. Un ácido nucleico, caracterizado porque codifica para el polipéptido anticuerpo de conformidad con cualquiera de las reivindicaciones 1-23.

25. Un vector, caracterizado porque comprende el
25 ácido nucleico de conformidad con la reivindicación 24.

26. Una célula hospedera aislada, caracterizada porque comprende el vector de conformidad con la reivindicación 25.

27. Una composición farmacéutica, caracterizada
5 porque comprende una cantidad terapéuticamente efectiva del polipéptido anticuerpo de conformidad con la reivindicación 1 y un portador farmacéuticamente aceptable.

28. La composición farmacéutica de conformidad con la reivindicación 27, caracterizada porque comprende una
10 agente inmunosupresor/inmunomodulador y/o anti-inflamatorio.

29. Un método de tratamiento de un trastorno inmunitario en un paciente en necesidad de tal tratamiento, caracterizado porque comprende administrar al paciente una cantidad terapéuticamente efectiva de la composición
15 farmacéutica de conformidad con la reivindicación 27.

30. El método de conformidad con la reivindicación 29, caracterizado porque la composición farmacéutica es administrada en combinación con un agente inmunosupresor/inmunomodulador y/o anti-inflamatorio.

20 31. El método de conformidad con la reivindicación 29, caracterizado porque el trastorno inmunitario es un trastorno autoinmunitario o un trastorno relacionado a injertos.

32. El método de conformidad con la
25 reivindicación 29, caracterizado porque el trastorno

inmunitario se selecciona del grupo que consiste de enfermedad de Addison, alergias, espondilitis anquilosante, asma, aterosclerosis, trastornos autoinmunitarios del oído, trastornos autoinmunitarios del ojo, hepatitis autoinmunitaria, parotitis autoinmunitaria, colitis, trastorno cardíaco coronario, enfermedad de Crohn, diabetes, incluyendo diabetes Tipo 1 y/o Tipo 2, epididimitis, glomerulonefritis, enfermedad de Graves, síndrome de Guillain-Barre, enfermedad de Hashimoto, anemia hemolítica, púrpura trombocitopénica idiopática, enfermedad inflamatoria del intestino, respuesta inmunitaria a productos farmacéuticos recombinantes, lupus eritematoso sistémico, infertilidad masculina, esclerosis múltiple, miastenia gravis, pénfigo, psoriasis, fiebre reumática, artritis reumatoide, sarcoidosis, esclerodermia, síndrome de Sjogren, espondiloartropatías, tiroiditis, rechazo de trasplante, vasculitis, SIDA, alergia atópica, asma bronquial, eczema, lepra, esquizofrenia, depresión heredada, trasplantes de tejidos y órganos, síndrome de fatiga crónica, enfermedad de Alzheimer, enfermedad de Parkinson, infarto del miocardio, apoplejía, autismo, epilepsia, fenómeno de Arthus, anafilaxis, adicción al alcohol, y adicción a drogas.

RESUMEN DE LA INVENCION

Se proporcionan los polipéptidos anticuerpos que se enlazan específicamente a un nuevo epítipo de CD40 humano. Los polipéptidos anticuerpos no muestran actividad agonista de CD40. Los polipéptidos anticuerpos son útiles en el tratamiento de trastornos que involucran la activación de CD40, tales como los trastornos autoinmunitarios. Los polipéptidos anticuerpos pueden ser anticuerpos de dominio (dAbs) que comprenden un dominio simple de V_L o V_H . La vida media de los polipéptidos anticuerpos puede ser incrementada por modificación de los polipéptidos anticuerpos para ser reactivos específicos dobles que pueden también reticularse a la albúmina sérica humana (HSA).

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